



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2018 – 01:38 pm GMT

PDB ID : 1QDN  
Title : AMINO TERMINAL DOMAIN OF THE N-ETHYLMALEIMIDE SENSITIVE FUSION PROTEIN (NSF)  
Authors : May, A.P.; Misura, K.M.S.; Whiteheart, S.W.; Weis, W.I.  
Deposited on : 1999-05-21  
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

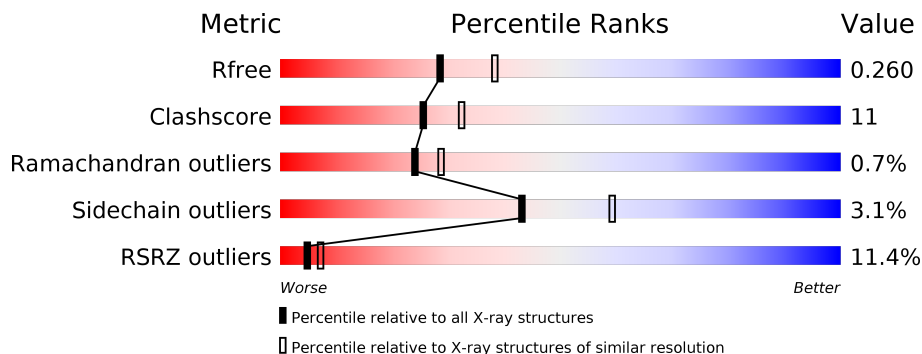
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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.

Mol	Chain	Length	Quality of chain
1	A	204	 6% 73% 19% • 7%
1	B	204	 11% 71% 21% • 7%
1	C	204	 15% 69% 23% • 7%

## 2 Entry composition [i](#)

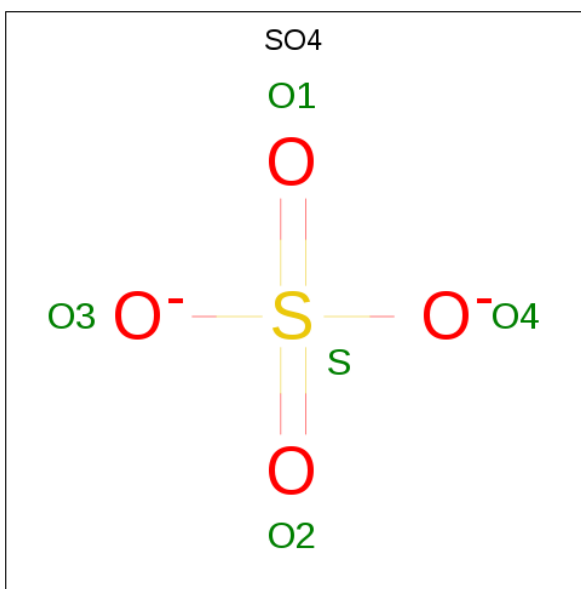
There are 4 unique types of molecules in this entry. The entry contains 4742 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (N-ETHYLMALEIMIDE SENSITIVE FUSION PROTEIN (NSF)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	189	Total 1472	C 931	N 249	O 284	S 8	0	1	0
1	B	189	Total 1476	C 933	N 251	O 284	S 8	0	2	0
1	C	190	Total 1488	C 940	N 252	O 288	S 8	0	3	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



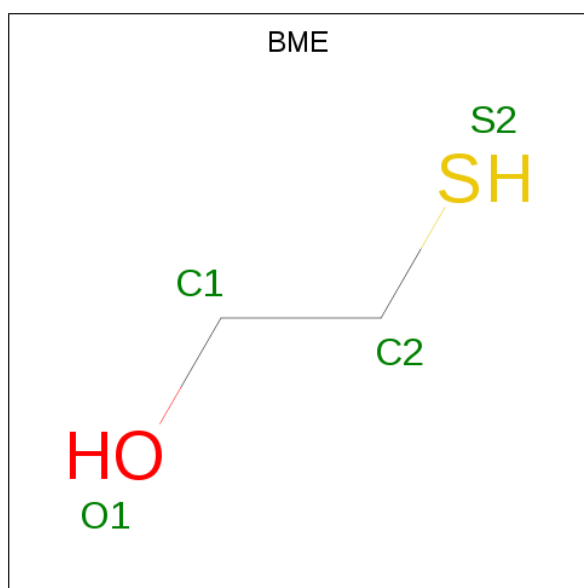
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	Total 5	O 4	S 1	0	0
2	A	1	Total 5	O 4	S 1	0	0
2	A	1	Total 5	O 4	S 1	0	0

*Continued on next page...*

Continued from previous page...

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

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

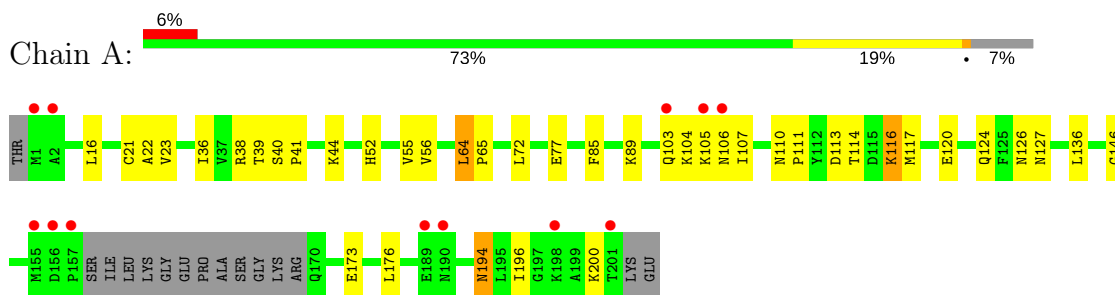
- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	93	Total 93	O 93	0	0
4	B	79	Total 79	O 79	0	0
4	C	70	Total 70	O 70	0	0

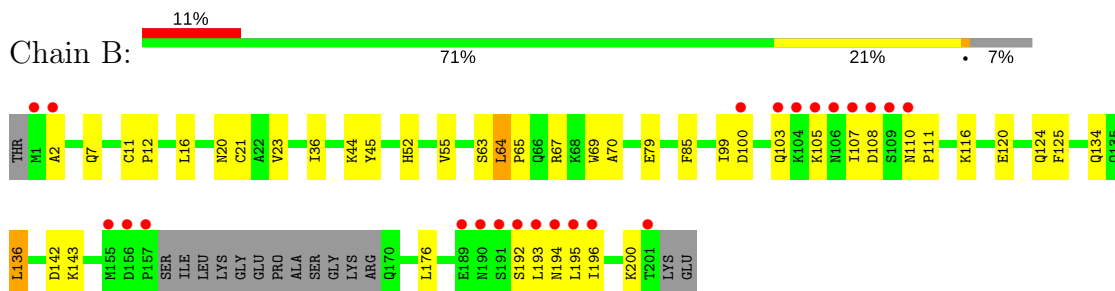
### 3 Residue-property plots [i](#)

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.

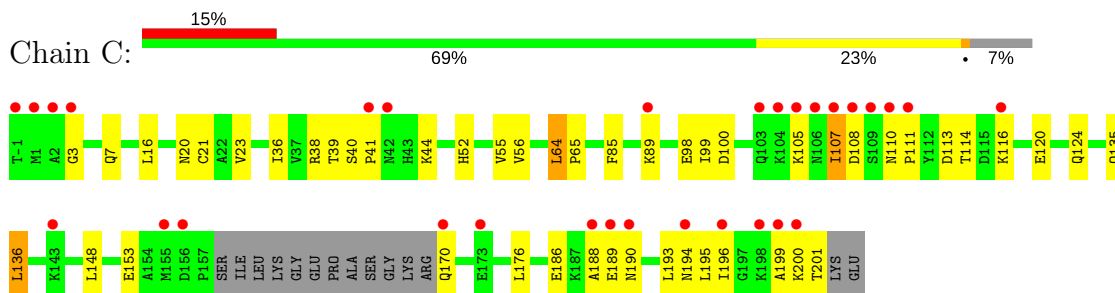
- Molecule 1: PROTEIN (N-ETHYLMALEIMIDE SENSITIVE FUSION PROTEIN (NSF))



- Molecule 1: PROTEIN (N-ETHYLMALEIMIDE SENSITIVE FUSION PROTEIN (NSF))



- Molecule 1: PROTEIN (N-ETHYLMALEIMIDE SENSITIVE FUSION PROTEIN (NSF))



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.90Å 101.90Å 126.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 29.95 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-2.30) 94.1 (29.95-2.30)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.09 (at 2.31Å)	Xtrriage
Refinement program	CNS 0.5	Depositor
R, $R_{free}$	0.220 , 0.260 0.221 , 0.260	Depositor DCC
$R_{free}$ test set	1675 reflections (5.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.1	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4742	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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: SO4, BME

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	0.35	0/1501	0.61	1/2024 (0.0%)
1	B	0.35	0/1509	0.61	0/2035
1	C	0.33	0/1525	0.60	0/2057
All	All	0.34	0/4535	0.61	1/6116 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	ALA	N-CA-C	-5.10	97.24	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	1472	0	1465	32	0
1	B	1476	0	1469	36	0
1	C	1488	0	1478	41	0
2	A	15	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
3	A	8	0	10	2	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	8	0	10	2	0
3	C	8	0	10	2	0
4	A	93	0	0	2	1
4	B	79	0	0	1	0
4	C	70	0	0	2	1
All	All	4742	0	4442	102	2

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 11.

All (102) 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)
1:C:85:PHE:HB3	3:C:401:BME:H12	1.47	0.96
1:A:85:PHE:HB3	3:A:401:BME:H12	1.44	0.95
1:B:85:PHE:HB3	3:B:401:BME:H12	1.46	0.94
1:C:38:ARG:HH21	1:C:44:LYS:HE2	1.38	0.86
1:A:21:CYS:O	3:A:400:BME:H12	1.79	0.82
1:B:20[B]:ASN:OD1	1:B:136:LEU:HD22	1.81	0.81
1:B:21:CYS:O	3:B:400:BME:H12	1.81	0.79
1:C:135:GLN:NE2	1:C:148:LEU:HB2	1.98	0.78
1:C:21:CYS:O	3:C:400:BME:H12	1.83	0.78
1:A:89:LYS:HG3	4:A:525:HOH:O	1.89	0.73
1:B:2:ALA:HB1	1:B:79:GLU:OE2	1.89	0.73
1:C:107:ILE:O	1:C:107:ILE:HG12	1.89	0.72
1:C:135:GLN:HE21	1:C:148:LEU:HD13	1.58	0.69
1:C:38:ARG:HH21	1:C:44:LYS:CE	2.05	0.69
1:C:135:GLN:HE22	1:C:148:LEU:HB2	1.58	0.68
1:C:23:VAL:HG12	1:C:55:VAL:HG21	1.76	0.67
1:B:23:VAL:HG12	1:B:55:VAL:HG21	1.75	0.66
1:A:38:ARG:NH2	1:A:44:LYS:HE3	2.14	0.63
1:C:113:ASP:HA	1:C:196:ILE:HG13	1.80	0.63
1:A:23:VAL:HG12	1:A:55:VAL:HG21	1.81	0.62
1:C:41:PRO:HA	4:C:547:HOH:O	1.99	0.62
1:B:111:PRO:HB3	1:B:194:ASN:ND2	2.14	0.61
1:A:38:ARG:HH21	1:A:44:LYS:HE3	1.65	0.61
1:C:111:PRO:CA	1:C:194:ASN:HD22	2.14	0.60
1:A:105:LYS:HD3	1:A:105:LYS:O	2.02	0.60
1:C:111:PRO:HB2	1:C:196:ILE:HD13	1.85	0.58
1:C:111:PRO:HA	1:C:194:ASN:HD22	1.67	0.58
1:A:113:ASP:O	1:A:117:MET:HG3	2.04	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:VAL:CG1	1:B:124:GLN:HB3	2.36	0.56
1:B:111:PRO:HB3	1:B:194:ASN:HD22	1.71	0.56
1:A:120:GLU:O	1:A:124:GLN:HG2	2.06	0.56
1:C:38:ARG:NH2	1:C:44:LYS:HE2	2.15	0.55
1:A:114:THR:HG21	1:A:200:LYS:HG2	1.89	0.55
1:C:100:ASP:OD2	1:C:188:ALA:HB3	2.05	0.55
1:C:20[B]:ASN:ND2	1:C:136:LEU:HD22	2.22	0.54
1:A:104:LYS:O	1:A:107:ILE:HG13	2.07	0.54
1:A:103:GLN:HB2	1:A:106:ASN:ND2	2.22	0.54
1:C:120:GLU:O	1:C:124:GLN:HG2	2.08	0.54
1:A:56:VAL:HG13	1:B:124:GLN:HB3	1.90	0.53
1:C:110:ASN:O	1:C:194:ASN:HB3	2.09	0.53
1:B:36:ILE:HD11	1:B:44:LYS:HD3	1.90	0.53
1:C:186:GLU:HB3	1:C:201:THR:OG1	2.09	0.53
1:B:107:ILE:HG21	1:B:192:SER:HB2	1.91	0.52
1:B:120:GLU:O	1:B:124:GLN:HG2	2.10	0.51
1:B:111:PRO:HB2	1:B:196:ILE:HD13	1.92	0.51
1:A:36:ILE:HD11	1:A:44:LYS:HB3	1.92	0.50
1:C:99:ILE:HG12	1:C:100:ASP:N	2.26	0.50
1:C:89:LYS:HG3	4:C:533:HOH:O	2.12	0.50
1:B:69:TRP:CE3	1:B:134:GLN:HG3	2.47	0.50
1:B:193:LEU:HD22	1:B:195:LEU:CD1	2.41	0.50
1:B:99:ILE:HG12	1:B:100:ASP:N	2.27	0.49
1:A:111:PRO:HB2	1:A:196:ILE:HD13	1.95	0.49
1:A:146:GLY:HA3	4:A:577:HOH:O	2.11	0.49
1:A:56:VAL:HG13	1:B:124:GLN:CB	2.42	0.49
1:B:64:LEU:HB3	1:B:65:PRO:HD3	1.95	0.49
1:C:114:THR:OG1	1:C:199:ALA:HB3	2.13	0.49
1:A:40:SER:HB2	1:A:41:PRO:HD2	1.95	0.48
1:A:39:THR:HG22	1:A:72:LEU:HD21	1.94	0.48
1:A:120:GLU:OE1	1:C:7:GLN:NE2	2.47	0.48
1:B:195:LEU:N	1:B:195:LEU:HD12	2.28	0.48
1:B:108:ASP:OD2	1:B:110:ASN:HB2	2.14	0.47
1:B:16:LEU:HD11	1:B:52:HIS:CD2	2.49	0.47
1:B:7[B]:GLN:HG2	4:B:560:HOH:O	2.15	0.47
1:A:103:GLN:HB2	1:A:106:ASN:HD22	1.80	0.46
1:A:36:ILE:CG1	1:A:44:LYS:HB3	2.44	0.46
1:B:36:ILE:HD11	1:B:44:LYS:HB3	1.97	0.46
1:B:195:LEU:O	1:B:200:LYS:HE3	2.15	0.46
1:B:193:LEU:HD22	1:B:195:LEU:HD12	1.97	0.46
1:B:20[A]:ASN:ND2	1:B:125:PHE:CZ	2.83	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:LEU:HD11	1:A:52:HIS:CD2	2.51	0.46
1:C:99:ILE:HG23	1:C:193:LEU:HD13	1.98	0.46
1:C:195:LEU:HB3	1:C:200:LYS:HE2	1.98	0.45
1:C:16:LEU:HD11	1:C:52:HIS:CD2	2.51	0.45
1:B:63:SER:O	1:B:67:ARG:HG3	2.16	0.45
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.98	0.45
1:A:124:GLN:HB3	1:C:56:VAL:HG13	1.98	0.45
1:B:69:TRP:CD2	1:B:134:GLN:HG3	2.51	0.45
1:C:99:ILE:CG1	1:C:100:ASP:N	2.80	0.44
1:C:186:GLU:HG3	1:C:186:GLU:O	2.17	0.44
1:B:103:GLN:C	1:B:105:LYS:N	2.70	0.44
1:B:103:GLN:C	1:B:105:LYS:H	2.21	0.43
1:A:126:ASN:O	1:A:127:ASN:HB2	2.18	0.43
1:C:189:GLU:O	1:C:190:ASN:HB2	2.19	0.42
1:B:45:TYR:CZ	1:B:70:ALA:HA	2.55	0.42
1:A:110:ASN:O	1:A:194:ASN:HB3	2.20	0.42
1:A:113:ASP:OD1	1:A:116:LYS:HE3	2.19	0.42
1:C:64:LEU:HB3	1:C:65:PRO:HD3	2.01	0.42
1:C:110:ASN:HB3	1:C:111:PRO:HD2	2.01	0.42
1:B:142:ASP:C	1:B:143:LYS:HD2	2.40	0.42
1:C:98:GLU:HA	1:C:186:GLU:O	2.19	0.42
1:A:36:ILE:HD11	1:A:44:LYS:CB	2.50	0.42
1:B:99:ILE:CG1	1:B:100:ASP:N	2.83	0.41
1:C:111:PRO:HA	1:C:194:ASN:ND2	2.34	0.41
1:B:7[A]:GLN:NE2	1:C:120:GLU:OE1	2.52	0.41
1:B:200:LYS:NZ	1:B:200:LYS:HB2	2.36	0.41
1:C:64:LEU:CB	1:C:65:PRO:HD3	2.51	0.41
1:A:120:GLU:HG2	1:A:124:GLN:HE21	1.86	0.41
1:C:153:GLU:HA	1:C:170:GLN:O	2.21	0.41
1:A:124:GLN:HB3	1:C:56:VAL:CG1	2.51	0.41
1:C:36:ILE:HD11	1:C:44:LYS:HD3	2.02	0.40
1:B:11:CYS:HA	1:B:12:PRO:HD3	1.97	0.40
1:C:39:THR:O	1:C:40:SER:HB3	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:516:HOH:O	4:C:516:HOH:O[7_555]	1.04	1.16
4:A:553:HOH:O	4:A:553:HOH:O[7_555]	1.67	0.53

## 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	186/204 (91%)	182 (98%)	4 (2%)	0	100	100
1	B	187/204 (92%)	178 (95%)	9 (5%)	0	100	100
1	C	189/204 (93%)	178 (94%)	7 (4%)	4 (2%)	8	6
All	All	562/612 (92%)	538 (96%)	20 (4%)	4 (1%)	24	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	105	LYS
1	C	108	ASP
1	C	107	ILE
1	C	3	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	164/175 (94%)	156 (95%)	8 (5%)	27	38
1	B	165/175 (94%)	161 (98%)	4 (2%)	52	69
1	C	167/175 (95%)	163 (98%)	4 (2%)	52	69
All	All	496/525 (94%)	480 (97%)	16 (3%)	43	58

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	LEU
1	A	77	GLU
1	A	116	LYS
1	A	136	LEU
1	A	173[A]	GLU
1	A	173[B]	GLU
1	A	176	LEU
1	A	194	ASN
1	B	64	LEU
1	B	116	LYS
1	B	136	LEU
1	B	176	LEU
1	C	64	LEU
1	C	116	LYS
1	C	136	LEU
1	C	176	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	126	ASN
1	A	127	ASN
1	A	182	GLN
1	A	194	ASN
1	B	43	HIS
1	B	126	ASN
1	B	127	ASN
1	B	135	GLN
1	B	194	ASN
1	C	7	GLN
1	C	135	GLN
1	C	194	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](#)

14 ligands are modelled in this entry.

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	BME	A	400	1	3,3,3	0.51	0	1,2,2	1.72	0
3	BME	A	401	1	3,3,3	0.49	0	1,2,2	1.34	0
2	SO4	A	501	-	4,4,4	0.36	0	6,6,6	0.13	0
2	SO4	A	502	-	4,4,4	0.38	0	6,6,6	0.12	0
2	SO4	A	505	-	4,4,4	0.35	0	6,6,6	0.08	0
3	BME	B	400	1	3,3,3	0.57	0	1,2,2	1.61	0
3	BME	B	401	1	3,3,3	0.49	0	1,2,2	1.29	0
2	SO4	B	503	-	4,4,4	0.34	0	6,6,6	0.06	0
2	SO4	B	506	-	4,4,4	0.34	0	6,6,6	0.07	0
2	SO4	B	507	-	4,4,4	0.34	0	6,6,6	0.11	0
3	BME	C	400	1	3,3,3	0.64	0	1,2,2	1.63	0
3	BME	C	401	1	3,3,3	0.44	0	1,2,2	1.21	0
2	SO4	C	504	-	4,4,4	0.38	0	6,6,6	0.09	0
2	SO4	C	508	-	4,4,4	0.33	0	6,6,6	0.11	0

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	BME	A	400	1	-	0/1/1/1	0/0/0/0
3	BME	A	401	1	-	0/1/1/1	0/0/0/0
2	SO4	A	501	-	-	0/0/0/0	0/0/0/0
2	SO4	A	502	-	-	0/0/0/0	0/0/0/0
2	SO4	A	505	-	-	0/0/0/0	0/0/0/0
3	BME	B	400	1	-	0/1/1/1	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BME	B	401	1	-	0/1/1/1	0/0/0/0
2	SO4	B	503	-	-	0/0/0/0	0/0/0/0
2	SO4	B	506	-	-	0/0/0/0	0/0/0/0
2	SO4	B	507	-	-	0/0/0/0	0/0/0/0
3	BME	C	400	1	-	0/1/1/1	0/0/0/0
3	BME	C	401	1	-	0/1/1/1	0/0/0/0
2	SO4	C	504	-	-	0/0/0/0	0/0/0/0
2	SO4	C	508	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	400	BME	1	0
3	A	401	BME	1	0
3	B	400	BME	1	0
3	B	401	BME	1	0
3	C	400	BME	1	0
3	C	401	BME	1	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

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	189/204 (92%)	0.17	12 (6%) 20 26	15, 28, 54, 63	0
1	B	189/204 (92%)	0.44	23 (12%) 4 6	15, 28, 65, 82	0
1	C	190/204 (93%)	0.51	30 (15%) 2 2	15, 32, 76, 87	0
All	All	568/612 (92%)	0.37	65 (11%) 5 7	15, 30, 66, 87	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	106	ASN	5.6
1	B	190	ASN	5.5
1	C	1	MET	4.8
1	C	-1	THR	4.7
1	B	107	ILE	4.5
1	C	107	ILE	4.4
1	B	156	ASP	4.3
1	B	105	LYS	4.2
1	C	196	ILE	4.1
1	B	109	SER	4.1
1	C	111	PRO	3.9
1	C	105	LYS	3.9
1	C	155	MET	3.9
1	B	108	ASP	3.9
1	B	155	MET	3.9
1	C	103	GLN	3.7
1	C	198	LYS	3.7
1	C	190	ASN	3.6
1	C	104	LYS	3.6
1	A	103	GLN	3.6
1	B	157	PRO	3.6
1	B	106	ASN	3.5
1	B	192	SER	3.4

*Continued on next page...*



*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	1	MET	3.4
1	B	104	LYS	3.4
1	B	110	ASN	3.3
1	B	103	GLN	3.3
1	B	194	ASN	3.3
1	C	194	ASN	3.2
1	B	193	LEU	3.2
1	A	2	ALA	3.2
1	A	156	ASP	3.2
1	C	2	ALA	3.1
1	A	190	ASN	3.1
1	B	195	LEU	3.1
1	B	201	THR	3.1
1	C	42	ASN	3.0
1	A	157	PRO	2.9
1	B	189	GLU	2.9
1	C	156	ASP	2.9
1	B	2	ALA	2.8
1	A	105	LYS	2.8
1	C	199	ALA	2.8
1	C	173	GLU	2.8
1	C	89	LYS	2.7
1	A	1	MET	2.7
1	A	155	MET	2.7
1	C	110	ASN	2.7
1	C	189	GLU	2.6
1	A	189	GLU	2.6
1	A	201	THR	2.5
1	A	198	LYS	2.5
1	C	200	LYS	2.4
1	C	109	SER	2.4
1	C	188	ALA	2.3
1	C	3	GLY	2.3
1	C	116	LYS	2.3
1	C	143	LYS	2.2
1	B	196	ILE	2.2
1	A	106	ASN	2.2
1	C	41	PRO	2.1
1	B	100	ASP	2.1
1	C	108	ASP	2.0
1	C	170	GLN	2.0
1	B	191	SER	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	503	5/5	0.86	0.17	74,75,75,76	0
2	SO4	B	507	5/5	0.88	0.27	89,89,90,90	0
2	SO4	B	506	5/5	0.93	0.16	76,77,77,77	0
3	BME	C	400	4/4	0.93	0.15	25,25,26,30	0
3	BME	C	401	4/4	0.94	0.13	26,26,28,30	0
2	SO4	A	505	5/5	0.95	0.13	68,69,69,70	0
3	BME	B	401	4/4	0.95	0.13	27,27,28,28	0
2	SO4	C	504	5/5	0.96	0.12	52,53,54,54	0
3	BME	B	400	4/4	0.96	0.18	24,25,27,29	0
2	SO4	A	501	5/5	0.96	0.11	41,41,42,43	0
2	SO4	C	508	5/5	0.96	0.28	93,93,94,94	0
3	BME	A	401	4/4	0.97	0.12	24,27,27,29	0
3	BME	A	400	4/4	0.97	0.16	20,23,26,30	0
2	SO4	A	502	5/5	0.99	0.09	20,20,21,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.