



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:39 PM UTC

PDB ID : 3EEQ / pdb_00003eeq
Title : Crystal structure of a putative cobalamin biosynthesis protein G homolog from *Sulfolobus solfataricus*
Authors : Bonanno, J.B.; Gilmore, M.; Bain, K.T.; Chang, S.; Romero, R.; Wasserman, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2008-09-05
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

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

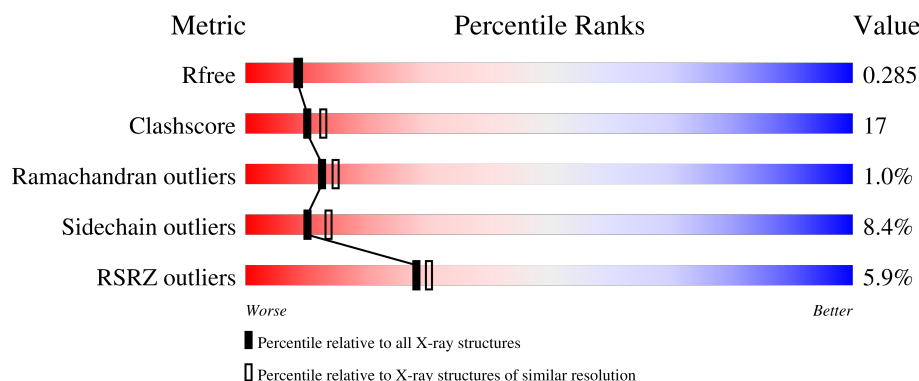
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	336	4% 64% 25% • 7%
1	B	336	6% 61% 24% 5% 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4721 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 Cobalamin biosynthesis protein G homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	2	0
			2358	1516	395	435	12			
1	B	304	Total	C	N	O	S	0	1	0
			2299	1478	385	425	11			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	SER	-	expression tag	UNP Q97WD0
A	9	LEU	-	expression tag	UNP Q97WD0
A	127	ILE	-	expression tag	UNP Q97WD0
A	128	THR	-	expression tag	UNP Q97WD0
A	129	THR	-	expression tag	UNP Q97WD0
A	337	HIS	-	expression tag	UNP Q97WD0
A	338	HIS	-	expression tag	UNP Q97WD0
A	339	HIS	-	expression tag	UNP Q97WD0
A	340	HIS	-	expression tag	UNP Q97WD0
A	341	HIS	-	expression tag	UNP Q97WD0
A	342	HIS	-	expression tag	UNP Q97WD0
B	8	SER	-	expression tag	UNP Q97WD0
B	9	LEU	-	expression tag	UNP Q97WD0
B	127	ILE	-	expression tag	UNP Q97WD0
B	128	THR	-	expression tag	UNP Q97WD0
B	129	THR	-	expression tag	UNP Q97WD0
B	337	HIS	-	expression tag	UNP Q97WD0
B	338	HIS	-	expression tag	UNP Q97WD0
B	339	HIS	-	expression tag	UNP Q97WD0
B	340	HIS	-	expression tag	UNP Q97WD0
B	341	HIS	-	expression tag	UNP Q97WD0
B	342	HIS	-	expression tag	UNP Q97WD0

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



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

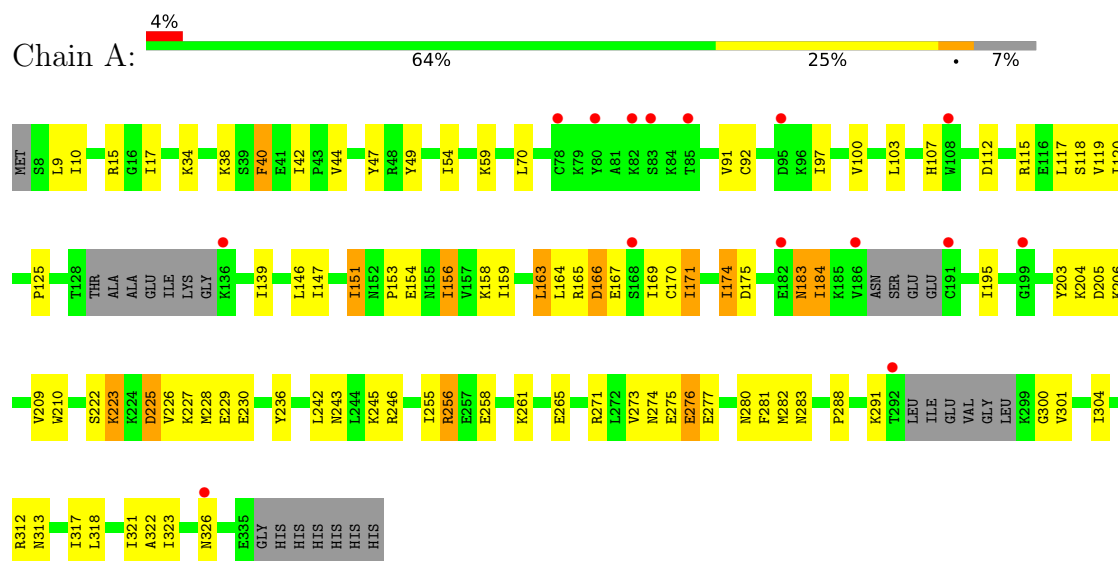
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	O	0	0
			15	15		
3	B	19	Total	O	0	0
			19	19		

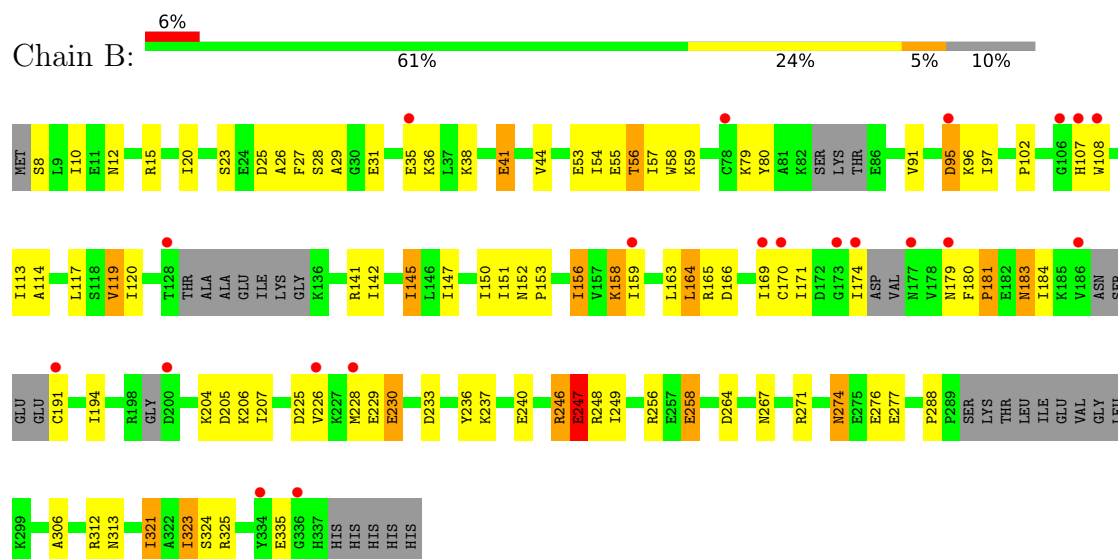
3 Residue-property plots [i](#)

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: putative Cobalamin biosynthesis protein G homolog



- Molecule 1: putative Cobalamin biosynthesis protein G homolog



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.02Å 97.50Å 107.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.30) 99.6 (20.00-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.54 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.237 , 0.284 0.238 , 0.285	Depositor DCC
R_{free} test set	1534 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4721	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 8.94% 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	1.03	0/2393	1.20	8/3247 (0.2%)
1	B	0.99	1/2329 (0.0%)	1.15	9/3161 (0.3%)
All	All	1.01	1/4722 (0.0%)	1.18	17/6408 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	306	ALA	CA-CB	5.40	1.61	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	323	ILE	N-CA-C	-11.01	102.98	111.90
1	B	323	ILE	N-CA-C	-7.02	106.65	113.53
1	A	291	LYS	N-CA-C	-6.28	104.49	111.71
1	B	288	PRO	O-C-N	6.07	124.00	121.15
1	A	301	VAL	N-CA-C	6.06	116.84	110.72
1	B	20	ILE	CB-CA-C	-5.98	103.62	110.73
1	B	152	ASN	CA-C-N	5.96	126.74	120.12
1	B	152	ASN	C-N-CA	5.96	126.74	120.12
1	A	276	GLU	N-CA-C	-5.88	104.21	111.33
1	B	41	GLU	CA-C-N	-5.75	118.45	122.59
1	B	41	GLU	C-N-CA	-5.75	118.45	122.59
1	B	150	ILE	CB-CA-C	-5.69	104.42	111.08
1	A	146	LEU	N-CA-C	-5.55	106.18	113.17
1	B	240	GLU	CB-CA-C	-5.43	102.60	110.96
1	A	317	ILE	CB-CA-C	-5.27	106.44	111.44
1	A	156	ILE	CB-CA-C	-5.26	104.97	112.22
1	A	40	PHE	N-CA-C	-5.05	106.36	112.88

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	2358	0	2361	82	1
1	B	2299	0	2274	78	1
2	A	20	0	0	0	0
2	B	10	0	0	0	0
3	A	15	0	0	0	0
3	B	19	0	0	0	0
All	All	4721	0	4635	160	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 17.

All (160) 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:223:LYS:HE2	1:A:326:ASN:CB	1.42	1.47
1:A:227:LYS:HE3	1:A:229:GLU:OE1	1.41	1.20
1:A:163:LEU:HD13	1:A:169:ILE:CD1	1.78	1.13
1:A:228:MET:HE3	1:A:258:GLU:HG2	1.22	1.11
1:B:141:ARG:O	1:B:145:ILE:HG12	1.49	1.11
1:A:163:LEU:CD1	1:A:169:ILE:HD13	1.80	1.10
1:A:223:LYS:CE	1:A:326:ASN:CB	2.31	1.08
1:A:226:VAL:CG1	1:A:228:MET:HE2	1.92	0.98
1:B:180:PHE:O	1:B:181:PRO:O	1.80	0.97
1:A:228:MET:CE	1:A:258:GLU:HG2	1.94	0.97
1:A:227:LYS:CE	1:A:229:GLU:OE1	2.16	0.94
1:A:38:LYS:HD3	1:A:44:VAL:CG1	1.97	0.93
1:A:163:LEU:CD1	1:A:169:ILE:CD1	2.43	0.93
1:A:163:LEU:HD13	1:A:169:ILE:HD13	1.42	0.91
1:A:312:ARG:O	1:A:313:ASN:HB2	1.72	0.90
1:A:226:VAL:HG11	1:A:228:MET:HE2	1.53	0.89
1:A:163:LEU:HD11	1:A:169:ILE:HD13	1.55	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:ASN:HD22	1:B:276:GLU:H	1.25	0.83
1:A:49:TYR:HE1	1:A:54:ILE:HD11	1.45	0.82
1:A:163:LEU:HD13	1:A:169:ILE:HD11	1.62	0.81
1:A:226:VAL:HG12	1:A:228:MET:HE2	1.64	0.80
1:B:141:ARG:O	1:B:145:ILE:CG1	2.29	0.79
1:A:300:GLY:O	1:A:304:ILE:HG13	1.84	0.78
1:A:153:PRO:HA	1:A:156:ILE:HG13	1.64	0.77
1:B:95:ASP:OD2	1:B:95:ASP:C	2.30	0.75
1:A:236:TYR:OH	1:A:246:ARG:NH2	2.19	0.74
1:A:203:TYR:HB3	1:A:206:LYS:HG3	1.69	0.74
1:B:163:LEU:HD23	1:B:169:ILE:HD13	1.69	0.74
1:A:49:TYR:CE1	1:A:54:ILE:HD11	2.22	0.73
1:A:34:LYS:O	1:A:38:LYS:HG2	1.88	0.73
1:A:245:LYS:HE2	1:A:246:ARG:H	1.55	0.72
1:B:183:ASN:OD1	1:B:183:ASN:N	2.18	0.72
1:A:282[A]:MET:HE3	1:A:283:ASN:H	1.53	0.71
1:B:226:VAL:HG11	1:B:228:MET:CE	2.20	0.71
1:B:38:LYS:HD3	1:B:44:VAL:HG12	1.71	0.70
1:B:274:ASN:ND2	1:B:276:GLU:H	1.88	0.70
1:B:246:ARG:O	1:B:248:ARG:N	2.24	0.69
1:B:163:LEU:CD2	1:B:169:ILE:HD13	2.22	0.69
1:A:70:LEU:HD11	1:A:103:LEU:HD21	1.76	0.67
1:A:226:VAL:HG11	1:A:228:MET:CE	2.24	0.67
1:B:226:VAL:CG1	1:B:228:MET:CE	2.75	0.65
1:A:222:SER:HB3	1:A:256:ARG:HG3	1.80	0.63
1:B:274:ASN:HD21	1:B:276:GLU:HB2	1.64	0.62
1:B:184:ILE:HD12	1:B:184:ILE:H	1.64	0.62
1:B:184:ILE:HD12	1:B:184:ILE:N	2.15	0.62
1:A:38:LYS:HD3	1:A:44:VAL:HG12	1.82	0.61
1:B:204:LYS:O	1:B:205:ASP:HB2	2.01	0.61
1:B:10:ILE:HD11	1:B:117:LEU:HD13	1.83	0.61
1:B:191:CYS:O	1:B:206:LYS:NZ	2.23	0.60
1:A:321:ILE:HG22	1:A:322:ALA:O	2.02	0.60
1:B:226:VAL:HG21	1:B:258:GLU:HG2	1.84	0.60
1:B:38:LYS:HD3	1:B:44:VAL:CG1	2.31	0.59
1:B:163:LEU:HD23	1:B:169:ILE:CD1	2.32	0.59
1:B:233:ASP:O	1:B:237:LYS:HG3	2.02	0.59
1:B:246:ARG:C	1:B:248:ARG:N	2.59	0.59
1:B:225:ASP:O	1:B:226:VAL:C	2.46	0.59
1:A:204:LYS:O	1:A:205:ASP:HB2	2.02	0.58
1:B:27:PHE:C	1:B:27:PHE:CD2	2.81	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ILE:HG13	1:A:184:ILE:HG23	1.84	0.58
1:A:38:LYS:HD3	1:A:44:VAL:HG11	1.84	0.58
1:A:49:TYR:HE1	1:A:54:ILE:CD1	2.15	0.57
1:B:142:ILE:HA	1:B:145:ILE:HG13	1.87	0.56
1:A:164:LEU:C	1:A:166:ASP:H	2.14	0.56
1:B:31:GLU:O	1:B:35:GLU:HG2	2.06	0.56
1:A:255:ILE:HG22	1:A:273:VAL:O	2.05	0.56
1:B:274:ASN:HD22	1:B:276:GLU:N	1.99	0.56
1:A:275:GLU:O	1:A:276:GLU:C	2.46	0.55
1:A:9:LEU:HD23	1:A:112:ASP:HB2	1.89	0.55
1:A:271:ARG:NH1	1:A:277:GLU:OE2	2.40	0.55
1:B:113:ILE:O	1:B:117:LEU:HB2	2.07	0.55
1:B:246:ARG:C	1:B:248:ARG:H	2.14	0.54
1:A:174:ILE:HG22	1:A:175:ASP:N	2.22	0.54
1:B:246:ARG:O	1:B:247:GLU:C	2.50	0.54
1:A:184:ILE:CD1	1:A:184:ILE:N	2.71	0.54
1:A:70:LEU:CD1	1:A:103:LEU:HD21	2.37	0.54
1:A:228:MET:HE3	1:A:258:GLU:CG	2.16	0.53
1:B:264:ASP:O	1:B:267:ASN:N	2.38	0.53
1:A:10:ILE:HD11	1:A:117:LEU:HD13	1.90	0.53
1:A:91:VAL:HG11	1:A:100:VAL:CG1	2.38	0.53
1:A:223:LYS:CD	1:A:326:ASN:CB	2.86	0.53
1:A:229:GLU:H	1:A:229:GLU:CD	2.17	0.52
1:A:112:ASP:OD1	1:A:115:ARG:NH2	2.42	0.52
1:A:70:LEU:HD11	1:A:103:LEU:CD2	2.40	0.52
1:B:274:ASN:ND2	1:B:276:GLU:HB2	2.26	0.51
1:B:274:ASN:ND2	1:B:274:ASN:C	2.69	0.51
1:B:55:GLU:HG3	1:B:80:TYR:HE1	1.74	0.50
1:A:318:LEU:HD21	1:A:321:ILE:HD12	1.92	0.50
1:B:274:ASN:HD22	1:B:274:ASN:C	2.19	0.50
1:A:171:ILE:HA	1:A:195:ILE:O	2.12	0.50
1:A:174:ILE:CG2	1:A:175:ASP:N	2.74	0.50
1:B:184:ILE:H	1:B:184:ILE:CD1	2.23	0.50
1:B:228:MET:HA	1:B:228:MET:HE2	1.92	0.50
1:B:226:VAL:HG21	1:B:258:GLU:CG	2.41	0.49
1:B:180:PHE:C	1:B:181:PRO:O	2.52	0.49
1:B:171:ILE:HG22	1:B:174:ILE:HG12	1.95	0.49
1:B:274:ASN:ND2	1:B:276:GLU:N	2.60	0.48
1:A:245:LYS:HE2	1:A:246:ARG:N	2.24	0.48
1:A:312:ARG:O	1:A:313:ASN:CB	2.46	0.48
1:B:230:GLU:OE1	1:B:324:SER:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ILE:HG22	1:A:322:ALA:N	2.29	0.47
1:B:26:ALA:O	1:B:29:ALA:HB3	2.15	0.47
1:B:108:TRP:CD1	1:B:141:ARG:NH1	2.83	0.47
1:A:223:LYS:NZ	1:A:225:ASP:OD2	2.38	0.47
1:B:23:SER:O	1:B:26:ALA:HB3	2.13	0.47
1:A:227:LYS:O	1:A:230:GLU:HB3	2.14	0.47
1:A:281:PHE:CD2	1:A:304:ILE:HG23	2.50	0.47
1:A:223:LYS:HE3	1:A:223:LYS:HB2	1.41	0.47
1:A:40:PHE:CE2	1:A:120:ILE:HG23	2.49	0.47
1:A:183:ASN:OD1	1:A:183:ASN:N	2.25	0.46
1:B:324:SER:OG	1:B:325:ARG:N	2.46	0.46
1:B:158:LYS:HB3	1:B:158:LYS:HE3	1.53	0.46
1:B:36:LYS:HE3	1:B:36:LYS:HB3	1.58	0.46
1:B:153:PRO:HA	1:B:156:ILE:HG13	1.96	0.46
1:B:15:ARG:NH2	1:B:59:LYS:O	2.48	0.46
1:B:102:PRO:HD3	1:B:114:ALA:CB	2.46	0.46
1:B:170:CYS:HB2	1:B:194:ILE:HD13	1.97	0.46
1:B:226:VAL:HG11	1:B:228:MET:HE1	1.96	0.45
1:B:229:GLU:HA	1:B:229:GLU:OE1	2.16	0.45
1:B:233:ASP:HA	1:B:236:TYR:HD1	1.81	0.45
1:A:281:PHE:CD2	1:A:281:PHE:C	2.94	0.45
1:B:158:LYS:HD3	1:B:207:ILE:HD13	1.99	0.45
1:B:180:PHE:O	1:B:181:PRO:C	2.53	0.45
1:A:47:TYR:OH	1:A:288:PRO:HG3	2.17	0.44
1:B:53:GLU:HB3	1:B:56:THR:OG1	2.17	0.44
1:B:54:ILE:O	1:B:58:TRP:HB2	2.17	0.44
1:A:139:ILE:HG12	1:A:209:VAL:HG11	1.98	0.44
1:B:56:THR:O	1:B:57:ILE:C	2.59	0.44
1:B:312:ARG:O	1:B:313:ASN:HB2	2.17	0.44
1:B:321:ILE:HG21	1:B:321:ILE:HD13	1.52	0.44
1:B:184:ILE:N	1:B:184:ILE:CD1	2.81	0.43
1:B:27:PHE:C	1:B:27:PHE:HD2	2.25	0.43
1:B:246:ARG:O	1:B:249:ILE:N	2.37	0.42
1:B:145:ILE:HG12	1:B:145:ILE:H	1.46	0.42
1:B:226:VAL:CG1	1:B:228:MET:HE2	2.50	0.42
1:A:91:VAL:HG12	1:A:92:CYS:N	2.35	0.42
1:A:118:SER:OG	1:A:125:PRO:HD3	2.20	0.42
1:B:119:VAL:O	1:B:120:ILE:C	2.62	0.42
1:A:165:ARG:O	1:A:166:ASP:C	2.61	0.42
1:B:164:LEU:C	1:B:166:ASP:H	2.28	0.42
1:A:17:ILE:HD12	1:A:42:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ILE:CG2	1:A:322:ALA:N	2.83	0.41
1:B:27:PHE:O	1:B:28:SER:C	2.62	0.41
1:A:242:LEU:O	1:A:243:ASN:HB2	2.19	0.41
1:B:8:SER:O	1:B:12:ASN:ND2	2.54	0.41
1:B:226:VAL:HG12	1:B:228:MET:HE2	2.01	0.41
1:A:227:LYS:NZ	1:A:229:GLU:OE1	2.52	0.41
1:A:169:ILE:HG22	1:A:170:CYS:N	2.36	0.41
1:A:222:SER:O	1:A:256:ARG:NH1	2.53	0.41
1:A:15:ARG:NH2	1:A:59:LYS:O	2.54	0.41
1:A:151:ILE:HG12	1:A:210:TRP:O	2.20	0.41
1:A:119:VAL:O	1:A:120:ILE:C	2.61	0.41
1:A:167:GLU:O	1:A:183:ASN:HB3	2.20	0.41
1:B:226:VAL:CG1	1:B:228:MET:HE3	2.51	0.41
1:B:271:ARG:NH1	1:B:277:GLU:OE2	2.49	0.41
1:B:230:GLU:HG3	1:B:323:ILE:HG21	2.04	0.40
1:A:222:SER:O	1:A:256:ARG:HD2	2.21	0.40
1:A:261:LYS:O	1:A:265:GLU:HG3	2.21	0.40
1:B:108:TRP:CD2	1:B:141:ARG:NH2	2.90	0.40
1:A:91:VAL:HG11	1:A:100:VAL:HG13	2.03	0.40
1:A:147:ILE:HG22	1:A:147:ILE:O	2.22	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:280:ASN:ND2	1:B:206:LYS:O[3_645]	1.99	0.21

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	305/336 (91%)	287 (94%)	18 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	291/336 (87%)	270 (93%)	15 (5%)	6 (2%)	5	4
All	All	596/672 (89%)	557 (94%)	33 (6%)	6 (1%)	12	15

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	181	PRO
1	B	107	HIS
1	B	247	GLU
1	B	179	ASN
1	B	147	ILE
1	B	119	VAL

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	245/293 (84%)	229 (94%)	16 (6%)	15	22
1	B	237/293 (81%)	213 (90%)	24 (10%)	7	9
All	All	482/586 (82%)	442 (92%)	40 (8%)	10	14

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ILE
1	A	107	HIS
1	A	151	ILE
1	A	154	GLU
1	A	158	LYS
1	A	159	ILE
1	A	163	LEU
1	A	166	ASP
1	A	171	ILE
1	A	174	ILE

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Mol	Chain	Res	Type
1	A	183	ASN
1	A	184	ILE
1	A	223	LYS
1	A	225	ASP
1	A	256	ARG
1	A	274	ASN
1	B	25	ASP
1	B	41	GLU
1	B	56	THR
1	B	79	LYS
1	B	91	VAL
1	B	95	ASP
1	B	96	LYS
1	B	97	ILE
1	B	145	ILE
1	B	151	ILE
1	B	156	ILE
1	B	158	LYS
1	B	159	ILE
1	B	164	LEU
1	B	165	ARG
1	B	183	ASN
1	B	230	GLU
1	B	246	ARG
1	B	247	GLU
1	B	256	ARG
1	B	258	GLU
1	B	274	ASN
1	B	321	ILE
1	B	335	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	122	ASN
1	A	274	ASN
1	A	279	ASN
1	B	12	ASN
1	B	274	ASN
1	B	279	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](#)

6 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	2	-	4,4,4	0.20	0	6,6,6	0.24	0
2	SO4	A	1	-	4,4,4	0.28	0	6,6,6	0.53	0
2	SO4	B	4	-	4,4,4	0.40	0	6,6,6	0.65	0
2	SO4	B	6	-	4,4,4	0.57	0	6,6,6	0.41	0
2	SO4	A	3	-	4,4,4	0.38	0	6,6,6	0.52	0
2	SO4	A	5	-	4,4,4	0.51	0	6,6,6	0.61	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.

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	311/336 (92%)	0.41	15 (4%) 35 37	28, 49, 73, 81	2 (0%)
1	B	304/336 (90%)	0.69	21 (6%) 23 25	31, 55, 75, 81	1 (0%)
All	All	615/672 (91%)	0.55	36 (5%) 28 30	28, 51, 75, 81	3 (0%)

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	186	VAL	4.5
1	B	186	VAL	3.8
1	B	177	ASN	3.8
1	B	191	CYS	3.7
1	B	108	TRP	3.4
1	A	136	LYS	3.4
1	B	200	ASP	3.1
1	B	173	GLY	3.0
1	A	85	THR	2.9
1	A	199	GLY	2.8
1	A	326	ASN	2.6
1	B	336	GLY	2.6
1	B	170	CYS	2.6
1	A	182	GLU	2.6
1	A	95	ASP	2.5
1	B	95	ASP	2.5
1	B	78[A]	CYS	2.5
1	A	292	THR	2.5
1	B	106	GLY	2.5
1	A	168	SER	2.4
1	A	83	SER	2.4
1	B	169	ILE	2.3
1	B	159	ILE	2.3
1	B	334	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	107	HIS	2.3
1	B	179	ASN	2.2
1	A	191	CYS	2.2
1	B	174	ILE	2.2
1	A	108	TRP	2.2
1	A	78[A]	CYS	2.2
1	B	228	MET	2.1
1	A	80	TYR	2.1
1	B	226	VAL	2.1
1	A	82	LYS	2.0
1	B	35	GLU	2.0
1	B	128	THR	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(Å ²)	Q<0.9
2	SO4	B	4	5/5	0.74	0.12	81,81,82,83	0
2	SO4	A	3	5/5	0.75	0.14	69,72,75,76	0
2	SO4	B	6	5/5	0.80	0.16	65,67,69,72	0
2	SO4	A	5	5/5	0.83	0.16	58,60,62,63	0
2	SO4	A	2	5/5	0.92	0.17	68,69,70,70	0
2	SO4	A	1	5/5	0.95	0.08	56,58,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.