



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:36 AM UTC

PDB ID : 7F00 / pdb_00007f00
Title : Crystal structure of SPD_0310
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Deposited on : 2021-06-03
Resolution : 2.70 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

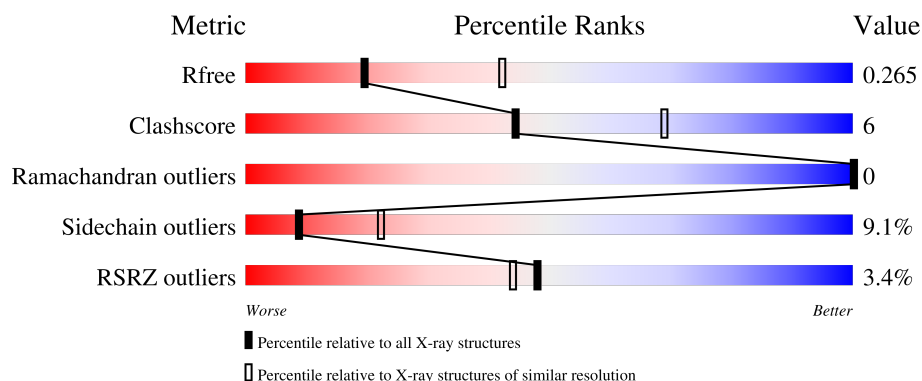
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	496	3% 76% 17% • •
1	B	496	3% 77% 15% • 6%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7357 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.

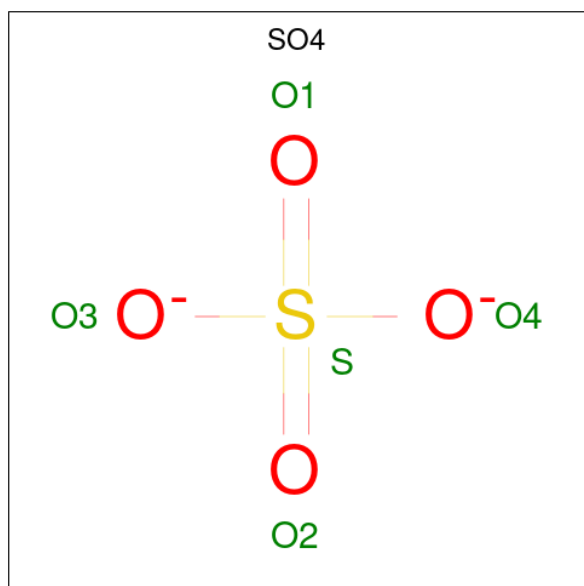
- Molecule 1 is a protein called UPF0371 protein SPRM200_0309.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	0	0	0
			3695	2349	627	707	12			
1	B	468	Total	C	N	O	S	0	0	0
			3627	2304	612	699	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP A0A2U3RY31
A	0	SER	-	expression tag	UNP A0A2U3RY31
B	-1	GLY	-	expression tag	UNP A0A2U3RY31
B	0	SER	-	expression tag	UNP A0A2U3RY31

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



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

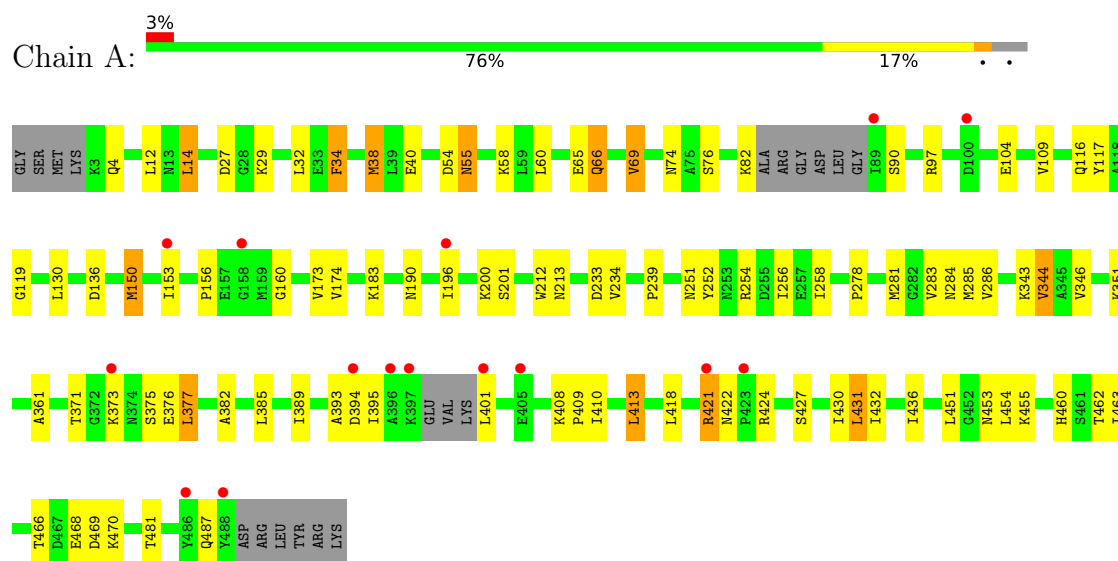
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	6	Total O 6 6	0	0
3	B	9	Total O 9 9	0	0

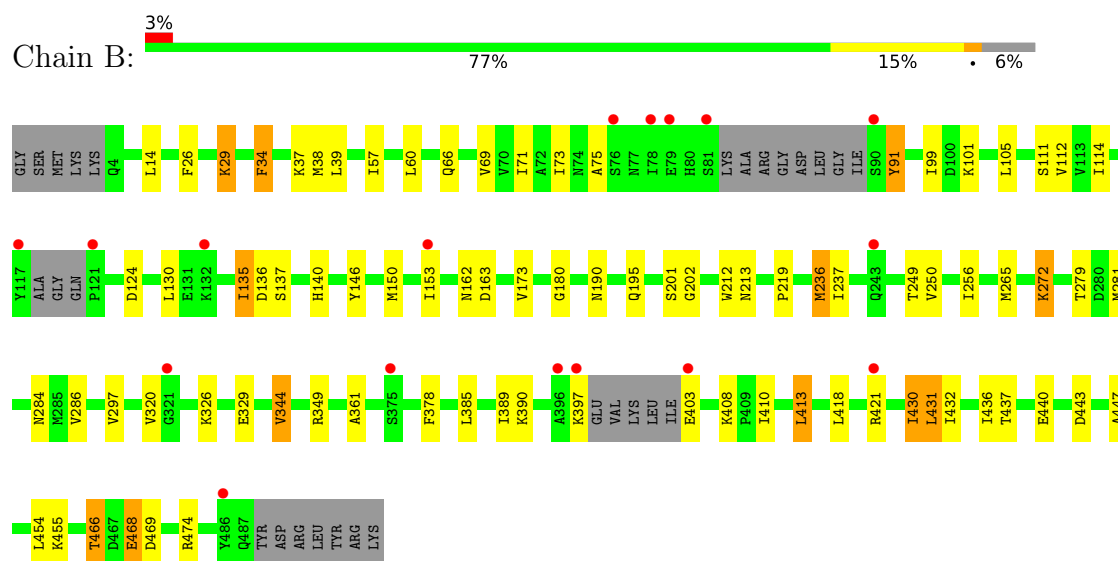
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: UPF0371 protein SPRM200_0309



• Molecule 1: UPF0371 protein SPRM200_0309



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	87.85Å 87.85Å 326.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.01 – 2.70 50.01 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.0 (50.01-2.70) 98.1 (50.01-2.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.97 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0123	Depositor
R, R_{free}	0.221 , 0.265 0.221 , 0.265	Depositor DCC
R_{free} test set	1795 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.8	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	0.92	EDS
Total number of atoms	7357	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.08% 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: 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	0.35	0/3765	0.63	1/5104 (0.0%)
1	B	0.37	0/3696	0.63	0/5009
All	All	0.36	0/7461	0.63	1/10113 (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	393	ALA	N-CA-C	-5.59	99.62	108.73

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	3695	0	3665	50	0
1	B	3627	0	3573	43	0
2	A	5	0	0	0	0
2	B	15	0	0	1	0
3	A	6	0	0	0	0
3	B	9	0	0	0	0
All	All	7357	0	7238	87	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 6.

All (87) 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:38:MET:HE1	1:B:60:LEU:HD11	1.66	0.77
1:A:421:ARG:HD2	1:A:422:ASN:H	1.50	0.74
1:A:233:ASP:OD2	1:A:254:ARG:NH1	2.26	0.68
1:B:236:MET:HG3	1:B:256:ILE:HD12	1.77	0.64
1:B:29:LYS:HD3	1:B:201:SER:HB3	1.79	0.63
1:A:278:PRO:HA	1:A:281:MET:HG2	1.81	0.63
1:A:431:LEU:HB3	1:B:413:LEU:HD11	1.83	0.60
1:A:413:LEU:HD11	1:B:431:LEU:HB3	1.84	0.60
1:B:249:THR:HG21	1:B:279:THR:OG1	2.02	0.60
1:A:409:PRO:HG2	1:B:436:ILE:HD13	1.84	0.59
1:A:104:GLU:OE2	1:B:421:ARG:NH2	2.34	0.59
1:B:150:MET:HE1	1:B:265:MET:HA	1.85	0.57
1:B:403:GLU:HG2	1:B:437:THR:HG21	1.87	0.55
1:A:38:MET:HE1	1:A:60:LEU:HD11	1.86	0.55
1:B:73:ILE:HD11	1:B:91:TYR:HB3	1.89	0.53
1:B:75:ALA:HA	1:B:114:ILE:HD11	1.89	0.53
1:B:112:VAL:O	1:B:137:SER:HA	2.08	0.53
1:B:39:LEU:HD21	1:B:101:LYS:HG2	1.90	0.53
1:A:27:ASP:HB2	1:A:200:LYS:HD3	1.92	0.52
1:A:239:PRO:HD2	1:A:256:ILE:HD12	1.92	0.52
1:A:38:MET:CE	1:A:60:LEU:HD11	2.40	0.52
1:B:99:ILE:HD13	1:B:135:ILE:HD12	1.91	0.52
1:A:252:TYR:O	1:A:256:ILE:HG12	2.10	0.52
1:A:65:GLU:HG3	1:A:66:GLN:HG2	1.93	0.51
1:B:284:ASN:OD1	1:B:286:VAL:HG12	2.11	0.51
1:A:150:MET:HE2	1:A:153:ILE:HD11	1.92	0.51
1:A:117:TYR:CZ	1:A:119:GLY:HA2	2.45	0.51
1:A:389:ILE:HD11	1:A:451:LEU:HD23	1.94	0.50
1:A:466:THR:HG23	1:A:469:ASP:H	1.76	0.50
1:B:413:LEU:HD22	1:B:418:LEU:HD13	1.93	0.50
1:A:156:PRO:HA	1:A:160:GLY:HA3	1.93	0.50
1:A:69:VAL:HG22	1:A:109:VAL:HA	1.96	0.48
1:A:74:ASN:ND2	1:A:116:GLN:HG3	2.29	0.47
1:A:54:ASP:OD2	1:A:58:LYS:HE2	2.15	0.47
1:A:212:TRP:CZ3	1:A:213:ASN:HB3	2.49	0.47
1:A:251:ASN:HB3	1:A:256:ILE:HD11	1.97	0.47
1:B:34:PHE:CE2	1:B:38:MET:HE3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:LYS:O	1:A:346:VAL:HG22	2.15	0.46
1:A:183:LYS:HE3	1:A:183:LYS:HB2	1.75	0.46
1:A:14:LEU:HD13	1:A:285:MET:HE3	1.97	0.46
1:B:326:LYS:HD3	1:B:329:GLU:OE1	2.16	0.46
1:A:34:PHE:CE2	1:A:38:MET:HE3	2.50	0.46
1:B:146:TYR:CE1	1:B:265:MET:HE1	2.50	0.46
1:B:29:LYS:HD3	1:B:201:SER:CB	2.44	0.46
1:B:26:PHE:CD1	1:B:202:GLY:HA3	2.51	0.46
1:A:34:PHE:CD2	1:A:38:MET:HE3	2.51	0.45
1:A:422:ASN:OD1	1:A:424:ARG:NE	2.50	0.45
1:A:34:PHE:CD1	1:A:173:VAL:HG13	2.52	0.45
1:B:180:GLY:N	2:B:501:SO4:O2	2.32	0.45
1:B:466:THR:OG1	1:B:468:GLU:HG2	2.16	0.45
1:B:71:ILE:HB	1:B:112:VAL:HG22	1.97	0.45
1:A:12:LEU:HD21	1:A:55:ASN:HB2	1.97	0.45
1:A:233:ASP:OD1	1:A:254:ARG:HD3	2.17	0.45
1:B:389:ILE:HG21	1:B:447:ALA:HB1	1.99	0.45
1:A:410:ILE:HG12	1:B:432:ILE:HG23	1.99	0.45
1:A:375:SER:O	1:A:424:ARG:HD3	2.17	0.45
1:B:140:HIS:ND1	1:B:162:ASN:HB3	2.31	0.45
1:B:466:THR:HG23	1:B:469:ASP:H	1.81	0.45
1:B:219:PRO:HG2	1:B:297:VAL:HG13	1.98	0.45
1:B:212:TRP:HB2	1:B:249:THR:HG23	1.99	0.45
1:A:254:ARG:O	1:A:258:ILE:HG12	2.17	0.44
1:A:29:LYS:HB3	1:A:201:SER:HB3	1.99	0.44
1:A:432:ILE:HG23	1:B:410:ILE:HG12	1.99	0.44
1:A:394:ASP:C	1:A:395:ILE:HG13	2.42	0.44
1:A:377:LEU:HD22	1:A:377:LEU:H	1.82	0.44
1:A:375:SER:OG	1:A:376:GLU:N	2.50	0.44
1:B:212:TRP:CZ3	1:B:213:ASN:HB3	2.53	0.44
1:A:430:ILE:HD13	1:A:430:ILE:HA	1.91	0.43
1:A:382:ALA:HB1	1:A:430:ILE:HG13	2.00	0.43
1:A:463:ILE:HG21	1:A:487:GLN:HG2	1.99	0.43
1:A:460:HIS:HA	1:A:481:THR:O	2.19	0.43
1:A:284:ASN:OD1	1:A:286:VAL:HG12	2.18	0.43
1:B:150:MET:HE1	1:B:265:MET:HG2	2.00	0.43
1:B:430:ILE:HA	1:B:430:ILE:HD12	1.77	0.43
1:A:351:LYS:HG3	1:A:371:THR:HG21	2.00	0.43
1:B:390:LYS:NZ	1:B:397:LYS:HA	2.34	0.42
1:B:378:PHE:CE2	1:B:430:ILE:HD11	2.54	0.42
1:A:385:LEU:HD12	1:A:427:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:VAL:O	1:A:361:ALA:HB3	2.19	0.42
1:A:174:VAL:HG12	1:A:183:LYS:HG2	2.02	0.41
1:B:140:HIS:HE1	1:B:163:ASP:O	2.03	0.41
1:B:212:TRP:CE3	1:B:213:ASN:HB3	2.55	0.41
1:B:344:VAL:O	1:B:361:ALA:HB3	2.21	0.41
1:B:34:PHE:CD1	1:B:173:VAL:HG13	2.55	0.41
1:B:57:ILE:HG23	1:B:105:LEU:HD13	2.01	0.41
1:A:212:TRP:CE3	1:A:213:ASN:HB3	2.56	0.40
1:B:272:LYS:HE2	1:B:272:LYS:HB2	1.86	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	471/496 (95%)	459 (98%)	12 (2%)	0	100	100
1	B	460/496 (93%)	446 (97%)	14 (3%)	0	100	100
All	All	931/992 (94%)	905 (97%)	26 (3%)	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	392/417 (94%)	356 (91%)	36 (9%)	8	22
1	B	384/417 (92%)	349 (91%)	35 (9%)	9	22
All	All	776/834 (93%)	705 (91%)	71 (9%)	9	22

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	14	LEU
1	A	32	LEU
1	A	34	PHE
1	A	38	MET
1	A	40	GLU
1	A	55	ASN
1	A	66	GLN
1	A	69	VAL
1	A	76	SER
1	A	82	LYS
1	A	90	SER
1	A	97	ARG
1	A	130	LEU
1	A	136	ASP
1	A	150	MET
1	A	190	ASN
1	A	196	ILE
1	A	234	VAL
1	A	283	VAL
1	A	344	VAL
1	A	373	LYS
1	A	377	LEU
1	A	401	LEU
1	A	408	LYS
1	A	413	LEU
1	A	418	LEU
1	A	421	ARG
1	A	431	LEU
1	A	436	ILE
1	A	453	ASN
1	A	454	LEU
1	A	455	LYS
1	A	462	THR
1	A	468	GLU

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Mol	Chain	Res	Type
1	A	470	LYS
1	B	14	LEU
1	B	29	LYS
1	B	34	PHE
1	B	37	LYS
1	B	66	GLN
1	B	69	VAL
1	B	91	TYR
1	B	111	SER
1	B	124	ASP
1	B	130	LEU
1	B	135	ILE
1	B	136	ASP
1	B	153	ILE
1	B	190	ASN
1	B	195	GLN
1	B	236	MET
1	B	237	ILE
1	B	250	VAL
1	B	272	LYS
1	B	281	MET
1	B	320	VAL
1	B	344	VAL
1	B	349	ARG
1	B	385	LEU
1	B	408	LYS
1	B	413	LEU
1	B	430	ILE
1	B	431	LEU
1	B	440	GLU
1	B	443	ASP
1	B	454	LEU
1	B	455	LYS
1	B	466	THR
1	B	468	GLU
1	B	474	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	ASN
1	A	116	GLN

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Mol	Chain	Res	Type
1	A	152	HIS
1	A	195	GLN
1	A	426	HIS
1	A	428	ASN
1	B	10	GLN
1	B	162	ASN
1	B	197	ASN
1	B	479	ASN
1	B	487	GLN

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](#)

4 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	B	502	-	4,4,4	0.42	0	6,6,6	0.28	0
2	SO4	B	503	-	4,4,4	0.43	0	6,6,6	0.36	0
2	SO4	B	501	-	4,4,4	0.35	0	6,6,6	0.30	0
2	SO4	A	501	-	4,4,4	0.44	0	6,6,6	0.27	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	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

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	477/496 (96%)	0.26	15 (3%) 51 48	23, 54, 83, 95	0
1	B	468/496 (94%)	0.27	17 (3%) 46 42	26, 53, 82, 99	0
All	All	945/992 (95%)	0.26	32 (3%) 48 44	23, 53, 83, 99	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	121	PRO	4.8
1	A	488	TYR	4.7
1	A	397	LYS	4.7
1	B	79	GLU	4.0
1	A	401	LEU	3.8
1	B	397	LYS	3.8
1	A	405	GLU	3.6
1	A	486	TYR	3.3
1	A	89	ILE	3.1
1	B	78	ILE	3.1
1	B	132	LYS	3.0
1	B	396	ALA	2.9
1	A	158	GLY	2.9
1	B	81	SER	2.8
1	A	394	ASP	2.8
1	A	100	ASP	2.7
1	B	486	TYR	2.7
1	B	375	SER	2.5
1	B	90	SER	2.5
1	A	421	ARG	2.4
1	B	321	GLY	2.4
1	A	396	ALA	2.4
1	A	153	ILE	2.3
1	B	76	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	243	GLN	2.3
1	B	421	ARG	2.2
1	A	423	PRO	2.2
1	B	117	TYR	2.1
1	B	403	GLU	2.0
1	B	153	ILE	2.0
1	A	373	LYS	2.0
1	A	196	ILE	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 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($\text{\AA}^2$)	Q<0.9
2	SO4	B	501	5/5	0.60	0.18	56,57,62,66	5
2	SO4	B	502	5/5	0.65	0.14	58,61,64,67	5
2	SO4	A	501	5/5	0.70	0.14	61,62,64,73	0
2	SO4	B	503	5/5	0.83	0.20	29,29,29,31	5

6.5 Other polymers [i](#)

There are no such residues in this entry.