



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 01:30 pm BST

PDB ID : 5B7S
Title : Apo structure of Cysteine Desulfurase from Thermococcus onnurineus NA1
Authors : Ho, T.-H.; Kang, L.W.
Deposited on : 2016-06-08
Resolution : 2.58 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

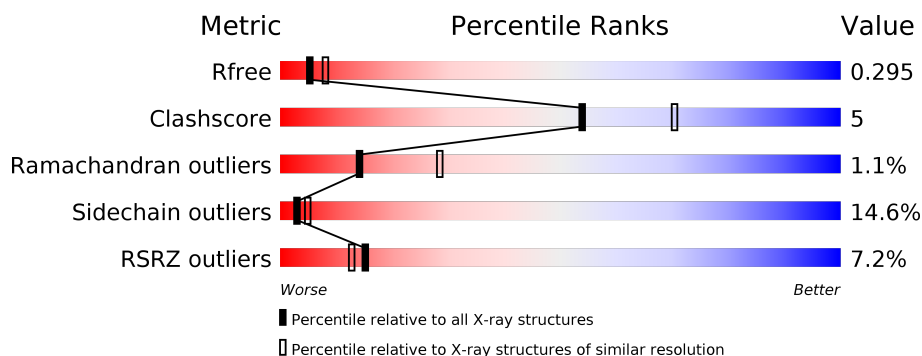
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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}	130704	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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 respectively. 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	419	<div> <div>7%</div> <div> <div></div> <div>73%</div> <div>17%</div> <div>5%</div> <div>5%</div> </div> </div>
1	B	419	<div> <div>7%</div> <div> <div></div> <div>77%</div> <div>16%</div> <div>• 5%</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6264 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 Cysteine desulfurase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	P	S	0	0	0
			3111	1982	538	581	1	9			
1	B	400	Total	C	N	O	P	S	0	0	0
			3040	1937	518	574	1	10			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP B6YT87
A	-18	HIS	-	expression tag	UNP B6YT87
A	-17	HIS	-	expression tag	UNP B6YT87
A	-16	HIS	-	expression tag	UNP B6YT87
A	-15	HIS	-	expression tag	UNP B6YT87
A	-14	HIS	-	expression tag	UNP B6YT87
A	-13	HIS	-	expression tag	UNP B6YT87
A	-12	SER	-	expression tag	UNP B6YT87
A	-11	SER	-	expression tag	UNP B6YT87
A	-10	GLU	-	expression tag	UNP B6YT87
A	-9	ASN	-	expression tag	UNP B6YT87
A	-8	LEU	-	expression tag	UNP B6YT87
A	-7	TYR	-	expression tag	UNP B6YT87
A	-6	PHE	-	expression tag	UNP B6YT87
A	-5	GLN	-	expression tag	UNP B6YT87
A	-4	GLY	-	expression tag	UNP B6YT87
A	-3	HIS	-	expression tag	UNP B6YT87
A	-2	MET	-	expression tag	UNP B6YT87
A	-1	ALA	-	expression tag	UNP B6YT87
A	0	SER	-	expression tag	UNP B6YT87
B	-19	MET	-	expression tag	UNP B6YT87
B	-18	HIS	-	expression tag	UNP B6YT87
B	-17	HIS	-	expression tag	UNP B6YT87
B	-16	HIS	-	expression tag	UNP B6YT87
B	-15	HIS	-	expression tag	UNP B6YT87

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP B6YT87
B	-13	HIS	-	expression tag	UNP B6YT87
B	-12	SER	-	expression tag	UNP B6YT87
B	-11	SER	-	expression tag	UNP B6YT87
B	-10	GLU	-	expression tag	UNP B6YT87
B	-9	ASN	-	expression tag	UNP B6YT87
B	-8	LEU	-	expression tag	UNP B6YT87
B	-7	TYR	-	expression tag	UNP B6YT87
B	-6	PHE	-	expression tag	UNP B6YT87
B	-5	GLN	-	expression tag	UNP B6YT87
B	-4	GLY	-	expression tag	UNP B6YT87
B	-3	HIS	-	expression tag	UNP B6YT87
B	-2	MET	-	expression tag	UNP B6YT87
B	-1	ALA	-	expression tag	UNP B6YT87
B	0	SER	-	expression tag	UNP B6YT87

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

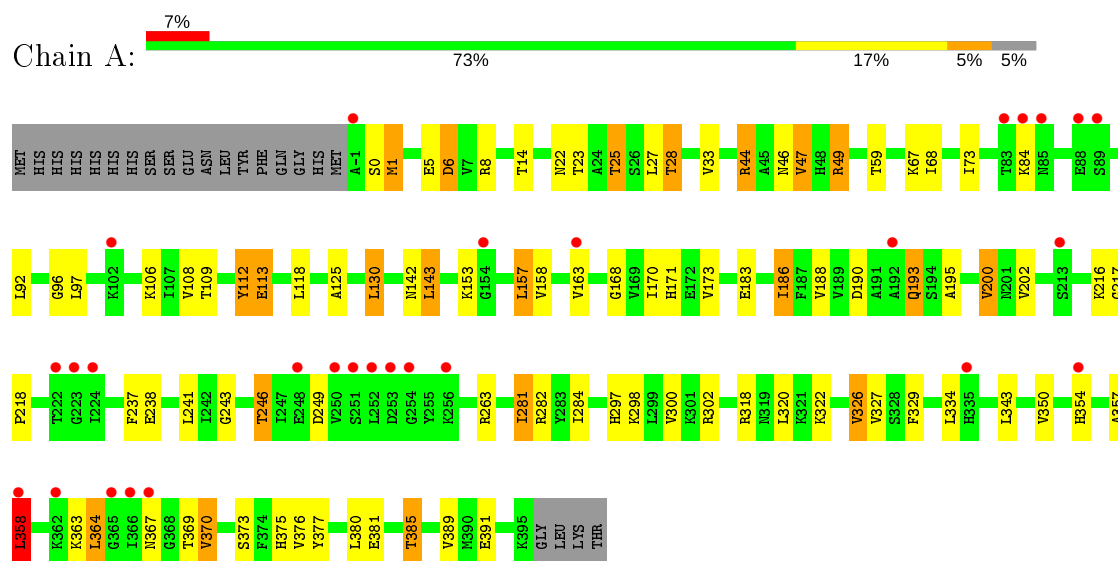
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total 57	O 57	0	0
3	B	44	Total 44	O 44	0	0

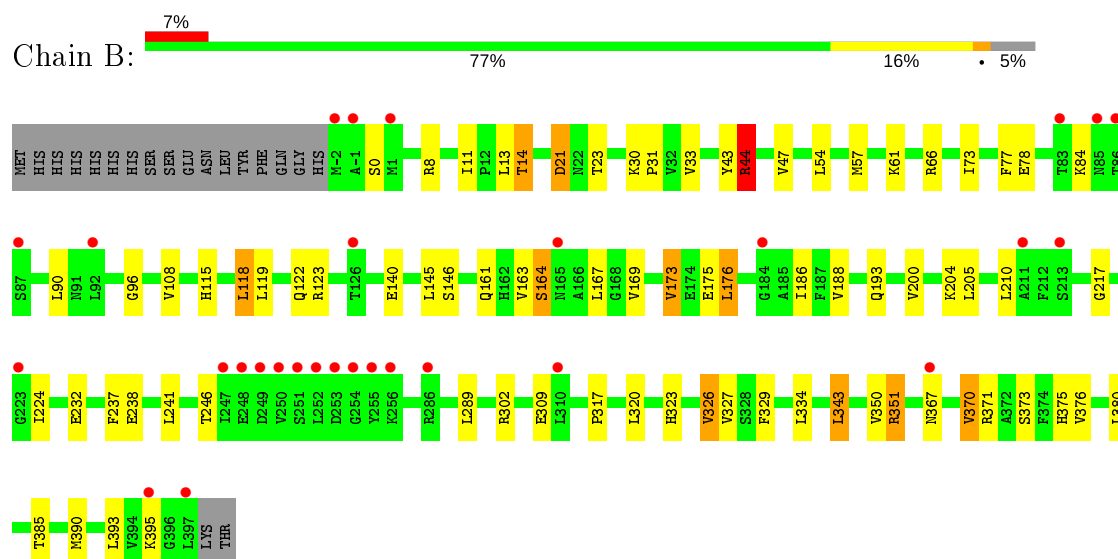
3 Residue-property plots [i](#)

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: Cysteine desulfurase



• Molecule 1: Cysteine desulfurase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.01Å 92.53Å 145.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.36 – 2.58 36.36 – 2.58	Depositor EDS
% Data completeness (in resolution range)	99.2 (36.36-2.58) 99.2 (36.36-2.58)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.20 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.203 , 0.295 0.208 , 0.295	Depositor DCC
R_{free} test set	1465 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6264	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, LLP

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	0.65	0/3153	0.92	7/4263 (0.2%)
1	B	0.61	0/3081	0.84	3/4187 (0.1%)
All	All	0.63	0/6234	0.88	10/8450 (0.1%)

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	A	0	2

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	44	ARG	NE-CZ-NH1	8.44	124.52	120.30
1	B	44	ARG	NE-CZ-NH2	-8.00	116.30	120.30
1	A	46	ASN	C-N-CA	6.62	138.26	121.70
1	A	47	VAL	CB-CA-C	6.32	123.40	111.40
1	A	113	GLU	N-CA-C	-6.19	94.30	111.00
1	A	44	ARG	NE-CZ-NH1	6.15	123.38	120.30
1	A	302	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	A	46	ASN	CA-C-N	5.20	128.65	117.20
1	B	21	ASP	CB-CG-OD1	5.11	122.90	118.30
1	A	357	ALA	N-CA-C	-5.03	97.42	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	0	SER	Peptide
1	A	112	TYR	Peptide

5.2 Too-close contacts ⓘ

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	3111	0	3107	37	0
1	B	3040	0	2939	31	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0
3	A	57	0	0	1	1
3	B	44	0	0	0	1
All	All	6264	0	6062	65	1

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 5.

All (65) 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:A:6:ASP:N	1:A:6:ASP:OD1	2.10	0.85
1:B:23:THR:HG23	1:B:373:SER:CB	2.20	0.71
1:B:23:THR:OG1	1:B:371:ARG:CZ	2.47	0.63
1:B:73:ILE:HD11	1:B:210:LEU:HD22	1.80	0.63
1:B:21:ASP:OD2	1:B:351:ARG:NH1	2.32	0.62
1:A:193:GLN:NE2	1:A:216:LLP:O3	2.32	0.62
1:A:153:LYS:HA	1:A:183:GLU:HG2	1.81	0.61
1:B:161:GLN:HE22	1:B:164:SER:HB2	1.66	0.60
1:A:193:GLN:HE22	1:A:216:LLP:C3	2.16	0.59
1:A:354:HIS:HB2	1:A:358:LEU:HD12	1.86	0.58
1:A:142:ASN:OD1	1:A:322:LYS:HE3	2.04	0.57
1:A:28:THR:CG2	1:B:44:ARG:HD3	2.35	0.57
1:A:23:THR:HG23	1:A:373:SER:CB	2.35	0.56
1:A:73:ILE:O	1:A:202:VAL:HG22	2.06	0.55
1:A:25:THR:OG1	1:B:44:ARG:NH2	2.41	0.53
1:A:193:GLN:HG3	3:A:548:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:343:LEU:HD21	1:B:390:MET:HE3	1.90	0.52
1:A:153:LYS:CA	1:A:183:GLU:HG2	2.38	0.52
1:A:375:HIS:CD2	1:A:376:VAL:H	2.27	0.52
1:A:363:LYS:HB3	1:A:364:LEU:HB2	1.92	0.52
1:A:5:GLU:O	1:A:8:ARG:HG3	2.10	0.52
1:A:297:HIS:HA	1:A:300:VAL:HG12	1.93	0.50
1:A:6:ASP:HA	1:A:8:ARG:H	1.75	0.50
1:B:140:GLU:CG	1:B:317:PRO:HA	2.42	0.50
1:B:23:THR:HG23	1:B:373:SER:HB3	1.94	0.50
1:B:8:ARG:HB3	1:B:14:THR:HG21	1.95	0.49
1:A:6:ASP:HA	1:A:8:ARG:N	2.27	0.49
1:B:23:THR:HG23	1:B:373:SER:HB2	1.93	0.48
1:B:11:ILE:O	1:B:14:THR:HB	2.14	0.48
1:A:125:ALA:HA	1:A:130:LEU:HB2	1.96	0.47
1:A:157:LEU:HB2	1:A:186:ILE:HG12	1.96	0.47
1:B:217:GLY:O	1:B:375:HIS:HE1	1.96	0.47
1:B:375:HIS:CD2	1:B:376:VAL:H	2.33	0.47
1:B:115:HIS:HA	1:B:118:LEU:CD2	2.44	0.46
1:B:78:GLU:H	1:B:78:GLU:CD	2.19	0.46
1:B:164:SER:HG	1:B:167:LEU:H	1.62	0.46
1:B:329:PHE:CZ	1:B:370:VAL:HG22	2.51	0.46
1:A:22:ASN:OD1	1:A:377:TYR:OH	2.25	0.45
1:A:28:THR:HG22	1:B:44:ARG:HD3	1.98	0.45
1:A:381:GLU:O	1:A:385:THR:HG23	2.16	0.45
1:A:217:GLY:O	1:A:375:HIS:HE1	1.99	0.45
1:B:43:TYR:OH	1:B:61:LYS:HG2	2.17	0.45
1:A:218:PRO:HA	1:A:284:ILE:CD1	2.46	0.45
1:A:96:GLY:HA3	1:A:237:PHE:CE1	2.52	0.44
1:A:195:ALA:HA	1:A:200:VAL:HG11	2.00	0.44
1:B:173:VAL:HA	1:B:176:LEU:HB2	1.99	0.43
1:B:323:HIS:HE1	1:B:326:VAL:O	2.00	0.43
1:B:96:GLY:HA3	1:B:237:PHE:CE1	2.52	0.43
1:A:68:ILE:HG22	1:A:281:ILE:HG12	2.00	0.43
1:B:115:HIS:HA	1:B:118:LEU:HD23	2.00	0.43
1:B:161:GLN:HE22	1:B:164:SER:CB	2.30	0.43
1:A:243:GLY:O	1:A:246:THR:HB	2.18	0.43
1:B:119:LEU:HA	1:B:122:GLN:HB2	2.00	0.43
1:A:143:LEU:HD22	1:A:171:HIS:CD2	2.54	0.43
1:A:157:LEU:CB	1:A:186:ILE:HG12	2.49	0.42
1:B:343:LEU:HD11	1:B:390:MET:HE3	2.00	0.42
1:A:190:ASP:OD2	1:A:216:LLP:N1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:PRO:HA	1:A:284:ILE:HD12	2.01	0.42
1:A:168:GLY:HA3	1:A:326:VAL:HG13	2.02	0.42
1:B:224:ILE:O	1:B:224:ILE:HG23	2.20	0.42
1:A:329:PHE:CZ	1:A:370:VAL:HG22	2.55	0.41
1:A:108:VAL:HG23	1:A:158:VAL:HG13	2.01	0.41
1:B:30:LYS:N	1:B:31:PRO:CD	2.84	0.41
1:A:49:ARG:HG3	1:A:59:THR:HG21	2.03	0.41
1:B:66:ARG:HD2	1:B:77:PHE:CE1	2.56	0.40

All (1) 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)
3:A:552:HOH:O	3:B:502:HOH:O[4_445]	2.05	0.15

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	394/419 (94%)	372 (94%)	16 (4%)	6 (2%)	10	20
1	B	397/419 (95%)	379 (96%)	15 (4%)	3 (1%)	19	37
All	All	791/838 (94%)	751 (95%)	31 (4%)	9 (1%)	14	28

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	VAL
1	A	113	GLU
1	A	358	LEU
1	A	1	MET
1	A	49	ARG

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Mol	Chain	Res	Type
1	A	112	TYR
1	B	0	SER
1	B	47	VAL
1	B	232	GLU

5.3.2 Protein sidechains ⓘ

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	329/350 (94%)	280 (85%)	49 (15%)	3	5
1	B	310/350 (89%)	266 (86%)	44 (14%)	3	5
All	All	639/700 (91%)	546 (85%)	93 (15%)	3	5

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	6	ASP
1	A	14	THR
1	A	25	THR
1	A	27	LEU
1	A	28	THR
1	A	33	VAL
1	A	44	ARG
1	A	67	LYS
1	A	84	LYS
1	A	92	LEU
1	A	97	LEU
1	A	106	LYS
1	A	109	THR
1	A	118	LEU
1	A	130	LEU
1	A	143	LEU
1	A	157	LEU
1	A	163	VAL

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Mol	Chain	Res	Type
1	A	170	ILE
1	A	173	VAL
1	A	186	ILE
1	A	188	VAL
1	A	193	GLN
1	A	200	VAL
1	A	238	GLU
1	A	241	LEU
1	A	246	THR
1	A	249	ASP
1	A	263	ARG
1	A	281	ILE
1	A	282	ARG
1	A	298	LYS
1	A	318	ARG
1	A	320	LEU
1	A	326	VAL
1	A	327	VAL
1	A	334	LEU
1	A	343	LEU
1	A	350	VAL
1	A	358	LEU
1	A	364	LEU
1	A	367	ASN
1	A	369	THR
1	A	370	VAL
1	A	380	LEU
1	A	385	THR
1	A	389	VAL
1	A	391	GLU
1	B	13	LEU
1	B	14	THR
1	B	33	VAL
1	B	44	ARG
1	B	54	LEU
1	B	57	MET
1	B	84	LYS
1	B	90	LEU
1	B	108	VAL
1	B	118	LEU
1	B	123	ARG
1	B	145	LEU

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Mol	Chain	Res	Type
1	B	146	SER
1	B	163	VAL
1	B	164	SER
1	B	169	VAL
1	B	173	VAL
1	B	175	GLU
1	B	176	LEU
1	B	186	ILE
1	B	188	VAL
1	B	193	GLN
1	B	200	VAL
1	B	204	LYS
1	B	205	LEU
1	B	238	GLU
1	B	241	LEU
1	B	246	THR
1	B	289	LEU
1	B	302	ARG
1	B	309	GLU
1	B	320	LEU
1	B	326	VAL
1	B	327	VAL
1	B	334	LEU
1	B	343	LEU
1	B	350	VAL
1	B	351	ARG
1	B	367	ASN
1	B	370	VAL
1	B	380	LEU
1	B	385	THR
1	B	393	LEU
1	B	395	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	A	193	GLN
1	A	337	HIS
1	A	375	HIS
1	B	114	HIS
1	B	161	GLN

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Mol	Chain	Res	Type
1	B	171	HIS
1	B	295	GLN
1	B	323	HIS
1	B	375	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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$
1	LLP	A	216	1	23,24,25	3.30	5 (21%)	25,32,34	1.95	7 (28%)
1	LLP	B	216	1	23,24,25	3.16	5 (21%)	25,32,34	1.43	3 (12%)

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
1	LLP	A	216	1	-	3/16/17/19	0/1/1/1
1	LLP	B	216	1	-	4/16/17/19	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	216	LLP	C3-C2	11.42	1.52	1.40
1	B	216	LLP	C3-C2	10.03	1.50	1.40
1	B	216	LLP	C4-C5	6.17	1.49	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	216	LLP	C4-C5	5.98	1.49	1.42
1	B	216	LLP	C4-C3	5.85	1.49	1.40
1	A	216	LLP	C4'-NZ	5.56	1.45	1.27
1	B	216	LLP	C4'-NZ	5.20	1.44	1.27
1	A	216	LLP	C4-C3	5.11	1.48	1.40
1	A	216	LLP	C4-C4'	4.27	1.54	1.46
1	B	216	LLP	C4-C4'	3.92	1.54	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	LLP	C3-C4-C5	-5.12	114.33	118.26
1	A	216	LLP	O3-C3-C2	3.80	125.77	117.49
1	B	216	LLP	C4-C3-C2	-3.63	117.94	120.19
1	B	216	LLP	C3-C4-C5	-3.24	115.77	118.26
1	A	216	LLP	C5-C4-C4'	2.80	126.17	121.56
1	A	216	LLP	C2'-C2-C3	2.75	124.28	120.89
1	A	216	LLP	OP4-P-OP1	-2.37	99.83	106.47
1	B	216	LLP	C6-N1-C2	2.24	123.31	119.17
1	A	216	LLP	C4-C4'-NZ	-2.18	114.31	124.31
1	A	216	LLP	C6-N1-C2	2.06	122.98	119.17

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	216	LLP	C4-C4'-NZ-CE
1	A	216	LLP	O-C-CA-CB
1	B	216	LLP	C4-C4'-NZ-CE
1	B	216	LLP	O-C-CA-CB
1	B	216	LLP	CG-CD-CE-NZ
1	A	216	LLP	C3-C4-C4'-NZ
1	B	216	LLP	C3-C4-C4'-NZ

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	216	LLP	3	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 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	$\# Z > 2$
2	GOL	A	401	-	5,5,5	0.49	0	5,5,5	0.45	0
2	GOL	B	401	-	5,5,5	0.54	0	5,5,5	0.34	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
2	GOL	A	401	-	-	0/4/4/4	-
2	GOL	B	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	GOL	C1-C2-C3-O3
2	B	401	GOL	O2-C2-C3-O3

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	396/419 (94%)	0.48	28 (7%) 16 13	28, 50, 82, 108	0
1	B	399/419 (95%)	0.43	29 (7%) 15 12	29, 50, 75, 106	0
All	All	795/838 (94%)	0.46	57 (7%) 15 13	28, 50, 79, 108	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	251	SER	5.0
1	B	250	VAL	4.9
1	B	248	GLU	3.9
1	B	253	ASP	3.9
1	B	-2	MET	3.8
1	A	253	ASP	3.7
1	A	250	VAL	3.6
1	B	247	ILE	3.5
1	A	354	HIS	3.3
1	A	83	THR	3.3
1	B	397	LEU	3.3
1	B	256	LYS	3.3
1	B	184	GLY	2.9
1	B	367	ASN	2.9
1	B	1	MET	2.8
1	A	154	GLY	2.7
1	A	362	LYS	2.7
1	A	224	ILE	2.7
1	A	254	GLY	2.6
1	B	83	THR	2.6
1	A	252	LEU	2.6
1	B	211	ALA	2.6
1	B	255	TYR	2.6
1	B	92	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	251	SER	2.5
1	A	88	GLU	2.5
1	A	365	GLY	2.5
1	B	286	ARG	2.5
1	A	163	VAL	2.4
1	A	85	ASN	2.4
1	B	223	GLY	2.4
1	A	192	ALA	2.4
1	A	213	SER	2.4
1	A	223	GLY	2.3
1	B	395	LYS	2.3
1	A	367	ASN	2.3
1	B	85	ASN	2.3
1	B	254	GLY	2.3
1	B	310	LEU	2.3
1	A	366	ILE	2.2
1	B	252	LEU	2.2
1	A	222	THR	2.2
1	B	126	THR	2.2
1	B	165	ASN	2.2
1	A	358	LEU	2.1
1	B	213	SER	2.1
1	B	249	ASP	2.1
1	A	-1	ALA	2.1
1	B	-1	ALA	2.1
1	B	86	THR	2.1
1	A	89	SER	2.1
1	A	84	LYS	2.1
1	A	102	LYS	2.1
1	A	256	LYS	2.1
1	A	248	GLU	2.0
1	B	87	SER	2.0
1	A	335	HIS	2.0

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

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
1	LLP	A	216	24/25	0.95	0.26	31,56,67,69	0
1	LLP	B	216	24/25	0.96	0.28	34,49,74,77	0

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	GOL	B	401	6/6	0.83	0.26	73,76,77,77	0
2	GOL	A	401	6/6	0.93	0.28	51,56,64,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.