



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 27, 2017 – 06:11 AM EDT

PDB ID : 1FO4  
Title : CRYSTAL STRUCTURE OF XANTHINE DEHYDROGENASE ISOLATED FROM BOVINE MILK  
Authors : Enroth, C.; Eger, B.T.; Okamoto, K.; Nishino, T.; Nishino, T.; Pai, E.F.  
Deposited on : unknown  
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

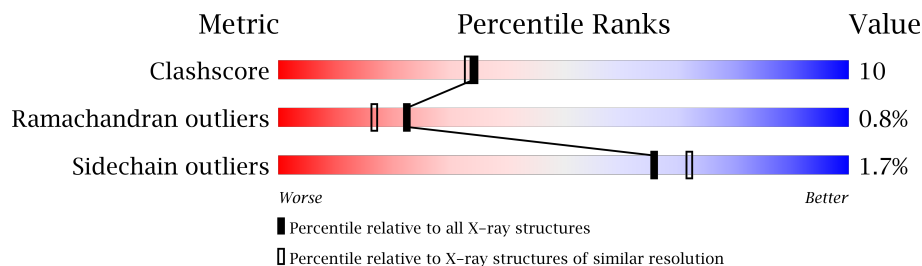
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain	
1	A	1332		78% 18% ..
1	B	1332		79% 17% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MOS	A	3004	-	-	X	-
5	MOS	B	4004	-	-	X	-
7	FAD	A	3006	X	-	-	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
7	FAD	B	4006	X	-	-	-
8	GOL	A	3007	-	X	X	-
8	GOL	A	3008	-	X	-	-
8	GOL	B	4007	-	X	X	-
8	GOL	B	4008	-	X	X	-

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 22402 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

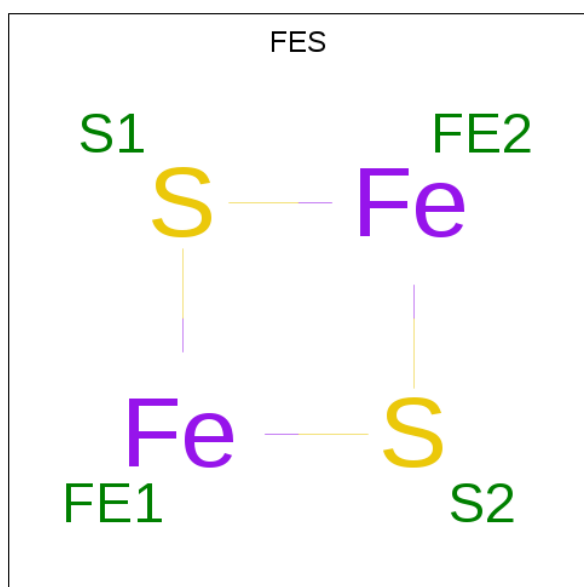
- Molecule 1 is a protein called XANTHINE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1299	10077	6404	1728	1884	61	0	0	0
1	B	1296	10054	6391	1724	1878	61	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

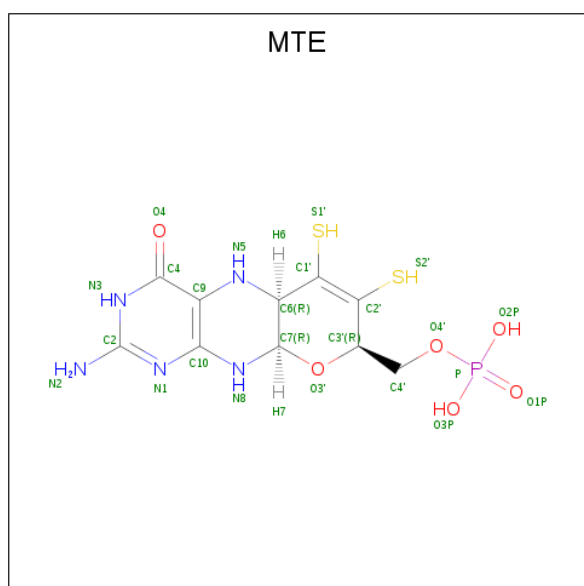
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>).



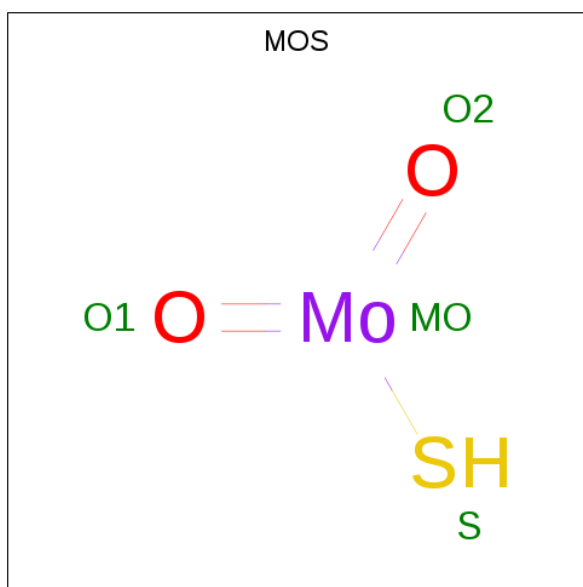
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A,9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: MTE) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>6</sub>P<sub>2</sub>S<sub>2</sub>).



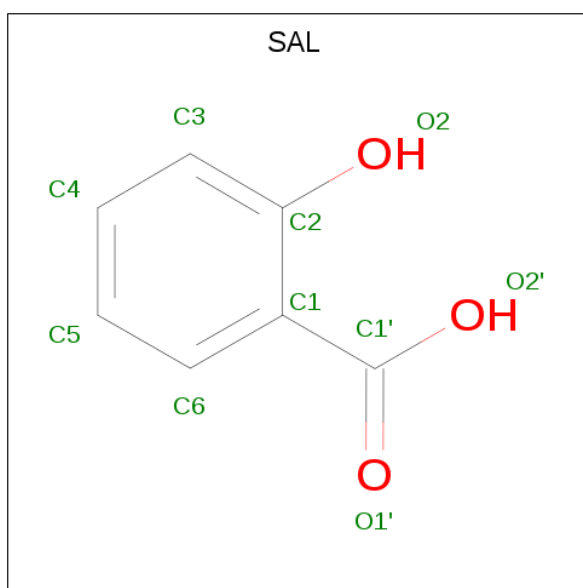
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
4	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 5 is DIOXOTHIO MOLYBDENUM(VI) ION (three-letter code: MOS) (formula: HMoO<sub>2</sub>S).



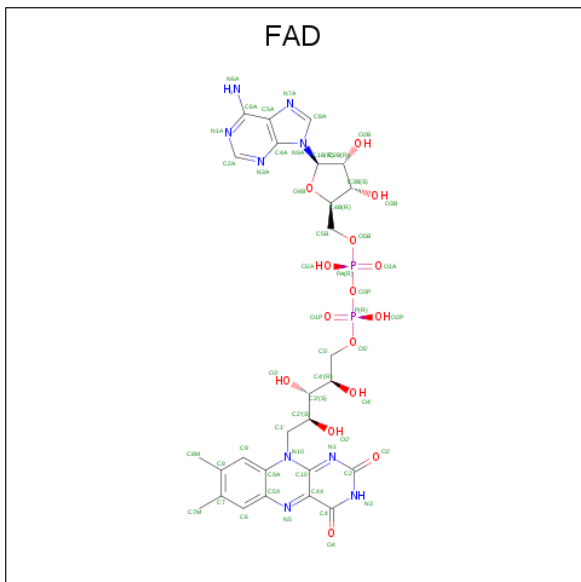
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	Mo	O	S		
5	A	1	4	1	2	1	0	0
5	B	1	4	1	2	1	0	0

- Molecule 6 is 2-HYDROXYBENZOIC ACID (three-letter code: SAL) (formula: C<sub>7</sub>H<sub>6</sub>O<sub>3</sub>).



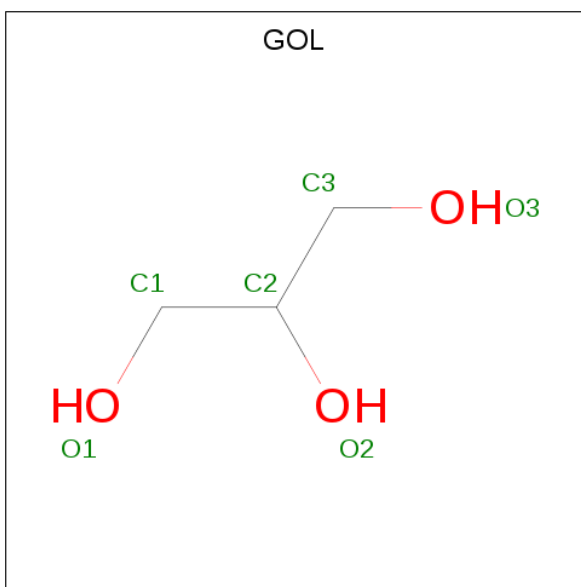
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	10	7	3	0	0
6	B	1	10	7	3	0	0

- Molecule 7 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
7	A	1	53	27	9	15	2	0	0
7	B	1	53	27	9	15	2	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1047	Total	O	0	0
			1047	1047		
9	B	1000	Total	O	0	0
			1000	1000		

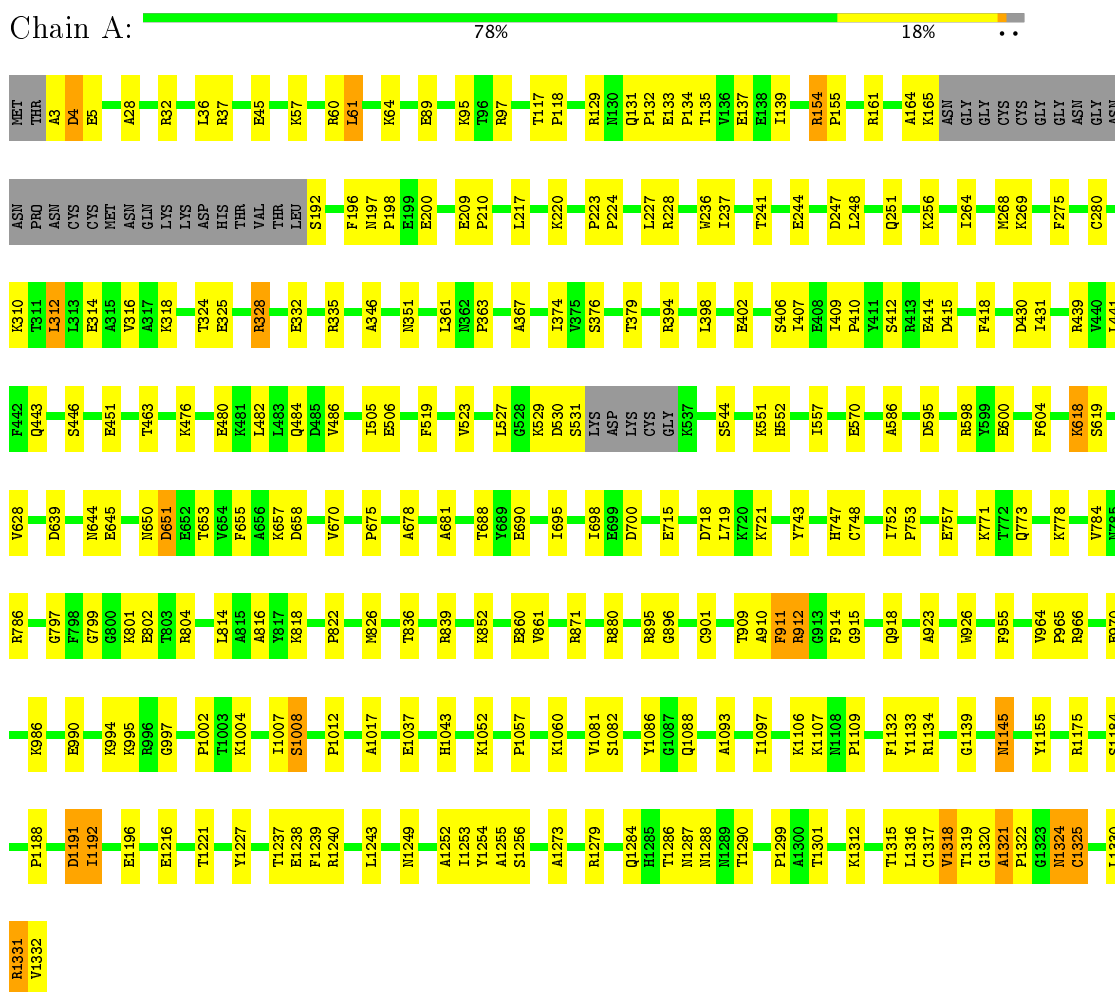


### 3 Residue-property plots

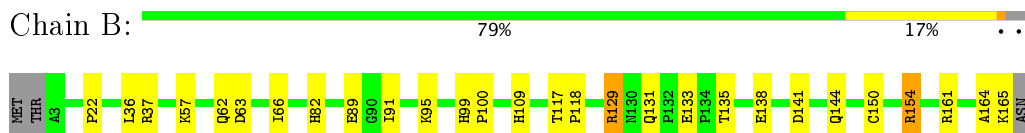
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: XANTHINE DEHYDROGENASE



- Molecule 1: XANTHINE DEHYDROGENASE



Gly	L313	R508	G837	L1054	F1239
ASN	E314	R509	G838	K1055	N1249
Gly	R328	T512	R839	P1072	A1252
ASN	L331	L527	R840	V1081	A1255
ASN	E332	G528	A844	S1082	S1256
CYS	R335	Lys	K847	I1085	E1261
CYS	R336	ASP	K852	Q1088	P1262
MET	F337	SER	E860	A1093	A1281
ASN	A338	LYS	E879	I1097	Q1284
GLN	G339	ASP	R880	N1106	H1285
LYS	K340	CYS	M885	P1109	T1286
LYS	A346	Gly	I894	M1287	M1288
ASP	A346	K537	R895	M1289	M1289
HIS	N851	L538	G896	T1290	K1291
THR	N851	L548	R899	S1126	E1292
VAL	L361	L548	I900	T1129	I1293
THR	L361	H552	C901	Y1133	F1294
LEU	I374	H552	T909	R1134	P1299
S192	S376	N565	A910	G1139	A1300
N197	R377	R569	F911	F1142	T1301
E200	G378	E600	R912	M1145	P1302
E209	T379	R606	F913	K1172	V1310
P210	R394	L607	G914	K1173	D1311
L217	L398	V608	F915	N1173	K1312
R218	E402	T609	I922	L1174	F1313
L219	I407	A615	R942	R1175	L1316
K220	R427	K616	F955	S1184	C1317
G231	E428	S1185	V964	L1186	V1318
T241	D429	K616	P965	N1187	A1321
L243	L441	S619	R980	P1188	P1322
E244	M451	V628	I787	A1189	G1323
K256	Q471	F634	K986	I1190	M1324
L257	K472	E645	F987	D1191	C1325
V258	Q473	E645	E990	I1192	K1326
I264	K476	M650	V1195	V1195	L1330
F275	E480	D651	E1196	E1196	R1331
I279	K481	V810	T1207	T1207	V1332
C280	L482	P822	L1208	L1208	
P281	L483	M633	T1221	T1221	
I284	Q484	I835	Y1227	Y1227	
L287	V486	T836	P1236	P1236	
K310					
T311					
L312					

## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.45Å 124.49Å 148.33Å 90.00° 90.94° 90.00°	Depositor
Resolution (Å)	25.00 – 2.10	Depositor
% Data completeness (in resolution range)	86.9 (25.00-2.10)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.198 , 0.238	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	22402	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SAL, MOS, CA, FES, FAD, MTE

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.37	0/10298	0.64	1/13939 (0.0%)
1	B	0.37	0/10275	0.64	1/13909 (0.0%)
All	All	0.37	0/20573	0.64	2/27848 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1191	ASP	N-CA-C	-5.23	96.89	111.00
1	B	243	LYS	N-CA-C	-5.00	97.49	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10077	0	10075	203	0
1	B	10054	0	10054	181	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	0	0	0
3	B	8	0	0	0	0
4	A	24	0	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	24	0	10	2	0
5	A	4	0	0	2	0
5	B	4	0	0	2	0
6	A	10	0	4	0	0
6	B	10	0	4	1	0
7	A	53	0	29	3	0
7	B	53	0	30	2	0
8	A	12	0	5	7	0
8	B	12	0	7	11	0
9	A	1047	0	0	21	0
9	B	1000	0	0	11	0
All	All	22402	0	20228	386	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (386) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:3008:GOL:C1	8:A:3008:GOL:O1	1.68	1.39
8:B:4008:GOL:C1	8:B:4008:GOL:O1	1.71	1.36
1:A:3:ALA:HB1	1:A:228:ARG:H	1.19	1.07
1:B:645:GLU:HG2	1:B:650:ASN:HD22	1.19	1.07
5:B:4004:MOS:MO	5:B:4004:MOS:S	1.66	1.06
1:B:243:LYS:O	1:B:244:GLU:HB2	1.62	0.99
1:B:1286:THR:HG22	1:B:1287:ASN:H	1.25	0.98
1:B:1321:ALA:HB1	1:B:1322:PRO:HD2	1.50	0.94
1:A:506:GLU:HG3	1:A:1319:THR:HB	1.47	0.93
5:A:3004:MOS:S	5:A:3004:MOS:MO	1.82	0.90
1:B:1312:LYS:O	1:B:1316:LEU:HD13	1.74	0.88
1:A:719:LEU:HD11	1:A:895:ARG:HB2	1.58	0.85
1:B:719:LEU:HD11	1:B:895:ARG:HB2	1.57	0.85
1:B:131:GLN:HE21	1:B:133:GLU:H	1.23	0.84
1:A:955:PHE:HA	1:A:1145:ASN:HD21	1.40	0.83
1:B:1088:GLN:HG2	1:B:1133:TYR:CD1	2.14	0.81
1:B:955:PHE:HA	1:B:1145:ASN:HD21	1.43	0.81
1:A:645:GLU:HG2	1:A:650:ASN:HD22	1.47	0.80
1:B:1191:ASP:O	1:B:1192:ILE:HB	1.78	0.80
1:B:719:LEU:HD11	1:B:895:ARG:CB	2.13	0.77
1:B:154:ARG:HD3	1:B:1196:GLU:OE2	1.85	0.77
1:B:839:ARG:HG3	8:B:4007:GOL:H11	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1191:ASP:O	1:A:1192:ILE:HB	1.85	0.75
1:A:131:GLN:HE21	1:A:133:GLU:H	1.34	0.75
1:A:154:ARG:HD3	1:A:1196:GLU:OE2	1.87	0.74
1:A:1331:ARG:O	1:A:1332:VAL:O	2.05	0.74
1:A:1088:GLN:HG2	1:A:1133:TYR:CD1	2.22	0.74
1:B:36:LEU:HD22	1:B:89:GLU:HG3	1.67	0.74
1:B:376:SER:HB3	1:B:379:THR:OG1	1.86	0.74
1:A:650:ASN:HD21	1:A:778:LYS:HE3	1.52	0.74
1:B:1207:THR:O	1:B:1208:LEU:HD12	1.89	0.72
1:B:552:HIS:CE1	1:B:1172:LYS:HZ3	2.07	0.72
1:B:164:ALA:O	1:B:165:LYS:HB2	1.89	0.71
1:B:328:ARG:HG2	1:B:328:ARG:HH11	1.53	0.71
1:A:506:GLU:CG	1:A:1319:THR:HB	2.20	0.71
1:A:1330:LEU:O	1:A:1331:ARG:HG2	1.89	0.71
1:A:3:ALA:HA	1:A:227:LEU:HD22	1.73	0.70
1:B:645:GLU:CG	1:B:650:ASN:HD22	2.01	0.70
1:B:1326:LYS:HD2	1:B:1326:LYS:N	2.06	0.70
1:B:264:ILE:HD11	7:B:4006:FAD:H3B	1.74	0.70
1:B:719:LEU:HD13	1:B:860:GLU:OE2	1.91	0.69
1:A:3:ALA:HB1	1:A:228:ARG:N	2.01	0.69
1:A:328:ARG:HH11	1:A:328:ARG:HG2	1.57	0.68
1:B:37:ARG:HD3	1:B:595:ASP:O	1.93	0.68
1:B:241:THR:OG1	1:B:243:LYS:O	2.12	0.67
1:B:918:GLN:HE22	8:B:4007:GOL:H12	1.60	0.66
1:A:719:LEU:HD11	1:A:895:ARG:CB	2.25	0.66
1:A:598:ARG:HG2	1:B:600:GLU:OE2	1.95	0.66
1:B:1191:ASP:O	1:B:1192:ILE:CB	2.44	0.65
1:B:761:GLU:HG3	1:B:788:LEU:HD23	1.78	0.65
1:B:1318:VAL:HG23	1:B:1321:ALA:HB2	1.78	0.65
1:B:721:LYS:O	1:B:725:GLU:HG3	1.96	0.65
1:A:619:SER:HB3	1:A:688:THR:OG1	1.96	0.65
1:B:1088:GLN:HG2	1:B:1133:TYR:CE1	2.31	0.65
1:A:753:PRO:HD3	1:A:816:ALA:HB1	1.78	0.65
1:A:264:ILE:HD11	7:A:3006:FAD:H3B	1.78	0.65
1:A:1324:ASN:HD22	1:A:1324:ASN:C	2.00	0.65
1:A:1332:VAL:OXT	1:A:1332:VAL:HG22	1.96	0.64
1:B:645:GLU:HG2	1:B:650:ASN:ND2	2.03	0.64
1:A:600:GLU:CD	1:B:598:ARG:HG2	2.17	0.64
1:A:752:ILE:CD1	1:A:822:PRO:HB3	2.28	0.63
1:B:1017:ALA:HB2	1:B:1085:ILE:HD12	1.81	0.62
1:B:880:ARG:HD2	1:B:914:PHE:HB3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:SER:HB3	1:A:379:THR:OG1	1.99	0.62
1:A:164:ALA:O	1:A:165:LYS:HB2	1.99	0.62
1:B:552:HIS:CE1	1:B:1172:LYS:NZ	2.68	0.61
1:B:131:GLN:HE21	1:B:133:GLU:N	1.96	0.61
1:A:880:ARG:HD2	1:A:914:PHE:HB3	1.82	0.61
1:A:36:LEU:HD22	1:A:89:GLU:HG3	1.84	0.60
1:B:980:ARG:NH1	1:B:1175:ARG:HD3	2.16	0.60
1:A:570:GLU:OE2	1:A:1057:PRO:HG3	2.02	0.59
1:B:707:PHE:CD2	1:B:899:ARG:HG3	2.37	0.59
1:A:441:LEU:HB3	1:A:451:GLU:HB2	1.85	0.59
1:A:197:ASN:O	1:A:200:GLU:HG2	2.03	0.59
1:A:557:ILE:HD12	1:A:1240:ARG:NE	2.18	0.59
1:A:1188:PRO:O	1:A:1191:ASP:O	2.21	0.58
1:B:1188:PRO:O	1:B:1191:ASP:O	2.20	0.58
1:B:129:ARG:HG3	1:B:129:ARG:HH11	1.67	0.58
1:A:1330:LEU:HD12	1:A:1331:ARG:N	2.18	0.58
1:B:747:HIS:CD2	1:B:836:THR:HG21	2.38	0.58
1:A:1191:ASP:O	1:A:1192:ILE:CB	2.51	0.58
1:B:1184:SER:HB3	8:B:4008:GOL:H11	1.84	0.57
1:B:281:PRO:HB2	1:B:287:LEU:CD1	2.34	0.57
1:A:618:LYS:HD2	1:A:690:GLU:OE1	2.05	0.57
1:A:1322:PRO:HG2	1:A:1324:ASN:CG	2.25	0.57
1:B:1286:THR:CG2	1:B:1287:ASN:H	2.04	0.57
1:B:209:GLU:HG3	1:B:210:PRO:HD2	1.86	0.57
1:A:314:GLU:O	1:A:318:LYS:HD3	2.05	0.57
1:A:394:ARG:HD2	9:A:4326:HOH:O	2.05	0.57
1:A:480:GLU:O	1:A:484:GLN:HG3	2.05	0.57
1:A:747:HIS:CD2	1:A:836:THR:HG21	2.39	0.57
1:B:1289:ASN:HB3	1:B:1292:GLU:HB2	1.87	0.56
1:B:628:VAL:HG21	1:B:681:ALA:HA	1.87	0.56
1:B:217:LEU:O	1:B:220:LYS:HG2	2.05	0.56
1:B:340:LYS:HE3	9:B:4667:HOH:O	2.04	0.56
1:A:217:LEU:O	1:A:220:LYS:HG2	2.04	0.56
1:B:1325:CYS:HB2	1:B:1326:LYS:HD2	1.86	0.56
1:A:1249:ASN:O	1:A:1255:ALA:HA	2.05	0.56
1:A:217:LEU:HD12	1:A:220:LYS:HD3	1.88	0.56
1:A:418:PHE:CD1	1:A:439:ARG:HB2	2.41	0.56
1:A:986:LYS:O	1:A:990:GLU:HG3	2.06	0.56
1:B:258:VAL:HG22	1:B:264:ILE:HG13	1.87	0.56
1:B:197:ASN:O	1:B:200:GLU:HG2	2.06	0.56
1:A:192:SER:HB2	9:A:4669:HOH:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1312:LYS:O	1:A:1316:LEU:HD23	2.06	0.55
1:B:1221:THR:HG22	1:B:1227:TYR:HB2	1.87	0.55
1:A:527:LEU:C	1:A:529:LYS:H	2.08	0.55
1:B:1326:LYS:N	1:B:1326:LYS:CD	2.69	0.55
1:B:995:LYS:NZ	1:B:1284:GLN:HE21	2.04	0.55
1:B:1287:ASN:O	1:B:1288:ASN:HB2	2.07	0.55
1:B:374:ILE:HD13	1:B:398:LEU:HD22	1.89	0.55
1:B:723:PHE:CE2	1:B:847:LYS:HE2	2.42	0.55
1:A:604:PHE:CD2	1:A:675:PRO:HG3	2.41	0.55
1:A:1082:SER:HB2	4:A:3003:MTE:O3P	2.07	0.55
1:A:1088:GLN:HG2	1:A:1133:TYR:CE1	2.42	0.55
1:A:1330:LEU:HD12	1:A:1331:ARG:H	1.70	0.55
1:A:1315:THR:O	1:A:1318:VAL:HG13	2.08	0.54
1:A:3:ALA:CB	1:A:228:ARG:H	2.06	0.54
1:B:1286:THR:HG22	1:B:1287:ASN:N	2.09	0.54
1:B:616:LYS:HA	1:B:659:THR:HG22	1.88	0.54
1:B:1312:LYS:HE3	1:B:1313:PHE:CZ	2.42	0.54
1:B:441:LEU:HB3	1:B:451:GLU:HB2	1.89	0.54
1:A:95:LYS:HE2	9:A:4796:HOH:O	2.06	0.54
1:A:443:GLN:HB2	1:A:446:SER:OG	2.07	0.54
1:B:1185:SER:O	8:B:4008:GOL:H12	2.08	0.54
1:A:752:ILE:HD13	1:A:822:PRO:HB3	1.90	0.54
1:A:1221:THR:HG22	1:A:1227:TYR:HB2	1.89	0.54
1:A:1008:SER:HA	1:A:1081:VAL:HG11	1.90	0.53
1:B:284:ILE:HB	1:B:287:LEU:HD12	1.90	0.53
1:A:799:GLY:HA2	5:A:3004:MOS:S	2.49	0.53
1:A:1093:ALA:O	1:A:1097:ILE:HG12	2.08	0.53
1:A:552:HIS:HB3	1:A:1237:THR:HG21	1.90	0.53
1:B:1294:PHE:HB2	9:B:4880:HOH:O	2.07	0.53
1:A:1012:PRO:HB2	9:A:4688:HOH:O	2.09	0.53
1:B:918:GLN:HE22	8:B:4007:GOL:C1	2.22	0.53
1:A:3:ALA:O	1:A:4:ASP:HB3	2.08	0.53
1:A:529:LYS:O	1:A:531:SER:N	2.42	0.53
1:A:406:SER:C	1:A:407:ILE:HD12	2.29	0.53
8:A:3008:GOL:C1	8:A:3008:GOL:HO1	2.12	0.53
1:A:430:ASP:OD1	1:A:431:ILE:N	2.42	0.53
1:B:802:GLU:OE1	6:B:4005:SAL:H4	2.09	0.52
1:A:316:VAL:HA	1:A:324:THR:HG21	1.92	0.52
8:B:4008:GOL:C1	8:B:4008:GOL:HO1	2.14	0.52
1:A:268:MET:HE1	9:A:4726:HOH:O	2.08	0.52
1:B:57:LYS:HE2	1:B:66:ILE:HD11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:GLN:NE2	1:B:133:GLU:H	2.00	0.52
1:A:3:ALA:HA	1:A:227:LEU:CD2	2.40	0.52
1:B:1326:LYS:HD3	1:B:1326:LYS:O	2.10	0.52
1:B:1007:ILE:O	1:B:1008:SER:CB	2.58	0.52
1:B:164:ALA:O	1:B:165:LYS:CB	2.57	0.51
1:A:1279:ARG:NH2	1:A:1290:THR:O	2.43	0.51
1:A:1332:VAL:OXT	1:A:1332:VAL:CG2	2.57	0.51
1:B:1287:ASN:O	1:B:1288:ASN:CB	2.58	0.51
1:A:552:HIS:HB2	9:A:4617:HOH:O	2.09	0.51
1:A:137:GLU:HG3	1:A:551:LYS:NZ	2.25	0.51
1:A:966:ARG:HG3	9:A:4860:HOH:O	2.11	0.51
1:B:695:ILE:HG23	1:B:700:ASP:HB3	1.93	0.51
1:A:407:ILE:N	1:A:407:ILE:HD12	2.26	0.51
1:A:241:THR:OG1	1:A:244:GLU:HG3	2.11	0.51
1:A:918:GLN:HE22	8:A:3007:GOL:C1	2.23	0.51
1:B:117:THR:HB	1:B:118:PRO:HD3	1.92	0.51
1:B:154:ARG:HD2	9:B:4305:HOH:O	2.11	0.50
1:A:374:ILE:HD13	1:A:398:LEU:CD2	2.41	0.50
1:A:670:VAL:HG11	1:A:681:ALA:HB3	1.93	0.50
1:A:60:ARG:O	1:A:61:LEU:HB2	2.09	0.50
1:A:839:ARG:NH1	8:A:3007:GOL:O1	2.44	0.50
1:B:1324:ASN:O	1:B:1326:LYS:N	2.44	0.50
1:B:1008:SER:HA	1:B:1081:VAL:HG11	1.92	0.50
1:A:346:ALA:HB1	7:A:3006:FAD:H4'	1.92	0.50
1:A:45:GLU:HG2	9:A:4719:HOH:O	2.12	0.50
1:A:655:PHE:HE1	1:A:814:LEU:HD23	1.77	0.50
1:A:752:ILE:HD12	1:A:822:PRO:HB3	1.93	0.50
1:B:1097:ILE:HD11	1:B:1129:THR:HG22	1.92	0.50
1:A:1322:PRO:HG2	1:A:1324:ASN:ND2	2.26	0.50
1:A:351:ASN:ND2	1:A:361:LEU:HB2	2.27	0.50
1:B:141:ASP:O	1:B:144:GLN:HG3	2.11	0.50
1:A:645:GLU:OE2	1:A:650:ASN:HB3	2.12	0.50
1:B:879:GLU:HG2	1:B:1142:PHE:CZ	2.46	0.49
1:A:964:VAL:HB	1:A:965:PRO:HD3	1.94	0.49
1:A:994:LYS:HE3	9:A:4560:HOH:O	2.12	0.49
1:B:885:MET:SD	1:B:896:GLY:HA3	2.52	0.49
1:A:135:THR:O	1:A:139:ILE:HG13	2.12	0.49
1:A:374:ILE:HG21	1:A:398:LEU:HD22	1.94	0.49
1:A:1007:ILE:O	1:A:1008:SER:CB	2.60	0.49
1:B:336:TRP:CZ3	1:B:427:ARG:HG2	2.48	0.49
1:B:713:LYS:HG3	1:B:714:ILE:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1037:GLU:HB2	1:A:1043:HIS:CD2	2.47	0.49
1:A:117:THR:HB	1:A:118:PRO:HD3	1.93	0.49
1:A:1184:SER:HB3	8:A:3008:GOL:H11	1.94	0.49
1:A:5:GLU:HB2	9:A:4797:HOH:O	2.12	0.49
1:B:980:ARG:HD2	9:B:4566:HOH:O	2.12	0.49
1:A:256:LYS:HG3	1:A:275:PHE:CD2	2.48	0.49
1:B:1249:ASN:O	1:B:1255:ALA:HA	2.13	0.49
1:A:955:PHE:CA	1:A:1145:ASN:HD21	2.21	0.49
1:B:840:HIS:N	8:B:4007:GOL:O3	2.38	0.49
1:A:915:GLY:H	8:A:3007:GOL:C1	2.26	0.49
1:B:154:ARG:CD	1:B:1196:GLU:OE2	2.59	0.49
1:B:719:LEU:HD11	1:B:895:ARG:HB3	1.93	0.49
1:B:839:ARG:NH1	8:B:4007:GOL:O1	2.46	0.49
1:A:1192:ILE:HG13	1:A:1243:LEU:HD11	1.95	0.48
1:A:312:LEU:O	1:A:316:VAL:HG23	2.13	0.48
1:A:418:PHE:HD1	1:A:439:ARG:HB2	1.78	0.48
1:A:651:ASP:OD1	1:A:871:ARG:NH1	2.45	0.48
1:A:995:LYS:NZ	1:A:1284:GLN:HE21	2.11	0.48
1:A:1320:GLY:O	1:A:1321:ALA:C	2.52	0.48
1:A:1320:GLY:O	1:A:1322:PRO:N	2.47	0.48
1:A:363:PRO:HG3	1:A:463:THR:HG23	1.94	0.48
1:A:600:GLU:OE2	1:B:598:ARG:HG2	2.13	0.48
1:A:367:ALA:O	1:A:439:ARG:HD3	2.14	0.48
1:A:3:ALA:HB2	1:A:227:LEU:HA	1.95	0.48
1:A:64:LYS:HE2	9:A:4653:HOH:O	2.14	0.48
1:B:129:ARG:HG3	1:B:129:ARG:NH1	2.29	0.48
1:B:117:THR:CG2	1:B:586:ALA:HA	2.44	0.48
1:A:1324:ASN:ND2	1:A:1324:ASN:C	2.68	0.47
1:A:909:THR:OG1	1:A:910:ALA:N	2.45	0.47
1:A:1017:ALA:HB1	1:A:1086:TYR:CD2	2.48	0.47
1:A:911:PHE:O	1:A:912:ARG:C	2.52	0.47
1:A:544:SER:HB2	1:A:994:LYS:HD2	1.95	0.47
1:B:150:CYS:SG	4:B:4003:MTE:N2	2.87	0.47
1:A:161:ARG:HD3	9:A:4840:HOH:O	2.13	0.47
1:A:719:LEU:CD1	1:A:895:ARG:HD3	2.44	0.47
1:A:325:GLU:HB2	1:A:412:SER:OG	2.14	0.47
1:A:657:LYS:O	1:A:658:ASP:HB2	2.15	0.47
1:B:739:GLN:HG2	1:B:911:PHE:CE1	2.50	0.47
1:B:473:GLN:O	1:B:476:LYS:HB2	2.14	0.47
1:B:332:GLU:CG	1:B:548:LEU:HD13	2.45	0.47
1:A:861:VAL:O	1:A:896:GLY:HA2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:GLN:O	1:A:134:PRO:HD3	2.15	0.47
1:B:129:ARG:NE	1:B:209:GLU:HG2	2.30	0.47
1:B:376:SER:HB2	1:B:402:GLU:HG2	1.96	0.47
1:A:1330:LEU:O	1:A:1331:ARG:CG	2.59	0.46
1:B:650:ASN:HD21	1:B:778:LYS:HE3	1.80	0.46
1:B:911:PHE:HD2	1:B:912:ARG:N	2.13	0.46
1:A:1318:VAL:HG23	1:A:1318:VAL:O	2.16	0.46
1:B:256:LYS:HG3	1:B:275:PHE:CD2	2.51	0.46
1:A:698:ILE:HG23	1:A:901:CYS:SG	2.55	0.46
1:A:923:ALA:HA	1:A:926:TRP:NE1	2.31	0.46
1:B:328:ARG:HG2	1:B:328:ARG:NH1	2.27	0.46
1:A:995:LYS:HZ3	1:A:1284:GLN:HE21	1.64	0.46
1:A:1134:ARG:HD3	1:B:1124:ARG:O	2.16	0.46
1:B:312:LEU:HB2	1:B:331:LEU:HD21	1.98	0.46
1:A:482:LEU:O	1:A:486:VAL:HG23	2.16	0.46
1:A:688:THR:HG23	9:A:4422:HOH:O	2.14	0.46
1:A:914:PHE:HA	8:A:3007:GOL:O2	2.15	0.46
1:B:1175:ARG:HG2	9:B:4751:HOH:O	2.16	0.46
1:B:1187:ASN:CG	1:B:1190:ILE:HG12	2.36	0.46
1:B:135:THR:OG1	1:B:138:GLU:HG3	2.16	0.46
1:A:1175:ARG:HG3	1:A:1238:GLU:HB2	1.98	0.46
1:A:506:GLU:CD	1:A:506:GLU:H	2.19	0.46
1:A:997:GLY:HA3	1:A:1273:ALA:O	2.15	0.45
1:A:747:HIS:CE1	1:A:801:LYS:HG2	2.51	0.45
1:B:915:GLY:H	8:B:4007:GOL:C1	2.29	0.45
1:A:718:ASP:HB3	1:A:721:LYS:HE3	1.97	0.45
1:B:705:ASN:HA	1:B:707:PHE:CE1	2.52	0.45
1:A:1317:CYS:O	1:A:1318:VAL:C	2.55	0.45
1:A:644:ASN:O	1:A:653:THR:HA	2.17	0.45
1:A:310:LYS:O	1:A:314:GLU:HG3	2.17	0.45
1:B:1261:GLU:N	1:B:1262:PRO:CD	2.79	0.45
1:B:757:GLU:HB3	1:B:786:ARG:HE	1.82	0.45
1:A:995:LYS:NZ	1:A:1284:GLN:NE2	2.64	0.45
1:B:1310:VAL:HG13	9:B:4809:HOH:O	2.16	0.45
1:B:37:ARG:HG2	1:B:37:ARG:HH11	1.82	0.45
1:A:519:PHE:O	1:A:523:VAL:HG23	2.17	0.44
1:B:377:ARG:HH11	1:B:377:ARG:HG2	1.82	0.44
1:B:740:ASP:OD2	1:B:833:MET:HG2	2.16	0.44
1:A:1330:LEU:O	1:A:1331:ARG:CB	2.66	0.44
1:B:779:MET:HG3	1:B:810:VAL:CG1	2.46	0.44
1:A:695:ILE:HG23	1:A:700:ASP:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:570:GLU:CD	1:A:1057:PRO:HG3	2.37	0.44
1:A:37:ARG:HG2	1:A:595:ASP:HA	1.99	0.44
1:B:1299:PRO:HG2	1:B:1301:THR:HG23	1.99	0.44
1:B:346:ALA:HB1	7:B:4006:FAD:H4'	1.99	0.44
1:A:247:ASP:O	1:A:251:GLN:HG3	2.18	0.44
1:B:1108:ASN:N	1:B:1109:PRO:HD3	2.33	0.44
1:A:328:ARG:NH1	1:A:328:ARG:HG2	2.28	0.44
1:A:527:LEU:C	1:A:529:LYS:N	2.71	0.44
1:B:1192:ILE:HA	1:B:1195:VAL:HB	1.98	0.44
1:B:82:HIS:CE1	1:B:219:LEU:HD13	2.52	0.44
1:B:909:THR:OG1	1:B:910:ALA:N	2.47	0.44
1:A:1286:THR:HG22	1:A:1287:ASN:N	2.32	0.44
1:A:1320:GLY:C	1:A:1322:PRO:HD3	2.38	0.44
1:A:557:ILE:HB	1:A:1240:ARG:HG2	1.99	0.44
1:B:1323:GLY:O	1:B:1324:ASN:C	2.57	0.43
1:B:480:GLU:O	1:B:484:GLN:HG3	2.18	0.43
1:B:885:MET:HE2	1:B:894:ILE:HD11	2.00	0.43
1:A:1253:ILE:HG23	1:A:1253:ILE:O	2.18	0.43
1:B:1082:SER:HB2	4:B:4003:MTE:O2P	2.19	0.43
1:B:332:GLU:HG2	1:B:548:LEU:HD13	2.01	0.43
9:A:4946:HOH:O	1:B:95:LYS:HE2	2.18	0.43
1:A:1299:PRO:HG2	1:A:1301:THR:HG23	2.00	0.43
1:A:1325:CYS:HA	9:A:4966:HOH:O	2.17	0.43
1:A:209:GLU:HG3	1:A:210:PRO:HD2	1.99	0.43
1:A:628:VAL:HG21	1:A:681:ALA:HA	2.00	0.43
1:B:914:PHE:HA	8:B:4007:GOL:O2	2.18	0.43
1:A:269:LYS:HE3	9:A:4958:HOH:O	2.18	0.43
1:B:606:ARG:HG2	1:B:679:GLU:HA	2.00	0.43
1:B:698:ILE:HG23	1:B:901:CYS:SG	2.58	0.43
1:B:91:ILE:O	1:B:99:HIS:HB2	2.19	0.43
1:A:715:GLU:CG	1:A:895:ARG:HG3	2.48	0.43
9:A:4908:HOH:O	1:B:1134:ARG:HD2	2.18	0.43
1:B:36:LEU:HD22	1:B:89:GLU:CG	2.44	0.43
1:B:509:ARG:HG2	1:B:509:ARG:HH11	1.84	0.43
1:B:407:ILE:HD12	1:B:407:ILE:N	2.33	0.43
1:B:1321:ALA:HB1	1:B:1322:PRO:CD	2.35	0.43
1:A:1175:ARG:NH2	1:A:1240:ARG:NH1	2.67	0.43
1:B:508:ARG:O	1:B:512:THR:HG23	2.19	0.43
1:A:505:ILE:HD12	1:A:505:ILE:N	2.35	0.42
1:A:715:GLU:HG3	1:A:895:ARG:HG3	2.01	0.42
1:B:1281:ALA:O	1:B:1284:GLN:HB3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:609:THR:HG21	1:B:835:ILE:HD11	2.00	0.42
1:A:1060:LYS:HA	9:A:4504:HOH:O	2.18	0.42
1:A:1107:LYS:C	1:A:1109:PRO:HD3	2.39	0.42
1:A:1252:ALA:HB3	1:A:1256:SER:O	2.19	0.42
1:A:966:ARG:O	1:A:970:GLU:HB2	2.19	0.42
1:B:62:GLN:O	1:B:63:ASP:C	2.58	0.42
1:B:752:ILE:CD1	1:B:822:PRO:HB3	2.48	0.42
1:A:137:GLU:HG3	1:A:551:LYS:HZ2	1.83	0.42
1:A:223:PRO:HA	1:A:224:PRO:HD3	1.85	0.42
1:A:237:ILE:HG21	1:A:248:LEU:HD11	2.01	0.42
1:A:1132:PHE:CD1	1:B:1126:SER:HB2	2.54	0.42
1:B:482:LEU:O	1:B:486:VAL:HG23	2.20	0.42
1:B:844:ALA:HB2	1:B:922:ILE:HD13	2.02	0.42
1:B:1316:LEU:HD11	9:B:4974:HOH:O	2.19	0.42
1:A:236:TRP:CZ2	1:A:280:CYS:HB2	2.55	0.42
1:B:911:PHE:O	1:B:912:ARG:C	2.58	0.42
1:A:639:ASP:HB3	1:A:818:LYS:HE3	2.01	0.42
1:A:757:GLU:HB3	1:A:786:ARG:HE	1.85	0.42
5:B:4004:MOS:O1	5:B:4004:MOS:S	2.78	0.42
1:A:719:LEU:HD12	1:A:895:ARG:HD3	2.02	0.42
1:A:748:CYS:HB2	1:A:826:MET:HG3	2.01	0.42
1:B:1054:LEU:O	1:B:1055:LYS:HB2	2.20	0.42
1:B:608:VAL:HG21	1:B:634:PHE:HE1	1.84	0.42
1:B:942:ARG:HD2	9:B:4351:HOH:O	2.20	0.42
1:A:131:GLN:HA	1:A:132:PRO:HD2	1.92	0.42
1:A:137:GLU:OE2	1:A:551:LYS:HD2	2.20	0.42
1:B:338:ALA:HA	1:B:429:ASP:OD1	2.20	0.42
1:B:964:VAL:HB	1:B:965:PRO:HD3	2.02	0.42
1:A:1132:PHE:CG	1:B:1126:SER:HB2	2.55	0.42
1:A:129:ARG:HG3	1:A:129:ARG:HH11	1.84	0.42
1:A:154:ARG:N	1:A:155:PRO:HD2	2.34	0.42
1:B:117:THR:HG22	1:B:586:ALA:HA	2.01	0.42
1:A:196:PHE:CE1	1:A:198:PRO:HG3	2.54	0.41
1:B:1207:THR:C	1:B:1208:LEU:HD12	2.40	0.41
1:B:447:MET:HG2	1:B:527:LEU:HD13	2.02	0.41
1:A:414:GLU:O	1:A:415:ASP:HB2	2.20	0.41
1:A:771:LYS:HD3	1:A:771:LYS:HA	1.92	0.41
1:B:1321:ALA:O	1:B:1322:PRO:C	2.58	0.41
1:B:161:ARG:HD3	9:B:4822:HOH:O	2.20	0.41
1:A:117:THR:CG2	1:A:586:ALA:HA	2.50	0.41
1:B:1252:ALA:HB3	1:B:1256:SER:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:727:ASP:OD2	1:B:852:LYS:HG2	2.20	0.41
1:A:1106:LYS:O	1:A:1109:PRO:HD3	2.21	0.41
1:A:28:ALA:O	1:A:32:ARG:HG2	2.20	0.41
1:A:409:ILE:HA	1:A:410:PRO:HD3	1.83	0.41
1:B:22:PRO:HD2	1:B:231:GLY:HA3	2.02	0.41
1:B:257:LEU:HA	1:B:279:ILE:O	2.20	0.41
1:B:310:LYS:O	1:B:314:GLU:HG3	2.20	0.41
1:A:129:ARG:NE	1:A:209:GLU:HG2	2.35	0.41
1:A:117:THR:HG22	1:A:586:ALA:HA	2.03	0.41
1:B:109:HIS:HA	9:B:4182:HOH:O	2.19	0.41
1:B:1173:ASN:O	1:B:1236:PRO:HA	2.21	0.41
1:B:351:ASN:ND2	1:B:361:LEU:HB2	2.36	0.41
1:B:482:LEU:HD23	1:B:482:LEU:C	2.41	0.41
1:B:670:VAL:HG11	1:B:681:ALA:HB3	2.02	0.41
1:B:1289:ASN:O	1:B:1290:THR:HB	2.20	0.41
1:B:741:HIS:CE1	1:B:838:GLY:HA2	2.56	0.41
1:A:678:ALA:HB3	9:A:4714:HOH:O	2.20	0.41
1:A:97:ARG:HB2	1:A:97:ARG:NH1	2.35	0.41
1:A:376:SER:HB2	1:A:402:GLU:HG2	2.03	0.41
1:A:719:LEU:HD13	1:A:860:GLU:OE2	2.21	0.41
1:B:394:ARG:HD2	9:B:4345:HOH:O	2.20	0.41
1:A:1052:LYS:HD3	1:A:1254:TYR:CZ	2.55	0.41
1:A:1004:LYS:HB2	1:A:1155:TYR:CE2	2.56	0.41
1:B:1301:THR:HB	1:B:1302:PRO:HD2	2.03	0.41
1:B:332:GLU:O	1:B:335:ARG:HB3	2.21	0.41
1:A:773:GLN:HG2	1:A:784:VAL:HG13	2.02	0.40
1:A:804:ARG:HG2	1:A:909:THR:HG21	2.02	0.40
1:B:1093:ALA:O	1:B:1097:ILE:HG12	2.20	0.40
1:B:986:LYS:O	1:B:990:GLU:HG3	2.22	0.40
1:A:332:GLU:O	1:A:335:ARG:HB3	2.22	0.40
1:A:644:ASN:HB2	9:A:4771:HOH:O	2.21	0.40
1:A:852:LYS:HE2	1:A:852:LYS:HB3	1.79	0.40
7:A:3006:FAD:HM73	9:A:4047:HOH:O	2.22	0.40
1:B:569:LYS:HE2	1:B:569:LYS:HB3	1.91	0.40
1:B:615:ALA:HB2	1:B:691:ASP:HA	2.04	0.40
1:B:987:PHE:CD2	1:B:996:ARG:HG3	2.57	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1293/1332 (97%)	1228 (95%)	54 (4%)	11 (1%)	20	14
1	B	1290/1332 (97%)	1236 (96%)	45 (4%)	9 (1%)	25	20
All	All	2583/2664 (97%)	2464 (95%)	99 (4%)	20 (1%)	22	17

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1008	SER
1	A	1331	ARG
1	B	244	GLU
1	B	1008	SER
1	B	1287	ASN
1	A	61	LEU
1	A	1192	ILE
1	A	1288	ASN
1	B	1192	ILE
1	B	1288	ASN
1	A	530	ASP
1	A	797	GLY
1	A	912	ARG
1	A	1318	VAL
1	B	912	ARG
1	B	1139	GLY
1	B	1325	CYS
1	A	1321	ALA
1	B	797	GLY
1	A	1139	GLY

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1101/1128 (98%)	1084 (98%)	17 (2%)	70	76
1	B	1098/1128 (97%)	1078 (98%)	20 (2%)	64	70
All	All	2199/2256 (98%)	2162 (98%)	37 (2%)	66	72

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	57	LYS
1	A	154	ARG
1	A	312	LEU
1	A	328	ARG
1	A	476	LYS
1	A	618	LYS
1	A	651	ASP
1	A	743	TYR
1	A	802	GLU
1	A	911	PHE
1	A	1002	PRO
1	A	1145	ASN
1	A	1216	GLU
1	A	1239	PHE
1	A	1324	ASN
1	A	1325	CYS
1	B	100	PRO
1	B	129	ARG
1	B	154	ARG
1	B	328	ARG
1	B	471	GLN
1	B	476	LYS
1	B	538	LEU
1	B	565	ASN
1	B	619	SER
1	B	651	ASP
1	B	743	TYR
1	B	744	LEU
1	B	899	ARG
1	B	911	PHE

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Mol	Chain	Res	Type
1	B	1072	PRO
1	B	1239	PHE
1	B	1324	ASN
1	B	1325	CYS
1	B	1326	LYS
1	B	1330	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	GLN
1	A	351	ASN
1	A	473	GLN
1	A	626	GLN
1	A	650	ASN
1	A	683	HIS
1	A	1095	GLN
1	A	1145	ASN
1	A	1212	HIS
1	A	1284	GLN
1	A	1289	ASN
1	A	1324	ASN
1	B	131	GLN
1	B	146	ASN
1	B	473	GLN
1	B	565	ASN
1	B	626	GLN
1	B	650	ASN
1	B	1145	ASN
1	B	1284	GLN
1	B	1287	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FES	A	3001	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FES	A	3002	1	0,4,4	0.00	-	0,4,4	0.00	-
4	MTE	A	3003	5	21,26,26	7.42	17 (80%)	19,40,40	3.15	8 (42%)
5	MOS	A	3004	4	0,3,3	0.00	-	0,3,3	0.00	-
6	SAL	A	3005	-	7,10,10	1.79	3 (42%)	9,13,13	1.18	0
7	FAD	A	3006	-	51,58,58	4.65	33 (64%)	54,89,89	2.77	20 (37%)
8	GOL	A	3007	-	5,5,5	7.48	5 (100%)	5,5,5	5.80	4 (80%)
8	GOL	A	3008	-	5,5,5	4.69	4 (80%)	5,5,5	5.74	3 (60%)
3	FES	B	4001	1	0,4,4	0.00	-	0,4,4	0.00	-
3	FES	B	4002	1	0,4,4	0.00	-	0,4,4	0.00	-
4	MTE	B	4003	5	21,26,26	7.41	13 (61%)	19,40,40	3.21	8 (42%)
5	MOS	B	4004	4	0,3,3	0.00	-	0,3,3	0.00	-
6	SAL	B	4005	-	7,10,10	1.76	3 (42%)	9,13,13	1.23	0
7	FAD	B	4006	-	51,58,58	4.50	33 (64%)	54,89,89	2.83	20 (37%)
8	GOL	B	4007	-	5,5,5	7.02	5 (100%)	5,5,5	5.72	3 (60%)
8	GOL	B	4008	-	5,5,5	4.55	3 (60%)	5,5,5	5.86	3 (60%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FES	A	3001	1	-	0/0/4/4	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FES	A	3002	1	-	0/0/4/4	0/1/1/1
4	MTE	A	3003	5	-	0/6/34/34	0/3/3/3
5	MOS	A	3004	4	-	0/0/0/0	0/0/0/0
6	SAL	A	3005	-	-	0/0/4/4	0/1/1/1
7	FAD	A	3006	-	2/2/9/9	0/28/50/50	0/6/6/6
8	GOL	A	3007	-	-	0/4/4/4	0/0/0/0
8	GOL	A	3008	-	-	0/4/4/4	0/0/0/0
3	FES	B	4001	1	-	0/0/4/4	0/1/1/1
3	FES	B	4002	1	-	0/0/4/4	0/1/1/1
4	MTE	B	4003	5	-	0/6/34/34	0/3/3/3
5	MOS	B	4004	4	-	0/0/0/0	0/0/0/0
6	SAL	B	4005	-	-	0/0/4/4	0/1/1/1
7	FAD	B	4006	-	2/2/9/9	0/28/50/50	0/6/6/6
8	GOL	B	4007	-	-	0/4/4/4	0/0/0/0
8	GOL	B	4008	-	-	0/4/4/4	0/0/0/0

All (119) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	3007	GOL	C3-C2	-13.99	1.00	1.52
8	B	4007	GOL	C3-C2	-13.06	1.03	1.52
7	A	3006	FAD	C5'-C4'	-8.95	1.38	1.51
8	A	3008	GOL	C3-C2	-7.53	1.24	1.52
7	B	4006	FAD	C5'-C4'	-7.46	1.40	1.51
8	B	4008	GOL	C3-C2	-6.78	1.27	1.52
4	A	3003	MTE	C4'-C3'	-6.47	1.42	1.52
4	A	3003	MTE	P-O4'	-5.86	1.41	1.60
7	B	4006	FAD	C8A-N7A	-5.78	1.23	1.34
8	A	3007	GOL	C1-C2	-5.78	1.30	1.52
4	B	4003	MTE	P-O4'	-5.51	1.42	1.60
4	A	3003	MTE	P-O3P	-5.42	1.32	1.54
8	B	4007	GOL	O2-C2	-5.04	1.28	1.43
8	A	3007	GOL	O2-C2	-5.02	1.28	1.43
7	A	3006	FAD	C8A-N7A	-4.90	1.25	1.34
8	A	3007	GOL	O3-C3	-4.64	1.22	1.42
7	B	4006	FAD	O5B-C5B	-4.60	1.26	1.44
4	B	4003	MTE	C4'-C3'	-4.46	1.45	1.52
7	B	4006	FAD	PA-O5B	-4.39	1.40	1.59
8	B	4007	GOL	O3-C3	-4.29	1.24	1.42
7	A	3006	FAD	O5B-C5B	-4.12	1.28	1.44
8	B	4007	GOL	C1-C2	-4.10	1.37	1.52
4	B	4003	MTE	P-O3P	-4.09	1.38	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	4006	FAD	O2B-C2B	-3.85	1.34	1.43
7	B	4006	FAD	C2B-C1B	-3.18	1.48	1.53
7	A	3006	FAD	PA-O2A	-3.17	1.39	1.55
7	B	4006	FAD	PA-O2A	-3.01	1.40	1.55
7	A	3006	FAD	PA-O5B	-2.80	1.47	1.59
7	A	3006	FAD	C6A-N6A	-2.77	1.22	1.34
8	B	4008	GOL	O3-C3	-2.72	1.30	1.42
7	A	3006	FAD	C5A-N7A	-2.69	1.30	1.39
7	B	4006	FAD	C2'-C3'	-2.65	1.48	1.53
4	A	3003	MTE	P-O2P	-2.62	1.44	1.54
7	A	3006	FAD	C2B-C1B	-2.50	1.49	1.53
7	A	3006	FAD	O4-C4	-2.46	1.18	1.24
7	B	4006	FAD	C5A-N7A	-2.39	1.31	1.39
8	A	3008	GOL	O3-C3	-2.38	1.32	1.42
8	A	3008	GOL	C1-C2	-2.32	1.43	1.52
7	A	3006	FAD	C2'-C3'	-2.17	1.49	1.53
7	B	4006	FAD	P-O2P	-2.07	1.44	1.55
8	A	3007	GOL	O1-C1	2.02	1.50	1.42
7	A	3006	FAD	C1'-N10	2.03	1.50	1.48
4	B	4003	MTE	O3'-C7	2.11	1.46	1.43
6	B	4005	SAL	C3-C2	2.12	1.43	1.39
6	A	3005	SAL	C6-C1	2.18	1.43	1.39
6	A	3005	SAL	C3-C2	2.22	1.43	1.39
7	A	3006	FAD	O2'-C2'	2.24	1.48	1.43
4	A	3003	MTE	C2'-C1'	2.33	1.50	1.35
6	B	4005	SAL	C6-C1	2.34	1.43	1.39
4	B	4003	MTE	C2'-C1'	2.37	1.50	1.35
7	A	3006	FAD	C6-C5X	2.40	1.45	1.41
4	A	3003	MTE	O4-C4	2.40	1.30	1.24
6	B	4005	SAL	C5-C6	2.72	1.44	1.38
7	B	4006	FAD	C5B-C4B	2.78	1.60	1.51
7	B	4006	FAD	C9-C8	2.80	1.45	1.37
6	A	3005	SAL	C5-C6	2.85	1.44	1.38
4	A	3003	MTE	C10-N1	2.92	1.39	1.34
4	A	3003	MTE	C2-N3	2.95	1.40	1.35
7	B	4006	FAD	C6-C7	3.15	1.46	1.37
7	B	4006	FAD	O2'-C2'	3.15	1.50	1.43
4	B	4003	MTE	C2-N1	3.21	1.41	1.35
7	B	4006	FAD	C6A-C5A	3.30	1.59	1.42
7	B	4006	FAD	O3'-C3'	3.31	1.50	1.43
7	A	3006	FAD	C6A-C5A	3.58	1.61	1.42
7	A	3006	FAD	C6-C7	3.59	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3003	MTE	C2-N1	3.80	1.42	1.35
8	B	4007	GOL	O1-C1	3.93	1.59	1.42
7	B	4006	FAD	C2-N3	3.98	1.46	1.38
7	B	4006	FAD	C10-N1	4.08	1.39	1.33
7	B	4006	FAD	C9-C9A	4.12	1.49	1.40
7	A	3006	FAD	C4X-N5	4.27	1.39	1.33
4	A	3003	MTE	O3'-C3'	4.35	1.49	1.43
7	B	4006	FAD	C4-C4X	4.44	1.49	1.41
7	A	3006	FAD	O4B-C4B	4.53	1.55	1.45
7	B	4006	FAD	C5A-C4A	4.60	1.50	1.40
7	B	4006	FAD	O4B-C4B	4.64	1.55	1.45
4	A	3003	MTE	O3'-C7	4.67	1.50	1.43
7	B	4006	FAD	C4X-N5	4.70	1.40	1.33
4	B	4003	MTE	C4-C9	4.71	1.46	1.41
7	A	3006	FAD	O3'-C3'	4.75	1.53	1.43
4	B	4003	MTE	C4-N3	5.05	1.42	1.33
7	B	4006	FAD	C5X-N5	5.06	1.43	1.35
7	A	3006	FAD	C5A-C4A	5.14	1.52	1.40
7	A	3006	FAD	C10-N1	5.25	1.40	1.33
7	A	3006	FAD	C9-C9A	5.25	1.51	1.40
4	B	4003	MTE	O3'-C3'	5.25	1.51	1.43
7	B	4006	FAD	C6-C5X	5.44	1.50	1.41
7	B	4006	FAD	C2A-N3A	5.46	1.41	1.32
7	A	3006	FAD	C4-C4X	5.49	1.51	1.41
4	B	4003	MTE	C9-N5	5.54	1.50	1.37
7	A	3006	FAD	C2-N3	5.71	1.49	1.38
7	A	3006	FAD	C5X-N5	5.78	1.44	1.35
4	A	3003	MTE	C4-N3	6.06	1.44	1.33
8	A	3008	GOL	O1-C1	6.23	1.68	1.42
4	A	3003	MTE	C4-C9	6.30	1.48	1.41
4	A	3003	MTE	C9-N5	6.60	1.52	1.37
7	A	3006	FAD	C8-C7	6.77	1.58	1.41
8	B	4008	GOL	O1-C1	6.78	1.71	1.42
7	A	3006	FAD	C2A-N1A	6.84	1.46	1.33
7	B	4006	FAD	C2A-N1A	6.95	1.47	1.33
7	B	4006	FAD	C4-N3	7.02	1.45	1.33
7	A	3006	FAD	O4B-C1B	7.20	1.51	1.41
7	B	4006	FAD	C8-C7	7.29	1.59	1.41
7	A	3006	FAD	C9A-C5X	7.39	1.57	1.42
7	A	3006	FAD	C4-N3	7.45	1.46	1.33
4	B	4003	MTE	C6-N5	7.61	1.55	1.45
7	A	3006	FAD	C2A-N3A	7.77	1.45	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3003	MTE	C6-N5	7.88	1.56	1.45
7	B	4006	FAD	C9A-C5X	8.01	1.59	1.42
7	A	3006	FAD	C4X-C10	8.31	1.55	1.41
7	B	4006	FAD	C4A-N3A	8.53	1.48	1.35
7	B	4006	FAD	C4X-C10	9.01	1.56	1.41
7	A	3006	FAD	C4A-N3A	9.27	1.49	1.35
7	A	3006	FAD	C9A-N10	12.33	1.54	1.38
7	B	4006	FAD	C9A-N10	13.10	1.55	1.38
4	A	3003	MTE	C9-C10	13.19	1.66	1.41
4	B	4003	MTE	C9-C10	14.46	1.69	1.41
4	A	3003	MTE	C7-C6	24.52	1.71	1.53
4	B	4003	MTE	C7-C6	26.07	1.72	1.53

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	3006	FAD	N3A-C2A-N1A	-6.56	123.14	128.86
7	B	4006	FAD	C4-C4X-C10	-6.29	114.87	119.96
7	A	3006	FAD	C4-C4X-C10	-6.16	114.98	119.96
7	B	4006	FAD	O5B-PA-O1A	-5.73	86.14	109.25
7	A	3006	FAD	C5X-C9A-N10	-5.60	113.50	117.66
7	B	4006	FAD	C5X-C9A-N10	-5.60	113.50	117.66
7	A	3006	FAD	O5B-PA-O1A	-5.31	87.81	109.25
7	B	4006	FAD	C4X-C10-N10	-4.84	117.16	120.52
4	B	4003	MTE	O3'-C7-C6	-4.82	105.75	108.96
7	A	3006	FAD	C4X-C10-N10	-4.67	117.28	120.52
7	B	4006	FAD	N3A-C2A-N1A	-4.42	125.01	128.86
4	A	3003	MTE	N3-C2-N1	-4.35	118.41	125.45
7	A	3006	FAD	O4B-C4B-C5B	-4.28	94.96	109.40
7	B	4006	FAD	C4X-C4-N3	-4.18	117.53	123.48
4	B	4003	MTE	N3-C2-N1	-3.69	119.46	125.45
7	B	4006	FAD	O4B-C4B-C5B	-3.57	97.36	109.40
4	A	3003	MTE	O3'-C7-C6	-3.54	106.60	108.96
7	A	3006	FAD	C4X-C4-N3	-3.48	118.53	123.48
7	A	3006	FAD	O3'-C3'-C2'	-3.39	100.41	108.82
7	B	4006	FAD	C4'-C3'-C2'	-3.27	106.36	113.41
7	B	4006	FAD	O3'-C3'-C2'	-3.15	101.01	108.82
7	B	4006	FAD	O4B-C4B-C3B	-2.88	99.43	105.17
7	A	3006	FAD	O4B-C4B-C3B	-2.50	100.20	105.17
7	A	3006	FAD	C8M-C8-C9	-2.48	114.11	120.34
7	B	4006	FAD	C8M-C8-C9	-2.47	114.15	120.34
7	A	3006	FAD	C4'-C3'-C2'	-2.18	108.72	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	3006	FAD	O2A-PA-O5B	2.15	118.29	108.14
7	B	4006	FAD	O2A-PA-O5B	2.20	118.52	108.14
8	A	3007	GOL	O2-C2-C1	2.25	119.45	108.84
7	B	4006	FAD	O5B-C5B-C4B	2.46	117.73	109.00
4	B	4003	MTE	O3P-P-O4'	2.47	113.32	106.73
7	A	3006	FAD	O2P-P-O5'	2.49	119.89	108.14
7	B	4006	FAD	O2P-P-O5'	2.56	120.25	108.14
7	B	4006	FAD	C2A-N1A-C6A	2.69	123.48	118.77
7	A	3006	FAD	C8M-C8-C7	2.72	126.43	120.72
7	B	4006	FAD	C5A-C6A-N6A	2.86	126.31	120.47
7	B	4006	FAD	C8M-C8-C7	2.99	127.00	120.72
7	A	3006	FAD	O5B-C5B-C4B	3.16	120.21	109.00
7	A	3006	FAD	C5A-C6A-N6A	3.20	126.98	120.47
7	A	3006	FAD	C2A-N1A-C6A	3.26	124.47	118.77
8	A	3007	GOL	O1-C1-C2	3.39	127.17	110.07
8	B	4007	GOL	O1-C1-C2	3.57	128.07	110.07
8	B	4008	GOL	O1-C1-C2	4.19	131.18	110.07
4	A	3003	MTE	N8-C10-N1	4.42	125.45	116.90
8	A	3008	GOL	O1-C1-C2	4.43	132.38	110.07
4	B	4003	MTE	N2-C2-N3	4.44	124.34	117.24
4	A	3003	MTE	O3P-P-O4'	4.52	118.76	106.73
7	B	4006	FAD	C4-C4X-N5	4.58	123.70	118.68
4	A	3003	MTE	N2-C2-N3	4.64	124.67	117.24
7	A	3006	FAD	C4-C4X-N5	4.73	123.86	118.68
4	B	4003	MTE	N8-C10-N1	5.01	126.59	116.90
8	A	3007	GOL	O2-C2-C3	5.16	133.20	108.84
8	B	4007	GOL	O2-C2-C3	5.23	133.55	108.84
4	B	4003	MTE	C2-N1-C10	5.24	126.32	114.51
4	A	3003	MTE	C4-N3-C2	5.39	123.82	116.06
4	A	3003	MTE	C2-N1-C10	5.45	126.78	114.51
4	A	3003	MTE	P-O4'-C4'	5.46	133.33	118.30
4	B	4003	MTE	C4-N3-C2	5.50	123.97	116.06
8	B	4008	GOL	O2-C2-C3	5.81	136.26	108.84
8	A	3008	GOL	O2-C2-C3	6.04	137.36	108.84
7	B	4006	FAD	C4X-N5-C5X	6.04	123.14	116.76
7	A	3006	FAD	C4X-N5-C5X	6.20	123.31	116.76
4	B	4003	MTE	P-O4'-C4'	6.74	136.86	118.30
7	A	3006	FAD	C4-N3-C2	7.80	121.98	115.16
7	B	4006	FAD	C4-N3-C2	9.91	123.83	115.16
8	A	3008	GOL	O3-C3-C2	10.41	162.50	110.07
8	B	4007	GOL	O3-C3-C2	10.91	165.04	110.07
8	B	4008	GOL	O3-C3-C2	10.97	165.33	110.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	3007	GOL	O3-C3-C2	11.13	166.16	110.07

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	B	4006	FAD	C2'
7	B	4006	FAD	C3'
7	A	3006	FAD	C2'
7	A	3006	FAD	C3'

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3003	MTE	1	0
5	A	3004	MOS	2	0
7	A	3006	FAD	3	0
8	A	3007	GOL	4	0
8	A	3008	GOL	3	0
4	B	4003	MTE	2	0
5	B	4004	MOS	2	0
6	B	4005	SAL	1	0
7	B	4006	FAD	2	0
8	B	4007	GOL	7	0
8	B	4008	GOL	4	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.