



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:11 PM UTC

PDB ID : 2ZJ2 / pdb_00002zj2
Title : Archaeal DNA helicase Hjm apo state in form 1
Authors : Oyama, T.; Oka, H.; Fujikane, R.; Ishino, Y.; Morikawa, K.
Deposited on : 2008-02-29
Resolution : 2.40 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

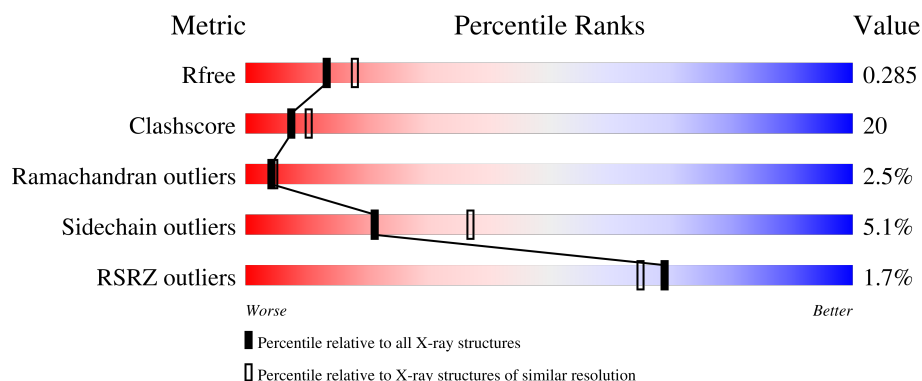
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of 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	720	

2 Entry composition [i](#)

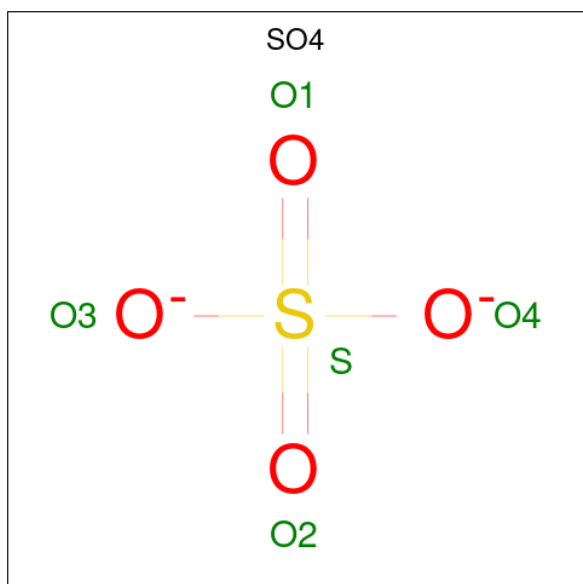
There are 3 unique types of molecules in this entry. The entry contains 5316 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Putative ski2-type helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	653	5201	3364	876	950	11	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	90	Total	O	0	0
			90	90		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.27Å 83.44Å 95.02Å 90.00° 120.69° 90.00°	Depositor
Resolution (Å)	44.86 – 2.40 44.86 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.2 (44.86-2.40) 96.3 (44.86-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.299 0.215 , 0.285	Depositor DCC
R_{free} test set	1506 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5316	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% 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: SO4

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	0.51	0/5306	1.00	23/7178 (0.3%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	75	VAL	CA-C-N	8.12	127.68	119.24
1	A	75	VAL	C-N-CA	8.12	127.68	119.24
1	A	474	GLU	N-CA-C	-7.79	103.78	113.28
1	A	374	TYR	N-CA-C	7.74	122.76	113.16
1	A	80	LEU	N-CA-C	-7.28	104.29	113.02
1	A	569	ARG	N-CA-C	-7.20	103.36	111.14
1	A	598	GLY	N-CA-C	-6.87	96.91	113.18
1	A	388	ASP	CA-C-N	6.45	127.91	119.84
1	A	388	ASP	C-N-CA	6.45	127.91	119.84
1	A	316	PHE	N-CA-C	-6.08	104.56	112.23
1	A	375	ASP	N-CA-C	6.08	119.40	109.24
1	A	5	GLU	N-CA-C	-5.92	106.05	113.28
1	A	376	GLU	N-CA-C	-5.86	106.17	113.38
1	A	327	THR	N-CA-C	-5.73	103.55	110.13
1	A	275	GLU	N-CA-C	-5.68	105.17	111.71
1	A	583	GLU	N-CA-C	5.63	119.20	111.54
1	A	381	ILE	N-CA-C	5.59	115.92	107.75
1	A	468	PHE	N-CA-C	-5.31	105.94	112.90
1	A	39	GLY	N-CA-C	5.27	121.35	115.08
1	A	176	SER	N-CA-C	5.21	116.90	109.14
1	A	572	LYS	N-CA-C	-5.20	105.70	111.36
1	A	526	THR	CA-C-N	5.09	125.02	119.78
1	A	526	THR	C-N-CA	5.09	125.02	119.78

There are no chirality outliers.

There are no planarity outliers.

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	5201	0	5244	212	1
2	A	25	0	0	1	0
3	A	90	0	0	3	0
All	All	5316	0	5244	212	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 20.

All (212) 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:495:THR:HG22	1:A:523:PRO:HD2	1.35	1.06
1:A:66:THR:C	1:A:67:GLN:HG2	2.05	0.82
1:A:654:VAL:HG12	1:A:655:GLY:N	1.94	0.81
1:A:276:LEU:HD21	1:A:311:LEU:HD11	1.65	0.78
1:A:306:ARG:O	1:A:310:VAL:HG23	1.84	0.78
1:A:76:PRO:C	1:A:77:LEU:HD12	2.09	0.77
1:A:653:LEU:O	1:A:654:VAL:HG23	1.84	0.77
1:A:385:THR:HG21	2:A:901:SO4:O3	1.85	0.76
1:A:495:THR:HG21	1:A:524:ASP:OD2	1.84	0.76
1:A:492:ASP:HB3	1:A:495:THR:HG23	1.69	0.75
1:A:97:ARG:HB3	1:A:115:TYR:HA	1.68	0.75
1:A:599:ASP:HA	1:A:602:ARG:NH1	2.02	0.74
1:A:177:ALA:HB2	1:A:364:GLN:NE2	2.04	0.72
1:A:243:PHE:CD2	1:A:365:MET:HE2	2.26	0.70
1:A:502:LYS:HE3	1:A:550:TYR:O	1.91	0.69
1:A:587:GLY:O	1:A:591:GLU:HG3	1.92	0.69
1:A:147:ILE:HG22	1:A:176:SER:HB3	1.77	0.67
1:A:153:ARG:H	1:A:153:ARG:CD	2.06	0.66
1:A:99:ALA:HB2	1:A:115:TYR:CD2	2.31	0.65
1:A:193:LEU:C	1:A:194:ILE:HD12	2.22	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ALA:HB3	1:A:294:ARG:NH1	2.12	0.65
1:A:583:GLU:HA	1:A:656:ARG:NH2	2.13	0.64
1:A:152:SER:C	1:A:407:GLN:HG3	2.24	0.63
1:A:554:PRO:HG3	1:A:567:PHE:CE2	2.32	0.63
1:A:635:VAL:HG11	1:A:646:ILE:HG23	1.81	0.63
1:A:520:SER:HA	1:A:525:ILE:HG21	1.81	0.63
1:A:78:LYS:HE3	1:A:102:THR:HB	1.81	0.62
1:A:553:ASP:OD2	1:A:556:ILE:HG13	1.99	0.62
1:A:79:ALA:HB1	1:A:306:ARG:NH1	2.14	0.62
1:A:46:ILE:HG22	1:A:196:SER:HB3	1.81	0.62
1:A:92:GLU:HG2	1:A:96:LEU:O	1.98	0.62
1:A:14:SER:HA	1:A:17:LYS:HD2	1.81	0.62
1:A:602:ARG:HH11	1:A:602:ARG:HB3	1.64	0.61
1:A:632:THR:O	1:A:636:ARG:HG3	1.99	0.60
1:A:3:VAL:HG23	1:A:22:GLU:C	2.26	0.60
1:A:56:ALA:O	1:A:60:MET:HG3	2.01	0.60
1:A:13:LYS:O	1:A:17:LYS:HG3	2.01	0.60
1:A:153:ARG:H	1:A:153:ARG:HD2	1.67	0.59
1:A:42:ALA:HA	1:A:191:ALA:HB1	1.85	0.59
1:A:403:LYS:HE2	1:A:405:PHE:CE2	2.37	0.59
1:A:309:ARG:NH1	1:A:330:LEU:HD13	2.17	0.59
1:A:28:GLN:HA	1:A:55:ILE:HD11	1.85	0.59
1:A:232:ASP:OD1	1:A:236:LYS:HE3	2.01	0.59
1:A:75:VAL:HG22	1:A:76:PRO:HD2	1.86	0.58
1:A:654:VAL:CG1	1:A:655:GLY:N	2.67	0.57
1:A:99:ALA:HB2	1:A:115:TYR:CG	2.39	0.57
1:A:161:VAL:HG21	1:A:417:GLN:HG2	1.86	0.57
1:A:521:LEU:HD12	1:A:566:LYS:HG2	1.85	0.57
1:A:590:VAL:HG13	1:A:595:VAL:O	2.05	0.57
1:A:583:GLU:OE1	1:A:660:ARG:HD3	2.04	0.56
1:A:654:VAL:O	1:A:657:ARG:HD3	2.05	0.56
1:A:644:GLU:CD	1:A:660:ARG:HH12	2.13	0.56
1:A:42:ALA:CA	1:A:191:ALA:HB1	2.35	0.56
1:A:650:GLN:O	1:A:651:LEU:O	2.23	0.56
1:A:662:LEU:O	1:A:664:ASN:N	2.39	0.56
1:A:180:GLY:C	1:A:182:PRO:HD3	2.30	0.56
1:A:287:GLU:O	1:A:290:ALA:HB3	2.05	0.56
1:A:528:PHE:CZ	1:A:603:ILE:HG13	2.41	0.55
1:A:649:MET:HE1	1:A:659:ALA:CB	2.34	0.55
1:A:157:ALA:O	1:A:161:VAL:HG23	2.06	0.55
1:A:129:LEU:HD23	1:A:136:ILE:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:LEU:O	1:A:13:LYS:HE2	2.07	0.55
1:A:244:VAL:HG13	1:A:245:ASN:N	2.22	0.55
1:A:16:LEU:O	1:A:19:ARG:HB2	2.06	0.54
1:A:586:GLU:OE1	1:A:601:TYR:OH	2.25	0.54
1:A:506:VAL:HG22	1:A:550:TYR:CE1	2.43	0.54
1:A:300:HIS:HE1	1:A:313:GLU:OE2	1.91	0.54
1:A:662:LEU:C	1:A:664:ASN:N	2.65	0.54
1:A:183:GLU:CD	1:A:183:GLU:H	2.15	0.54
1:A:182:PRO:HD2	1:A:183:GLU:OE2	2.08	0.53
1:A:555:TYR:O	1:A:556:ILE:C	2.51	0.53
1:A:599:ASP:HA	1:A:602:ARG:HH12	1.74	0.53
1:A:645:LEU:HD11	1:A:660:ARG:HD2	1.90	0.53
1:A:3:VAL:HG23	1:A:22:GLU:O	2.09	0.53
1:A:60:MET:O	1:A:63:ARG:HB3	2.08	0.53
1:A:654:VAL:HG12	1:A:655:GLY:H	1.70	0.53
1:A:662:LEU:C	1:A:664:ASN:H	2.14	0.53
1:A:27:PRO:HG3	1:A:198:TRP:HB3	1.91	0.53
1:A:153:ARG:HD2	1:A:153:ARG:N	2.24	0.53
1:A:622:GLY:O	1:A:624:TYR:N	2.38	0.53
1:A:527:PRO:HB2	1:A:569:ARG:HB3	1.91	0.52
1:A:592:LYS:HD3	1:A:593:TYR:CE1	2.44	0.52
1:A:209:TYR:CG	1:A:389:PRO:HG3	2.43	0.52
1:A:242:ILE:HD12	1:A:242:ILE:N	2.25	0.52
1:A:577:LEU:O	1:A:580:TRP:HB3	2.09	0.52
1:A:244:VAL:CG1	1:A:245:ASN:N	2.73	0.52
1:A:300:HIS:CE1	1:A:309:ARG:HG2	2.45	0.52
1:A:74:ILE:HA	1:A:120:ALA:O	2.10	0.51
1:A:83:GLU:O	1:A:87:GLU:HG2	2.09	0.51
1:A:76:PRO:CB	1:A:77:LEU:HD12	2.39	0.51
1:A:147:ILE:CG2	1:A:176:SER:HB3	2.40	0.51
1:A:647:PRO:C	1:A:649:MET:H	2.19	0.51
1:A:314:GLU:O	1:A:318:LYS:HG2	2.11	0.51
1:A:429:THR:HG22	1:A:431:GLU:N	2.25	0.51
1:A:232:ASP:O	1:A:236:LYS:HG3	2.12	0.50
1:A:381:ILE:N	1:A:381:ILE:HD12	2.26	0.50
1:A:6:LEU:HD23	1:A:8:VAL:HG21	1.94	0.50
1:A:47:PRO:HD3	1:A:196:SER:O	2.10	0.50
1:A:225:SER:O	1:A:228:GLU:HB2	2.10	0.50
1:A:415:ARG:HA	1:A:459:ILE:HD13	1.93	0.50
1:A:429:THR:HG22	1:A:431:GLU:H	1.76	0.50
1:A:495:THR:CG2	1:A:524:ASP:OD2	2.58	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:THR:OG1	1:A:268:PRO:HD2	2.12	0.49
1:A:77:LEU:O	1:A:79:ALA:N	2.39	0.49
1:A:471:ILE:HG22	1:A:472:SER:N	2.27	0.49
1:A:209:TYR:CD1	1:A:389:PRO:HG3	2.48	0.49
1:A:658:ARG:O	1:A:659:ALA:C	2.56	0.49
1:A:376:GLU:O	1:A:377:VAL:HG23	2.13	0.48
1:A:276:LEU:CD2	1:A:311:LEU:HD21	2.43	0.48
1:A:194:ILE:HD12	1:A:194:ILE:N	2.29	0.48
1:A:75:VAL:O	1:A:121:THR:HA	2.14	0.48
1:A:504:GLU:O	1:A:508:LYS:HG3	2.14	0.48
1:A:201:VAL:HG21	1:A:370:GLY:HA3	1.95	0.47
1:A:413:ASN:O	1:A:417:GLN:HB2	2.14	0.47
1:A:1:MET:CE	1:A:33:LYS:HE2	2.44	0.47
1:A:283:ASN:OD1	1:A:283:ASN:C	2.57	0.47
1:A:214:THR:HA	1:A:220:ILE:HD13	1.96	0.47
1:A:238:LYS:NZ	1:A:374:TYR:HB3	2.30	0.47
1:A:380:GLY:C	1:A:381:ILE:HD12	2.40	0.47
1:A:423:ALA:HB1	1:A:484:ILE:HA	1.97	0.47
1:A:485:ARG:HG2	1:A:620:VAL:HG21	1.95	0.47
1:A:6:LEU:HD23	1:A:8:VAL:CG2	2.45	0.47
1:A:209:TYR:CD2	1:A:389:PRO:HG2	2.49	0.47
1:A:241:LEU:HD12	1:A:242:ILE:N	2.30	0.47
1:A:160:GLU:OE2	1:A:440:THR:HB	2.14	0.47
1:A:150:ILE:HG22	1:A:404:LEU:HD13	1.96	0.47
1:A:308:GLU:CD	1:A:308:GLU:H	2.22	0.47
1:A:205:ARG:HD3	1:A:216:GLU:OE2	2.15	0.46
1:A:82:GLU:O	1:A:86:GLN:HG2	2.16	0.46
1:A:257:LEU:O	1:A:261:VAL:HG23	2.16	0.46
1:A:66:THR:O	1:A:67:GLN:HG2	2.15	0.46
1:A:602:ARG:NH1	1:A:602:ARG:HB3	2.30	0.46
1:A:8:VAL:O	1:A:13:LYS:HE3	2.16	0.46
1:A:502:LYS:CE	1:A:550:TYR:O	2.61	0.46
1:A:307:ASP:O	1:A:308:GLU:C	2.58	0.45
1:A:148:HIS:HA	1:A:404:LEU:HD11	1.97	0.45
1:A:265:LEU:O	1:A:270:ILE:HD11	2.16	0.45
1:A:317:ARG:CG	1:A:336:THR:HG21	2.47	0.45
1:A:25:TYR:HB3	1:A:27:PRO:HD2	1.98	0.45
1:A:29:ALA:O	1:A:33:LYS:HG3	2.17	0.45
1:A:622:GLY:HA2	1:A:624:TYR:CE1	2.52	0.45
1:A:599:ASP:O	1:A:603:ILE:HG12	2.17	0.45
1:A:266:THR:CB	1:A:268:PRO:HD2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:THR:O	1:A:330:LEU:HB2	2.17	0.45
1:A:547:ASP:HB3	3:A:1067:HOH:O	2.17	0.44
1:A:246:MET:HE3	3:A:1042:HOH:O	2.17	0.44
1:A:635:VAL:HG11	1:A:646:ILE:CG2	2.47	0.44
1:A:152:SER:O	1:A:407:GLN:HG3	2.17	0.44
1:A:362:VAL:HG21	1:A:396:TYR:CE2	2.53	0.44
1:A:626:ILE:HD12	1:A:630:LEU:HD11	2.00	0.44
1:A:53:THR:O	1:A:57:GLU:HG3	2.17	0.44
1:A:260:LYS:HG2	3:A:1073:HOH:O	2.17	0.44
1:A:495:THR:HG22	1:A:522:THR:HB	1.98	0.44
1:A:649:MET:HE1	1:A:659:ALA:HB2	1.99	0.44
1:A:661:ALA:O	1:A:662:LEU:C	2.61	0.44
1:A:110:GLU:OE2	1:A:134:SER:HB3	2.18	0.43
1:A:643:GLU:C	1:A:645:LEU:H	2.25	0.43
1:A:647:PRO:O	1:A:649:MET:N	2.52	0.43
1:A:269:GLU:O	1:A:273:LEU:HG	2.18	0.43
1:A:329:THR:O	1:A:330:LEU:CB	2.66	0.43
1:A:540:GLU:O	1:A:544:GLU:HB2	2.18	0.43
1:A:262:LYS:C	1:A:264:LEU:H	2.26	0.43
1:A:267:LYS:N	1:A:268:PRO:CD	2.82	0.43
1:A:299:PHE:HA	1:A:325:VAL:O	2.18	0.43
1:A:344:ARG:HG3	1:A:344:ARG:O	2.18	0.43
1:A:583:GLU:HA	1:A:656:ARG:HH21	1.82	0.43
1:A:52:LYS:HB3	1:A:175:LEU:HD22	2.01	0.43
1:A:97:ARG:HG3	1:A:97:ARG:HH11	1.83	0.43
1:A:153:ARG:CD	1:A:153:ARG:N	2.79	0.43
1:A:652:PRO:O	1:A:653:LEU:HB2	2.19	0.43
1:A:88:PHE:O	1:A:98:VAL:HG21	2.18	0.43
1:A:108:LYS:HG2	1:A:131:HIS:HB3	2.01	0.43
1:A:317:ARG:HG3	1:A:336:THR:HG21	2.00	0.43
1:A:474:GLU:O	1:A:475:ASP:HB2	2.19	0.43
1:A:655:GLY:C	1:A:657:ARG:N	2.72	0.43
1:A:39:GLY:O	1:A:171:GLN:HG3	2.18	0.43
1:A:471:ILE:CG2	1:A:472:SER:N	2.82	0.42
1:A:654:VAL:CG1	1:A:659:ALA:HB2	2.49	0.42
1:A:75:VAL:HA	1:A:76:PRO:HD3	1.90	0.42
1:A:599:ASP:HA	1:A:602:ARG:HH11	1.78	0.42
1:A:629:TYR:HD2	1:A:630:LEU:HD23	1.84	0.42
1:A:647:PRO:C	1:A:649:MET:N	2.77	0.42
1:A:535:PHE:CZ	1:A:539:GLU:HG3	2.54	0.42
1:A:400:LYS:HG2	1:A:401:PRO:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:SER:O	1:A:410:ASN:C	2.63	0.42
1:A:12:ILE:HD11	1:A:61:VAL:HG12	2.02	0.42
1:A:265:LEU:HD13	1:A:273:LEU:CD1	2.49	0.42
1:A:495:THR:CG2	1:A:522:THR:HB	2.49	0.42
1:A:516:PHE:HB3	1:A:574:ALA:HA	2.01	0.42
1:A:654:VAL:HG13	1:A:659:ALA:H	1.84	0.42
1:A:262:LYS:HE2	1:A:294:ARG:O	2.20	0.41
1:A:276:LEU:HD22	1:A:311:LEU:HD21	2.00	0.41
1:A:131:HIS:CE1	1:A:488:LYS:HB3	2.54	0.41
1:A:35:GLY:HA3	1:A:40:LYS:HD2	2.02	0.41
1:A:66:THR:C	1:A:67:GLN:CG	2.83	0.41
1:A:329:THR:C	1:A:330:LEU:HG	2.45	0.41
1:A:2:ARG:O	1:A:3:VAL:C	2.63	0.41
1:A:36:ILE:HD12	1:A:59:ALA:HB2	2.03	0.41
1:A:70:LYS:HG2	1:A:115:TYR:O	2.20	0.41
1:A:236:LYS:C	1:A:238:LYS:H	2.28	0.41
1:A:276:LEU:HD11	1:A:315:ASN:CG	2.46	0.41
1:A:585:PRO:O	1:A:586:GLU:C	2.62	0.41
1:A:346:ILE:HG13	1:A:347:TRP:CD1	2.55	0.41
1:A:602:ARG:HH11	1:A:602:ARG:CB	2.33	0.41
1:A:77:LEU:HD12	1:A:77:LEU:N	2.36	0.41
1:A:142:LEU:HD23	1:A:142:LEU:C	2.46	0.41
1:A:528:PHE:HE2	1:A:599:ASP:HB3	1.85	0.40
1:A:646:ILE:N	1:A:647:PRO:CD	2.84	0.40
1:A:317:ARG:HD2	1:A:336:THR:HG21	2.02	0.40
1:A:610:LEU:HA	1:A:610:LEU:HD23	1.86	0.40
1:A:472:SER:O	1:A:475:ASP:N	2.48	0.40
1:A:617:ILE:HD13	1:A:617:ILE:HA	1.92	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)
1:A:354:MET:CE	1:A:354:MET:CE[2_656]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

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	647/720 (90%)	594 (92%)	37 (6%)	16 (2%)	4 5

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	555	TYR
1	A	651	LEU
1	A	654	VAL
1	A	657	ARG
1	A	448	ASP
1	A	552	ASP
1	A	644	GLU
1	A	648	LEU
1	A	154	ASP
1	A	653	LEU
1	A	663	TYR
1	A	330	LEU
1	A	623	ALA
1	A	78	LYS
1	A	598	GLY
1	A	647	PRO

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	544/626 (87%)	516 (95%)	28 (5%)	21 37

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	GLU
1	A	67	GLN
1	A	75	VAL
1	A	97	ARG
1	A	153	ARG
1	A	154	ASP
1	A	155	ARG
1	A	183	GLU
1	A	227	GLU
1	A	228	GLU
1	A	235	ARG
1	A	244	VAL
1	A	246	MET
1	A	256	GLU
1	A	271	ARG
1	A	276	LEU
1	A	324	VAL
1	A	356	ARG
1	A	385	THR
1	A	448	ASP
1	A	449	THR
1	A	495	THR
1	A	547	ASP
1	A	586	GLU
1	A	602	ARG
1	A	644	GLU
1	A	654	VAL
1	A	656	ARG

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

Mol	Chain	Res	Type
1	A	171	GLN
1	A	190	ASN

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Mol	Chain	Res	Type
1	A	300	HIS
1	A	364	GLN
1	A	582	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	SO4	A	905	-	4,4,4	1.87	2 (50%)	6,6,6	0.80	0
2	SO4	A	904	-	4,4,4	1.84	1 (25%)	6,6,6	0.84	0
2	SO4	A	901	-	4,4,4	1.91	2 (50%)	6,6,6	0.93	0
2	SO4	A	903	-	4,4,4	1.92	1 (25%)	6,6,6	0.83	0
2	SO4	A	902	-	4,4,4	1.92	1 (25%)	6,6,6	0.84	0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	902	SO4	O1-S	3.41	1.65	1.44
2	A	903	SO4	O1-S	3.33	1.64	1.44
2	A	904	SO4	O1-S	3.19	1.63	1.44
2	A	905	SO4	O1-S	3.08	1.63	1.44
2	A	901	SO4	O1-S	3.06	1.63	1.44
2	A	901	SO4	O3-S	-2.23	1.29	1.48
2	A	905	SO4	O3-S	-2.10	1.30	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	SO4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	653/720 (90%)	0.01	11 (1%) 69 65	19, 39, 63, 89	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	556	ILE	3.1
1	A	650	GLN	2.9
1	A	654	VAL	2.8
1	A	652	PRO	2.6
1	A	658	ARG	2.5
1	A	329	THR	2.4
1	A	281	GLU	2.3
1	A	655	GLY	2.3
1	A	374	TYR	2.1
1	A	351	ASP	2.1
1	A	552	ASP	2.1

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 oligosaccharides 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(Å ²)	Q<0.9
2	SO4	A	902	5/5	0.88	0.13	50,60,66,93	0
2	SO4	A	903	5/5	0.89	0.12	44,55,73,93	0
2	SO4	A	904	5/5	0.92	0.14	39,51,69,81	0
2	SO4	A	901	5/5	0.93	0.18	30,51,64,73	5
2	SO4	A	905	5/5	0.96	0.09	33,49,67,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.