



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 07:13 pm GMT

PDB ID : 2XR1
Title : DIMERIC ARCHAEL CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR WITH N-TERMINAL KH DOMAINS (KH-CPSF) FROM METHANOSARCINA MAZEI
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Deposited on : 2010-09-08
Resolution : 2.59 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

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
Xtriage (Phenix) : 1.13
EDS : trunk30967
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) : trunk30967

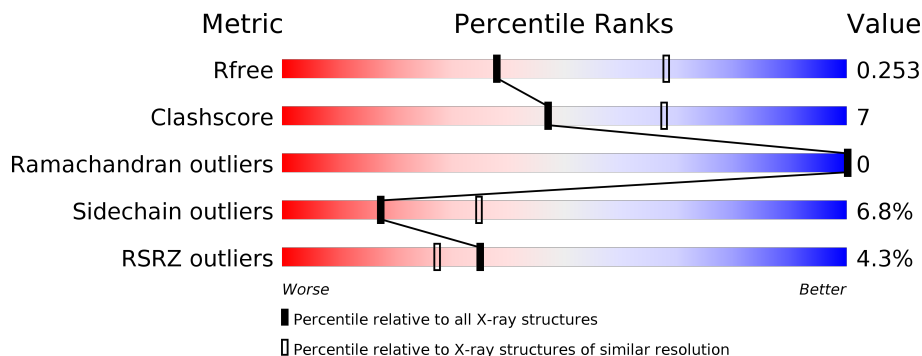
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

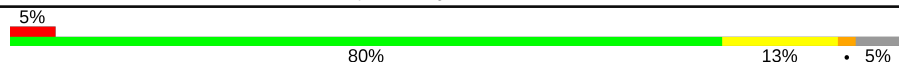

The reported resolution of this entry is 2.59 Å.

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	2767 (2.60-2.60)
Clashscore	122126	3110 (2.60-2.60)
Ramachandran outliers	120053	3062 (2.60-2.60)
Sidechain outliers	120020	3062 (2.60-2.60)
RSRZ outliers	108989	2706 (2.60-2.60)

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 ≥ 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	640	 5% 80% 13% • 5%
1	B	640	 3% 79% 14% • 5%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 9391 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 CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 100 KD SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	605	Total 4640	C 2964	N 791	O 864	S 21	0	1	0
1	B	611	Total 4705	C 3008	N 797	O 875	S 25	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q8PZ03
A	-1	SER	-	expression tag	UNP Q8PZ03
A	0	HIS	-	expression tag	UNP Q8PZ03
B	-2	GLY	-	expression tag	UNP Q8PZ03
B	-1	SER	-	expression tag	UNP Q8PZ03
B	0	HIS	-	expression tag	UNP Q8PZ03

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total 2	Zn 2	0	0
2	A	2	Total 2	Zn 2	0	0

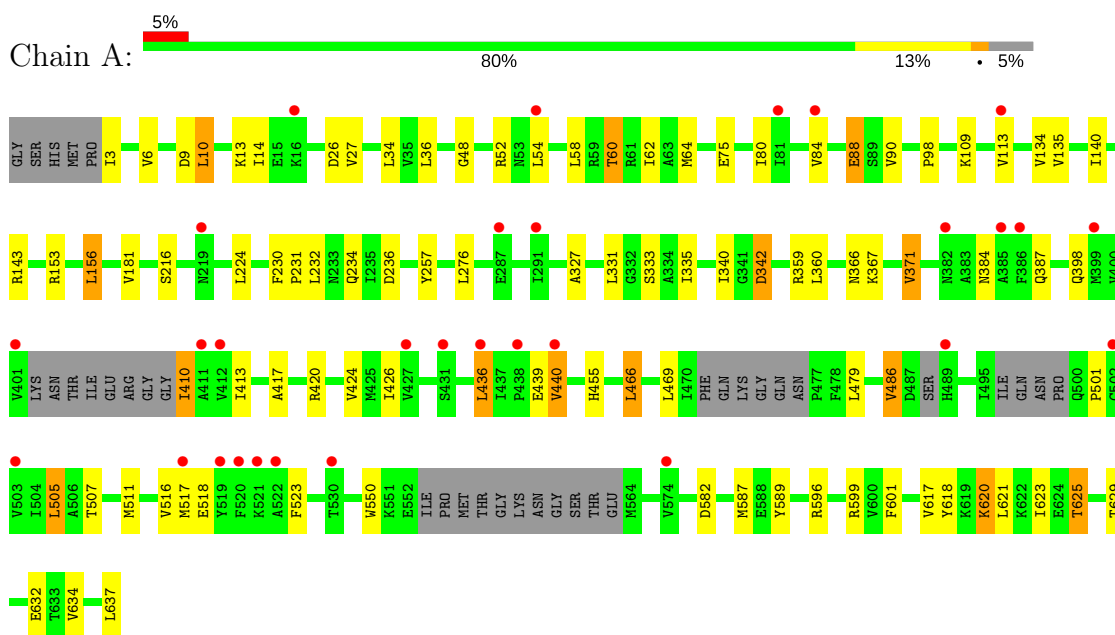
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	16	Total 16	O 16	0	0
3	B	26	Total 26	O 26	0	0

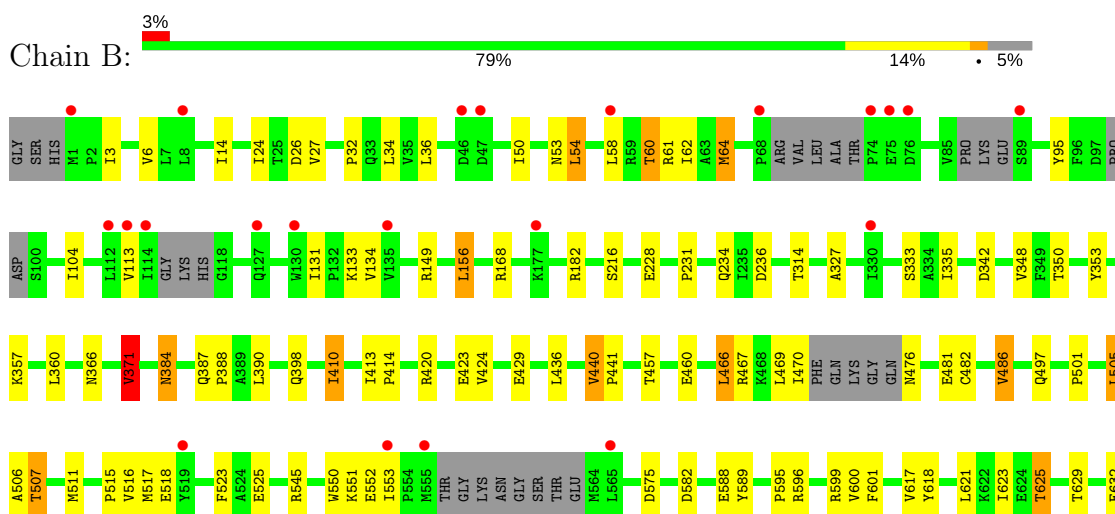
3 Residue-property plots [i](#)

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: CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 100 KD SUB-UNIT



• Molecule 1: CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 100 KD SUB-UNIT





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.66Å 97.72Å 90.72Å 90.00° 98.26° 90.00°	Depositor
Resolution (Å)	38.43 – 2.59 38.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.9 (38.43-2.59) 98.9 (38.43-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.209 , 0.267 0.204 , 0.253	Depositor DCC
R_{free} test set	2023 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtrriage
Anisotropy	0.061	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9391	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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:
ZN

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	0.67	0/4741	0.72	2/6450 (0.0%)
1	B	0.80	3/4807 (0.1%)	0.76	2/6529 (0.0%)
All	All	0.74	3/9548 (0.0%)	0.74	4/12979 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	482	CYS	CB-SG	6.76	1.93	1.82
1	B	423	GLU	CG-CD	6.09	1.61	1.51
1	B	588	GLU	CG-CD	5.48	1.60	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	371	VAL	CB-CA-C	-6.41	99.23	111.40
1	A	342	ASP	CB-CG-OD1	-6.30	112.63	118.30
1	A	371	VAL	CB-CA-C	-6.15	99.71	111.40
1	B	182	ARG	NE-CZ-NH2	-5.21	117.70	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	384	ASN	Peptide

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	4640	0	4523	57	0
1	B	4705	0	4597	67	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	16	0	0	0	0
3	B	26	0	0	0	0
All	All	9391	0	9120	124	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 7.

All (124) 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:B:410:ILE:HG22	1:B:501:PRO:HA	1.42	1.00
1:B:516:VAL:HG13	1:B:517:MET:HE2	1.53	0.90
1:A:360:LEU:HD23	1:A:466:LEU:HD12	1.57	0.86
1:A:516:VAL:HG13	1:A:517:MET:HE2	1.57	0.85
1:B:413:ILE:HB	1:B:505:LEU:HD12	1.61	0.80
1:A:360:LEU:HD23	1:A:466:LEU:CD1	2.14	0.77
1:B:360:LEU:HD23	1:B:466:LEU:CD1	2.16	0.76
1:B:360:LEU:HD23	1:B:466:LEU:HD12	1.68	0.75
1:A:398:GLN:NE2	1:A:436:LEU:HD23	2.06	0.71
1:A:413:ILE:HB	1:A:505:LEU:HD12	1.72	0.70
1:B:231:PRO:HD2	1:B:234:GLN:NE2	2.09	0.68
1:A:360:LEU:CD2	1:A:466:LEU:HD12	2.23	0.68
1:B:231:PRO:HD2	1:B:234:GLN:HE21	1.59	0.66
1:A:231:PRO:HD2	1:A:234:GLN:NE2	2.10	0.66
1:A:231:PRO:HD2	1:A:234:GLN:HE21	1.60	0.66
1:A:156:LEU:HD22	1:A:156:LEU:O	1.96	0.65
1:A:410:ILE:HG22	1:A:501:PRO:HA	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:VAL:HG22	1:B:441:PRO:HD2	1.79	0.64
1:B:511:MET:HB3	1:B:517:MET:HE3	1.80	0.64
1:A:98:PRO:HB2	1:A:156:LEU:HD21	1.82	0.62
1:B:113:VAL:CG1	1:B:134:VAL:HG11	2.30	0.61
1:A:3:ILE:O	1:A:6:VAL:HG22	2.01	0.61
1:B:507:THR:HG22	1:B:515:PRO:HD2	1.83	0.61
1:A:601:PHE:CZ	1:A:634:VAL:HG11	2.36	0.60
1:B:27:VAL:HG13	1:B:34:LEU:HD11	1.85	0.59
1:B:516:VAL:HG13	1:B:517:MET:CE	2.31	0.58
1:B:113:VAL:HG13	1:B:134:VAL:HG11	1.86	0.58
1:A:439:GLU:O	1:A:440:VAL:HG23	2.04	0.58
1:A:58:LEU:O	1:A:60:THR:HG23	2.04	0.57
1:A:398:GLN:CD	1:A:436:LEU:HD23	2.24	0.57
1:A:88:GLU:O	1:A:90:VAL:HG23	2.05	0.56
1:A:360:LEU:CD2	1:A:466:LEU:CD1	2.82	0.56
1:A:587:MET:CE	1:A:620:LYS:HE2	2.36	0.56
1:B:3:ILE:O	1:B:6:VAL:HG22	2.05	0.56
1:B:601:PHE:CZ	1:B:634:VAL:HG11	2.41	0.56
1:A:623:ILE:O	1:A:625:THR:HG23	2.05	0.56
1:A:587:MET:HE1	1:A:620:LYS:HE2	1.88	0.56
1:A:14:ILE:HG12	1:A:54:LEU:HD21	1.87	0.55
1:A:48:GLY:HA3	1:A:52:ARG:NH2	2.22	0.55
1:B:50:ILE:HG22	1:B:54:LEU:HD22	1.89	0.53
1:A:410:ILE:HD11	1:A:523:PHE:CD2	2.43	0.53
1:B:58:LEU:O	1:B:60:THR:HG22	2.09	0.53
1:A:617:VAL:CG1	1:A:625:THR:HG21	2.39	0.53
1:B:552:GLU:C	1:B:553:ILE:HD12	2.28	0.53
1:B:3:ILE:HG21	1:B:168:ARG:HD3	1.92	0.52
1:A:113:VAL:CG1	1:A:134:VAL:HG11	2.40	0.52
1:A:398:GLN:HE22	1:A:436:LEU:HD23	1.73	0.52
1:B:420:ARG:O	1:B:424:VAL:HG23	2.09	0.52
1:B:64:MET:CE	1:B:131:ILE:HD11	2.40	0.51
1:B:511:MET:CB	1:B:517:MET:HE3	2.40	0.51
1:B:617:VAL:CG1	1:B:625:THR:HG21	2.40	0.51
1:B:410:ILE:HG22	1:B:501:PRO:CA	2.28	0.51
1:A:58:LEU:HD12	1:A:62:ILE:HD11	1.92	0.51
1:B:156:LEU:O	1:B:156:LEU:HD22	2.11	0.51
1:A:335:ILE:HD13	1:A:589:TYR:OH	2.11	0.50
1:B:623:ILE:O	1:B:625:THR:HG23	2.11	0.50
1:B:360:LEU:HD23	1:B:466:LEU:HD11	1.92	0.49
1:A:420:ARG:O	1:A:424:VAL:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:PRO:HB3	1:B:314:THR:HG23	1.94	0.49
1:A:623:ILE:O	1:A:625:THR:CG2	2.61	0.49
1:B:457:THR:CG2	1:B:457:THR:O	2.59	0.49
1:B:617:VAL:HG13	1:B:621:LEU:HD12	1.94	0.49
1:B:14:ILE:HG21	1:B:24:ILE:HD13	1.95	0.49
1:B:470:ILE:HA	1:B:476:ASN:ND2	2.26	0.49
1:A:224:LEU:O	1:A:230:PHE:CE1	2.66	0.49
1:B:553:ILE:N	1:B:553:ILE:HD12	2.27	0.48
1:B:348:VAL:HG23	1:B:371:VAL:HG13	1.96	0.48
1:B:387:GLN:HG2	1:B:582:ASP:HB3	1.95	0.48
1:A:113:VAL:HG13	1:A:134:VAL:HG11	1.94	0.48
1:B:486:VAL:HG22	1:B:486:VAL:O	2.14	0.48
1:A:410:ILE:HD11	1:A:523:PHE:CE2	2.49	0.48
1:B:410:ILE:HD11	1:B:523:PHE:CE1	2.49	0.48
1:B:600:VAL:HG22	1:B:625:THR:HB	1.96	0.48
1:A:366:ASN:HB3	1:A:589:TYR:CE1	2.48	0.48
1:A:387:GLN:HG2	1:A:582:ASP:HB3	1.96	0.47
1:A:617:VAL:HG13	1:A:621:LEU:HD12	1.96	0.47
1:B:58:LEU:CD1	1:B:62:ILE:HD11	2.44	0.47
1:A:9:ASP:O	1:A:13:LYS:HB2	2.14	0.47
1:A:331:LEU:HD22	1:A:455:HIS:CG	2.49	0.47
1:A:156:LEU:CD2	1:A:156:LEU:O	2.63	0.47
1:A:327:ALA:HB3	1:A:333:SER:OG	2.15	0.47
1:B:366:ASN:HB3	1:B:589:TYR:CE1	2.49	0.47
1:A:27:VAL:HG13	1:A:34:LEU:HD11	1.96	0.47
1:A:80:ILE:O	1:A:84:VAL:HG23	2.15	0.47
1:A:232:LEU:HD12	1:A:257:TYR:O	2.15	0.46
1:B:231:PRO:CD	1:B:234:GLN:HE21	2.28	0.46
1:A:10:LEU:HD22	1:A:14:ILE:HD11	1.97	0.46
1:A:181:VAL:HG11	1:A:340:ILE:HD12	1.96	0.46
1:A:398:GLN:OE1	1:A:436:LEU:HD23	2.15	0.46
1:B:360:LEU:CD2	1:B:466:LEU:HD12	2.42	0.46
1:B:104:ILE:HD13	1:B:133:LYS:HB2	1.97	0.46
1:B:228:GLU:OE1	1:B:228:GLU:N	2.49	0.46
1:B:371:VAL:HG23	1:B:595:PRO:HD2	1.99	0.45
1:A:466:LEU:HD23	1:A:466:LEU:HA	1.74	0.45
1:A:511:MET:HB3	1:A:517:MET:HE3	1.98	0.45
1:B:64:MET:HE3	1:B:131:ILE:HD11	1.99	0.45
1:A:629:THR:HB	1:A:632:GLU:HG3	1.99	0.45
1:A:98:PRO:HB2	1:A:156:LEU:CD2	2.47	0.45
1:A:276:LEU:HD21	1:A:417:ALA:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:LEU:CD2	1:B:466:LEU:CD1	2.93	0.44
1:A:27:VAL:HG22	1:A:36:LEU:CD2	2.48	0.44
1:B:95:TYR:CE1	1:B:149:ARG:HB3	2.52	0.43
1:B:27:VAL:HG22	1:B:36:LEU:CD2	2.49	0.43
1:B:457:THR:HG22	1:B:457:THR:O	2.17	0.43
1:B:335:ILE:HD13	1:B:589:TYR:OH	2.18	0.43
1:B:58:LEU:HD12	1:B:62:ILE:HD11	1.99	0.43
1:B:414:PRO:HA	1:B:506:ALA:O	2.18	0.42
1:B:60:THR:OG1	1:B:61:ARG:N	2.52	0.42
1:B:623:ILE:O	1:B:625:THR:CG2	2.67	0.42
1:B:637:LEU:O	1:B:637:LEU:HD22	2.20	0.42
1:A:140:ILE:HG12	1:A:479:LEU:HD21	2.02	0.42
1:B:53:ASN:HA	1:B:53:ASN:HD22	1.68	0.42
1:B:398:GLN:NE2	1:B:436:LEU:HD23	2.34	0.42
1:A:27:VAL:HG22	1:A:36:LEU:HD22	2.02	0.41
1:B:327:ALA:HB3	1:B:333:SER:OG	2.20	0.41
1:B:440:VAL:CG2	1:B:501:PRO:O	2.68	0.41
1:B:32:PRO:HB3	1:B:314:THR:CG2	2.50	0.41
1:B:350:THR:HB	1:B:353:TYR:CD1	2.55	0.41
1:A:359:ARG:HG2	1:A:426:ILE:HG21	2.03	0.41
1:B:50:ILE:O	1:B:54:LEU:N	2.52	0.41
1:B:388:PRO:HD2	1:B:575:ASP:O	2.21	0.41
1:A:486:VAL:O	1:A:486:VAL:HG22	2.21	0.41
1:B:629:THR:HB	1:B:632:GLU:HG3	2.02	0.41
1:B:95:TYR:CZ	1:B:149:ARG:HG2	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	594/640 (93%)	567 (96%)	27 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	598/640 (93%)	570 (95%)	28 (5%)	0	100	100
All	All	1192/1280 (93%)	1137 (95%)	55 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	487/560 (87%)	454 (93%)	33 (7%)	17	35
1	B	495/560 (88%)	461 (93%)	34 (7%)	17	34
All	All	982/1120 (88%)	915 (93%)	67 (7%)	17	35

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	26	ASP
1	A	60	THR
1	A	64	MET
1	A	75	GLU
1	A	88	GLU
1	A	109	LYS
1	A	135	VAL
1	A	143	ARG
1	A	153	ARG
1	A	156	LEU
1	A	216	SER
1	A	236	ASP
1	A	342	ASP
1	A	367	LYS
1	A	371	VAL
1	A	384	ASN
1	A	410	ILE

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Mol	Chain	Res	Type
1	A	436	LEU
1	A	440	VAL
1	A	466	LEU
1	A	469	LEU
1	A	486	VAL
1	A	505	LEU
1	A	507	THR
1	A	518	GLU
1	A	550	TRP
1	A	596	ARG
1	A	599	ARG
1	A	618	TYR
1	A	620	LYS
1	A	625	THR
1	A	637	LEU
1	B	26	ASP
1	B	54	LEU
1	B	60	THR
1	B	64	MET
1	B	156	LEU
1	B	216	SER
1	B	236	ASP
1	B	342	ASP
1	B	357	LYS
1	B	371	VAL
1	B	384	ASN
1	B	390	LEU
1	B	410	ILE
1	B	429	GLU
1	B	440	VAL
1	B	460	GLU
1	B	466	LEU
1	B	467	ARG
1	B	469	LEU
1	B	481	GLU
1	B	486	VAL
1	B	497	GLN
1	B	505	LEU
1	B	507	THR
1	B	518	GLU
1	B	525	GLU
1	B	545	ARG

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Mol	Chain	Res	Type
1	B	550	TRP
1	B	551	LYS
1	B	596	ARG
1	B	599	ARG
1	B	618	TYR
1	B	625	THR
1	B	637	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
1	A	384	ASN
1	A	387	GLN
1	B	53	ASN
1	B	384	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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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, 95th 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 ²)	Q<0.9
1	A	605/640 (94%)	0.39	30 (4%) 29 22	28, 60, 121, 158	0
1	B	611/640 (95%)	0.25	22 (3%) 42 35	22, 46, 93, 119	0
All	All	1216/1280 (95%)	0.32	52 (4%) 35 27	22, 55, 107, 158	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	555	MET	5.1
1	A	520	PHE	5.0
1	A	411	ALA	4.1
1	B	8	LEU	3.9
1	A	440	VAL	3.8
1	A	431	SER	3.6
1	A	530	THR	3.5
1	A	517	MET	3.3
1	A	521	LYS	3.1
1	A	489	HIS	3.1
1	B	112	LEU	3.1
1	A	438	PRO	3.0
1	B	89	SER	3.0
1	B	47	ASP	2.9
1	B	76	ASP	2.9
1	A	81	ILE	2.9
1	A	427	VAL	2.9
1	B	75	GLU	2.9
1	A	385	ALA	2.9
1	B	114	ILE	2.8
1	B	130	TRP	2.7
1	B	68	PRO	2.7
1	B	46	ASP	2.6
1	A	401	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	553	ILE	2.6
1	A	113	VAL	2.6
1	B	74	PRO	2.6
1	B	177	LYS	2.6
1	A	399	MET	2.6
1	A	412	VAL	2.5
1	A	291	ILE	2.5
1	B	1	MET	2.5
1	A	436	LEU	2.5
1	A	502	CYS	2.4
1	B	113	VAL	2.4
1	B	565	LEU	2.4
1	B	330	ILE	2.4
1	A	16	LYS	2.3
1	A	522	ALA	2.3
1	B	519	TYR	2.3
1	A	503	VAL	2.2
1	A	219	ASN	2.2
1	A	84	VAL	2.2
1	A	574	VAL	2.2
1	A	382	ASN	2.2
1	A	386	PHE	2.1
1	B	135	VAL	2.1
1	A	54	LEU	2.1
1	B	58	LEU	2.1
1	A	287	GLU	2.1
1	A	519	TYR	2.0
1	B	127	GLN	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, 95th 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(\AA^2)	Q<0.9
2	ZN	A	1638	1/1	0.99	0.20	49,49,49,49	0
2	ZN	B	1638	1/1	0.99	0.18	34,34,34,34	0
2	ZN	A	1639	1/1	0.99	0.17	52,52,52,52	0
2	ZN	B	1639	1/1	0.99	0.16	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.