



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:30 PM UTC

PDB ID : 2E6C / pdb_00002e6c
Title : Crystal structure of the stationary phase survival protein SurE from *Thermus thermophilus* HB8 cocrystallized with manganese and AMP
Authors : Iwasaki, W.; Miki, K.
Deposited on : 2006-12-26
Resolution : 2.05 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

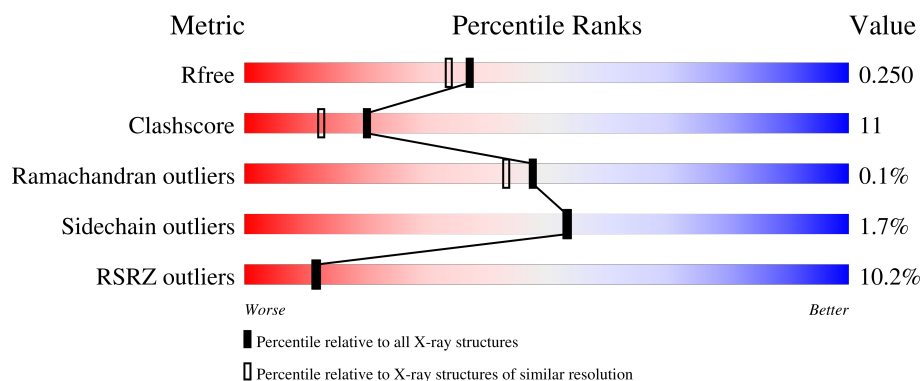
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	244	8% 78% 20% .
1	B	244	10% 80% 17% .
1	C	244	12% 75% 22% ..
1	D	244	10% 75% 19% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7741 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 5'-nucleotidase surE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1878	1214	330	331	3			
1	B	237	Total	C	N	O	S	0	0	0
			1840	1193	323	321	3			
1	C	238	Total	C	N	O	S	0	0	0
			1841	1190	323	325	3			
1	D	234	Total	C	N	O	S	0	0	0
			1817	1178	318	318	3			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

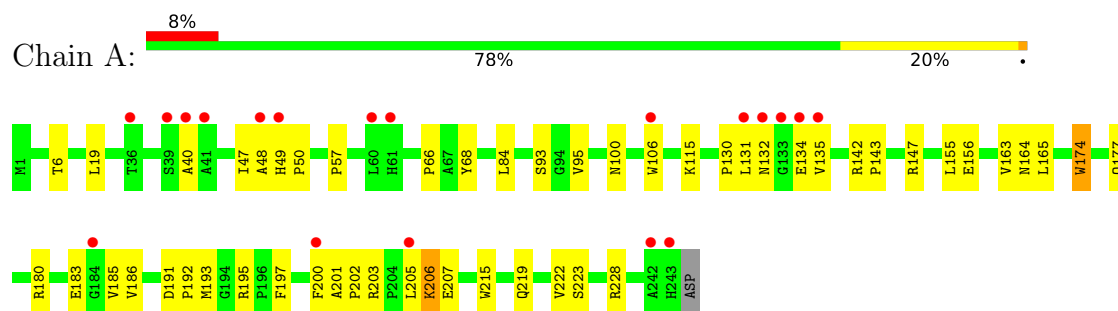
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	96	Total	O	0	0
			96	96		
5	B	63	Total	O	0	0
			63	63		
5	C	70	Total	O	0	0
			70	70		
5	D	75	Total	O	0	0
			75	75		

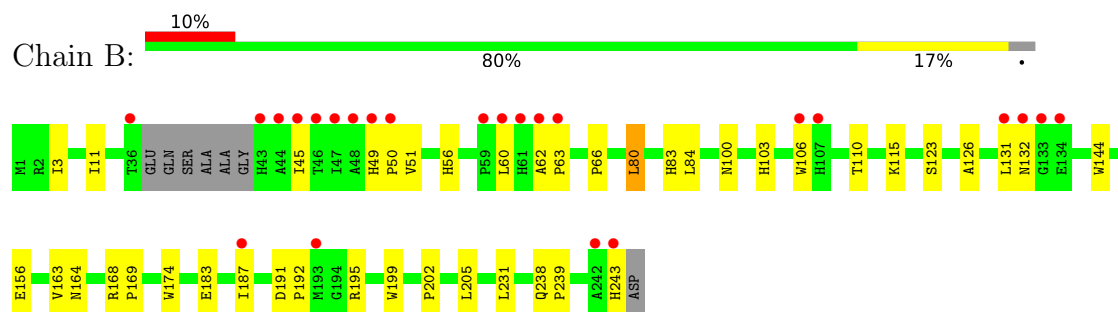
3 Residue-property plots

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.

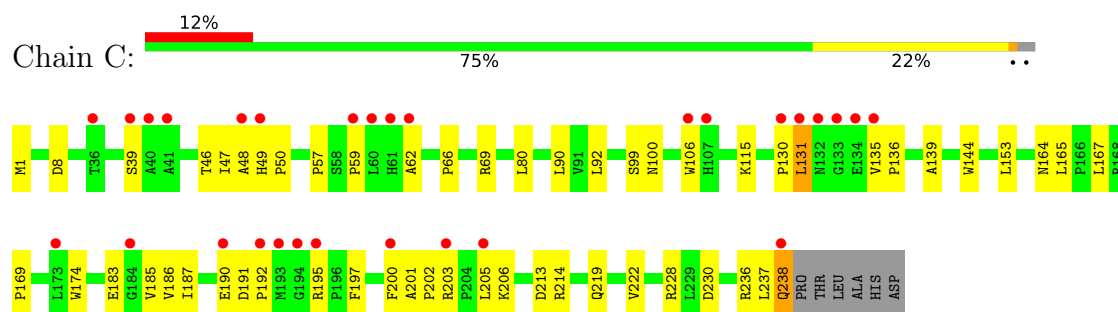
• Molecule 1: 5'-nucleotidase surE



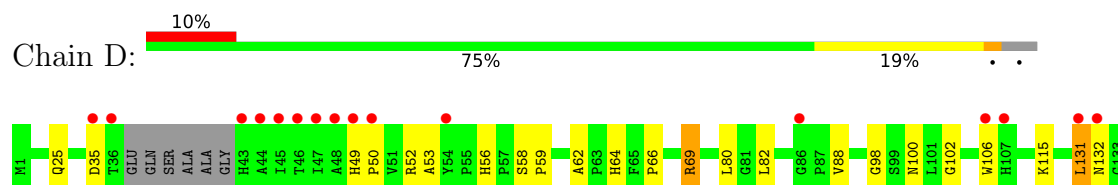
• Molecule 1: 5'-nucleotidase surE

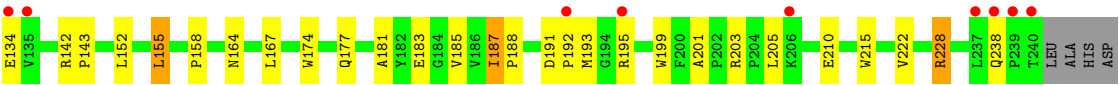


• Molecule 1: 5'-nucleotidase surE



• Molecule 1: 5'-nucleotidase surE





4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	132.60Å 132.60Å 130.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.56 – 2.05 46.56 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.56-2.05) 100.0 (46.56-2.05)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.45 (at 2.05Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.208 , 0.249 0.207 , 0.250	Depositor DCC
R_{free} test set	4228 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	27.2	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7741	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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: MN, SO4, GOL

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	0.52	0/1939	0.95	3/2658 (0.1%)
1	B	0.49	0/1900	0.98	6/2604 (0.2%)
1	C	0.52	0/1900	0.96	6/2603 (0.2%)
1	D	0.51	0/1876	0.99	6/2571 (0.2%)
All	All	0.51	0/7615	0.97	21/10436 (0.2%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	174	TRP	N-CA-C	-7.11	98.96	110.20
1	A	174	TRP	N-CA-C	-6.78	98.98	109.76
1	B	174	TRP	N-CA-C	-6.66	100.62	110.48
1	C	47	ILE	N-CA-C	6.41	118.25	108.71
1	D	174	TRP	N-CA-C	-6.14	100.50	110.20
1	B	163	VAL	N-CA-C	6.00	116.58	108.17
1	D	69	ARG	N-CA-C	-5.97	99.50	109.24
1	C	222	VAL	N-CA-C	-5.86	101.97	109.30
1	D	222	VAL	N-CA-C	-5.83	102.06	109.58
1	C	66	PRO	N-CA-C	-5.75	102.16	111.14
1	B	66	PRO	N-CA-C	-5.73	102.20	111.14
1	A	66	PRO	N-CA-C	-5.71	102.23	111.14
1	B	3	ILE	N-CA-C	5.46	115.75	108.11
1	A	222	VAL	N-CA-C	-5.35	102.68	109.58
1	D	66	PRO	N-CA-C	-5.26	102.94	111.03
1	D	238	GLN	CA-C-N	5.23	125.52	119.92
1	D	238	GLN	C-N-CA	5.23	125.52	119.92
1	C	139	ALA	N-CA-C	-5.17	105.56	111.14
1	B	156	GLU	N-CA-C	-5.05	102.80	110.28
1	B	123	SER	N-CA-C	-5.05	103.05	110.52

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	69	ARG	N-CA-C	-5.00	101.09	109.24

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	1878	0	1852	56	0
1	B	1840	0	1819	53	0
1	C	1841	0	1815	56	0
1	D	1817	0	1796	51	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	20	0	0	1	0
3	B	10	0	0	1	0
3	C	5	0	0	0	0
3	D	10	0	0	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
5	A	96	0	0	1	0
5	B	63	0	0	1	0
5	C	70	0	0	1	0
5	D	75	0	0	2	0
All	All	7741	0	7298	167	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 11.

All (167) 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:183:GLU:CD	1:A:203:ARG:HH12	1.71	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:238:GLN:H	1:C:238:GLN:NE2	1.65	0.94
1:A:40:ALA:HB2	1:C:39:SER:HB3	1.48	0.93
1:D:100:ASN:H	1:D:164:ASN:HD21	1.21	0.88
1:D:187:ILE:HG23	1:D:199:TRP:HB2	1.56	0.88
1:A:202:PRO:HG3	1:B:45:ILE:HG21	1.58	0.85
1:A:177:GLN:NE2	1:B:231:LEU:H	1.75	0.83
1:B:100:ASN:H	1:B:164:ASN:HD21	1.25	0.83
1:A:100:ASN:H	1:A:164:ASN:HD21	1.27	0.81
1:C:100:ASN:H	1:C:164:ASN:HD21	1.28	0.81
1:A:193:MET:HE3	1:A:195:ARG:CZ	2.12	0.79
1:A:135:VAL:HG21	1:C:57:PRO:HG3	1.66	0.77
1:C:59:PRO:HG2	1:C:62:ALA:HB3	1.66	0.77
1:A:203:ARG:HH11	1:A:203:ARG:HG2	1.49	0.75
1:A:177:GLN:HE22	1:B:231:LEU:H	1.31	0.75
1:D:187:ILE:CG2	1:D:199:TRP:HB2	2.17	0.74
1:A:191:ASP:HB2	1:A:192:PRO:HD2	1.68	0.74
1:A:57:PRO:HG3	1:C:135:VAL:HG21	1.70	0.73
1:C:228:ARG:NH1	5:C:2461:HOH:O	2.21	0.73
1:D:58:SER:OG	1:D:64:HIS:HD2	1.74	0.69
1:C:99:SER:HB3	1:C:130:PRO:HB3	1.74	0.68
1:C:200:PHE:HZ	1:D:80:LEU:HB2	1.56	0.68
1:B:49:HIS:HB2	1:B:50:PRO:HD2	1.74	0.68
1:D:191:ASP:OD1	1:D:195:ARG:HB2	1.94	0.68
1:C:191:ASP:HB2	1:C:192:PRO:HD2	1.75	0.67
1:B:191:ASP:HB2	1:B:192:PRO:HD2	1.76	0.67
1:A:200:PHE:HB3	1:B:45:ILE:HD11	1.77	0.66
1:C:228:ARG:HD3	1:C:230:ASP:O	1.96	0.66
1:D:131:LEU:H	1:D:131:LEU:HD22	1.60	0.66
1:C:228:ARG:NH1	1:D:228:ARG:NH1	2.45	0.65
1:C:190:GLU:HA	1:C:195:ARG:O	1.97	0.64
1:C:191:ASP:OD1	1:C:195:ARG:HB2	1.97	0.64
1:C:200:PHE:CZ	1:D:80:LEU:HB2	2.32	0.64
1:C:238:GLN:H	1:C:238:GLN:HE21	1.44	0.63
1:C:130:PRO:HD2	1:C:165:LEU:O	1.99	0.63
1:A:49:HIS:N	1:B:199:TRP:HZ3	1.98	0.62
1:D:102:GLY:O	1:D:177:GLN:NE2	2.31	0.61
1:A:135:VAL:CG2	1:C:57:PRO:HG3	2.30	0.61
1:B:80:LEU:HD13	1:B:84:LEU:CD1	2.30	0.61
1:A:203:ARG:HG2	1:A:203:ARG:NH1	2.15	0.60
1:B:50:PRO:HD3	1:C:50:PRO:HG3	1.83	0.60
1:A:180:ARG:HG2	1:A:206:LYS:HE2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:PHE:CD1	1:B:50:PRO:CB	2.84	0.60
1:D:152:LEU:O	1:D:155:LEU:HB2	2.02	0.59
1:C:1:MET:HE1	1:C:153:LEU:HD22	1.83	0.59
1:A:193:MET:HE2	1:C:48:ALA:HB3	1.83	0.59
1:C:186:VAL:HG22	1:C:200:PHE:CD2	2.39	0.58
1:A:115:LYS:HE2	1:B:106:TRP:CD2	2.39	0.58
1:D:192:PRO:C	1:D:193:MET:HE2	2.29	0.58
1:D:228:ARG:HG2	1:D:228:ARG:HH11	1.68	0.57
1:A:155:LEU:HD11	1:A:174:TRP:HH2	1.69	0.57
1:A:206:LYS:HD2	1:A:207:GLU:O	2.05	0.57
1:D:49:HIS:HB2	1:D:50:PRO:HD2	1.87	0.57
1:A:106:TRP:CE3	1:B:115:LYS:HE2	2.40	0.57
1:A:40:ALA:CB	1:C:39:SER:HB3	2.31	0.57
1:D:187:ILE:C	1:D:187:ILE:HD13	2.30	0.56
1:D:132:ASN:ND2	5:D:3470:HOH:O	2.38	0.56
1:D:203:ARG:HH21	1:D:203:ARG:HG3	1.72	0.55
1:C:197:PHE:CD1	1:D:50:PRO:HB2	2.41	0.55
1:C:236:ARG:NH1	1:D:158:PRO:O	2.39	0.55
1:D:187:ILE:HD13	1:D:188:PRO:O	2.07	0.55
1:D:98:GLY:HA2	1:D:131:LEU:CD2	2.37	0.55
1:B:11:ILE:HG12	1:B:56:HIS:CD2	2.43	0.54
1:B:60:LEU:H	1:B:60:LEU:HD22	1.72	0.54
1:B:131:LEU:O	1:B:132:ASN:HB2	2.06	0.54
1:A:131:LEU:HG	1:A:132:ASN:H	1.72	0.54
1:D:131:LEU:HD22	1:D:131:LEU:N	2.22	0.54
1:D:59:PRO:HG2	1:D:62:ALA:HB3	1.90	0.54
1:A:47:ILE:CD1	1:B:202:PRO:HD2	2.38	0.53
1:A:48:ALA:O	1:D:52:ARG:NH1	2.42	0.53
1:B:187:ILE:HB	1:B:199:TRP:HB2	1.90	0.53
1:D:56:HIS:HB2	1:D:69:ARG:HG3	1.90	0.53
1:C:205:LEU:C	1:C:206:LYS:HD2	2.34	0.53
1:B:144:TRP:CD1	1:B:169:PRO:HB2	2.44	0.53
1:A:200:PHE:HZ	1:B:80:LEU:HB2	1.75	0.52
1:C:131:LEU:HD13	1:C:131:LEU:O	2.11	0.52
1:D:183:GLU:HB2	1:D:205:LEU:HD21	1.90	0.52
1:A:106:TRP:CD2	1:B:115:LYS:HE2	2.46	0.51
1:A:130:PRO:HD2	1:A:165:LEU:O	2.10	0.51
1:A:48:ALA:C	1:B:199:TRP:HZ3	2.19	0.51
1:A:49:HIS:N	1:B:199:TRP:CZ3	2.79	0.51
1:A:197:PHE:CD1	1:B:50:PRO:HB2	2.46	0.50
1:C:186:VAL:HG22	1:C:200:PHE:HD2	1.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:PRO:HG3	1:D:50:PRO:HD3	1.94	0.50
1:A:200:PHE:CE2	1:B:80:LEU:HD23	2.46	0.50
1:C:131:LEU:O	1:C:131:LEU:CD1	2.59	0.50
1:C:185:VAL:HB	1:C:201:ALA:O	2.12	0.50
1:C:228:ARG:HH12	1:D:228:ARG:NH1	2.08	0.50
5:A:534:HOH:O	1:B:83:HIS:HD2	1.94	0.49
1:B:183:GLU:HB2	1:B:205:LEU:HD21	1.93	0.49
1:B:49:HIS:HB2	1:B:50:PRO:CD	2.43	0.49
1:C:50:PRO:HD3	1:D:199:TRP:CH2	2.48	0.49
1:C:183:GLU:OE1	1:C:203:ARG:HD3	2.13	0.49
1:D:98:GLY:HA2	1:D:131:LEU:HD21	1.95	0.48
1:B:50:PRO:HD3	1:C:50:PRO:CG	2.43	0.48
1:C:228:ARG:HH11	1:D:228:ARG:HD2	1.77	0.48
1:A:193:MET:HE2	1:C:48:ALA:CB	2.43	0.48
1:B:80:LEU:HD13	1:B:84:LEU:HD11	1.96	0.48
1:A:202:PRO:HG3	1:B:45:ILE:CG2	2.37	0.48
1:D:183:GLU:OE1	1:D:203:ARG:NH1	2.47	0.47
1:D:82:LEU:CD2	1:D:88:VAL:HB	2.43	0.47
1:C:185:VAL:CG2	1:C:203:ARG:HD2	2.44	0.47
1:C:197:PHE:CD1	1:D:50:PRO:CB	2.97	0.47
1:A:215:TRP:O	1:A:219:GLN:HG2	2.14	0.47
1:C:50:PRO:HD3	1:D:199:TRP:CZ3	2.49	0.47
1:D:35:ASP:OD2	1:D:69:ARG:NH2	2.39	0.47
1:A:183:GLU:CD	1:A:203:ARG:NH1	2.56	0.47
1:A:193:MET:HG3	1:C:48:ALA:HB2	1.97	0.47
1:C:185:VAL:HG21	1:C:203:ARG:HD2	1.97	0.46
1:C:106:TRP:CD2	1:D:115:LYS:HE2	2.49	0.46
1:C:228:ARG:NH1	1:D:228:ARG:CZ	2.78	0.46
1:A:68:TYR:CE2	1:A:84:LEU:HD13	2.50	0.46
1:A:115:LYS:HE2	1:B:106:TRP:CE3	2.49	0.46
1:A:195:ARG:NH2	1:C:48:ALA:HB3	2.30	0.46
1:A:203:ARG:NH1	1:A:203:ARG:CG	2.79	0.46
1:A:185:VAL:HB	1:A:201:ALA:O	2.15	0.45
1:A:200:PHE:CZ	1:B:80:LEU:HB2	2.50	0.45
1:B:60:LEU:HD22	1:B:60:LEU:N	2.31	0.45
1:B:80:LEU:HD13	1:B:84:LEU:HD12	1.98	0.45
1:A:228:ARG:HB3	3:A:403:SO4:O3	2.16	0.45
1:B:192:PRO:HB2	1:C:187:ILE:HD13	1.99	0.45
1:A:200:PHE:HB3	1:B:45:ILE:CD1	2.45	0.45
1:B:80:LEU:CD1	1:B:84:LEU:HD11	2.46	0.45
1:A:142:ARG:HB3	1:A:143:PRO:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:LEU:H	1:B:60:LEU:CD2	2.30	0.44
1:C:213:ASP:OD2	1:C:214:ARG:N	2.50	0.44
1:A:186:VAL:HG22	1:A:200:PHE:CD2	2.53	0.44
1:B:11:ILE:O	1:B:11:ILE:HG13	2.16	0.44
1:C:238:GLN:NE2	1:C:238:GLN:N	2.49	0.44
1:D:98:GLY:HA2	1:D:131:LEU:HD22	2.00	0.44
1:D:134:GLU:HG2	1:D:167:LEU:HD13	1.99	0.44
1:C:144:TRP:CD1	1:C:169:PRO:HB2	2.53	0.44
1:D:58:SER:OG	1:D:64:HIS:CD2	2.63	0.44
1:C:136:PRO:HA	1:C:167:LEU:HD22	2.00	0.43
1:D:53:ALA:HB2	1:D:80:LEU:HD21	2.00	0.43
1:B:115:LYS:NZ	5:B:1553:HOH:O	2.52	0.43
1:B:132:ASN:HD22	1:B:132:ASN:N	2.16	0.43
1:C:183:GLU:O	1:C:202:PRO:HA	2.19	0.43
1:C:238:GLN:H	1:C:238:GLN:CD	2.22	0.43
1:C:46:THR:HG22	1:C:49:HIS:HB3	2.01	0.42
1:A:6:THR:O	1:A:93:SER:HA	2.19	0.42
1:B:238:GLN:HE21	1:B:239:PRO:HD2	1.84	0.42
1:D:203:ARG:HG3	1:D:203:ARG:NH2	2.33	0.42
1:B:192:PRO:CB	1:C:187:ILE:HD13	2.49	0.42
1:B:243:HIS:ND1	1:B:243:HIS:O	2.53	0.42
1:A:147:ARG:HD3	1:A:147:ARG:C	2.45	0.42
1:D:25:GLN:NE2	5:D:3445:HOH:O	2.52	0.42
1:A:19:LEU:HB2	1:A:95:VAL:HG23	2.02	0.42
1:A:197:PHE:CD1	1:B:50:PRO:HB3	2.55	0.42
1:B:103:HIS:HD2	3:B:1401:SO4:O4	2.03	0.42
1:D:181:ALA:HB3	1:D:205:LEU:HD12	2.00	0.41
1:D:100:ASN:H	1:D:164:ASN:ND2	2.02	0.41
1:A:183:GLU:HB2	1:A:205:LEU:HD21	2.03	0.41
1:B:168:ARG:HG3	1:B:168:ARG:HH21	1.86	0.41
1:C:90:LEU:HD21	1:C:92:LEU:HD21	2.01	0.41
1:B:110:THR:HG22	1:B:126:ALA:HB1	2.01	0.41
1:B:106:TRP:CH2	1:B:231:LEU:HD13	2.56	0.41
1:A:200:PHE:CE1	1:B:51:VAL:HG21	2.55	0.41
1:D:185:VAL:HB	1:D:201:ALA:O	2.21	0.40
1:D:210:GLU:HA	1:D:215:TRP:CG	2.57	0.40
1:C:197:PHE:CD1	1:C:197:PHE:C	2.99	0.40
1:A:163:VAL:HA	1:A:223:SER:O	2.22	0.40
1:B:62:ALA:O	1:B:63:PRO:C	2.65	0.40
1:C:115:LYS:HE2	1:D:106:TRP:CD2	2.57	0.40
1:D:142:ARG:HB3	1:D:143:PRO:HD3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ASP:OD1	1:B:195:ARG:HB3	2.22	0.40
1:D:191:ASP:HB2	1:D:192:PRO:HD2	2.04	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	241/244 (99%)	231 (96%)	9 (4%)	1 (0%)	30	22
1	B	233/244 (96%)	223 (96%)	10 (4%)	0	100	100
1	C	236/244 (97%)	226 (96%)	10 (4%)	0	100	100
1	D	230/244 (94%)	227 (99%)	3 (1%)	0	100	100
All	All	940/976 (96%)	907 (96%)	32 (3%)	1 (0%)	48	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	GLU

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	193/194 (100%)	191 (99%)	2 (1%)	68	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	190/194 (98%)	189 (100%)	1 (0%)	81	85
1	C	189/194 (97%)	183 (97%)	6 (3%)	34	29
1	D	188/194 (97%)	184 (98%)	4 (2%)	47	46
All	All	760/776 (98%)	747 (98%)	13 (2%)	53	53

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	156	GLU
1	A	206	LYS
1	B	80	LEU
1	C	8	ASP
1	C	80	LEU
1	C	131	LEU
1	C	219	GLN
1	C	237	LEU
1	C	238	GLN
1	D	131	LEU
1	D	155	LEU
1	D	187	ILE
1	D	228	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	49	HIS
1	A	61	HIS
1	A	83	HIS
1	A	107	HIS
1	A	164	ASN
1	A	177	GLN
1	A	243	HIS
1	B	25	GLN
1	B	56	HIS
1	B	64	HIS
1	B	83	HIS
1	B	103	HIS
1	B	116	GLN
1	B	132	ASN

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Mol	Chain	Res	Type
1	B	164	ASN
1	B	238	GLN
1	C	49	HIS
1	C	61	HIS
1	C	83	HIS
1	C	164	ASN
1	C	219	GLN
1	C	238	GLN
1	D	25	GLN
1	D	64	HIS
1	D	100	ASN
1	D	107	HIS
1	D	116	GLN
1	D	132	ASN
1	D	164	ASN
1	D	219	GLN
1	D	238	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](#)

Of 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 for Mogul analysis.

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
3	SO4	D	3402	-	4,4,4	0.39	0	6,6,6	0.15	0
4	GOL	B	1501	-	5,5,5	0.38	0	5,5,5	0.51	0
3	SO4	D	3401	-	4,4,4	0.37	0	6,6,6	0.12	0
4	GOL	A	501	-	5,5,5	0.63	0	5,5,5	0.57	0
3	SO4	C	2401	-	4,4,4	0.29	0	6,6,6	0.15	0
3	SO4	A	401	-	4,4,4	0.32	0	6,6,6	0.09	0
3	SO4	B	1402	-	4,4,4	0.41	0	6,6,6	0.09	0
3	SO4	A	402	-	4,4,4	0.41	0	6,6,6	0.13	0
3	SO4	A	404	-	4,4,4	0.43	0	6,6,6	0.13	0
3	SO4	A	403	-	4,4,4	0.42	0	6,6,6	0.06	0
3	SO4	B	1401	-	4,4,4	0.40	0	6,6,6	0.24	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
4	GOL	B	1501	-	-	0/4/4/4	-
4	GOL	A	501	-	-	0/4/4/4	-

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	403	SO4	1	0
3	B	1401	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	243/244 (99%)	0.22	19 (7%)	19 19	16, 27, 49, 74	0
1	B	237/244 (97%)	0.35	24 (10%)	12 12	18, 28, 59, 73	0
1	C	238/244 (97%)	0.43	29 (12%)	8 7	17, 30, 62, 73	0
1	D	234/244 (95%)	0.35	25 (10%)	11 10	15, 28, 53, 68	0
All	All	952/976 (97%)	0.34	97 (10%)	12 12	15, 28, 57, 74	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	47	ILE	7.5
1	B	45	ILE	7.4
1	B	44	ALA	6.4
1	A	40	ALA	6.4
1	B	48	ALA	6.3
1	C	131	LEU	6.2
1	D	36	THR	6.1
1	C	40	ALA	5.8
1	B	46	THR	5.7
1	C	39	SER	5.7
1	B	49	HIS	5.6
1	B	62	ALA	5.4
1	A	200	PHE	5.3
1	D	240	THR	5.3
1	D	43	HIS	5.3
1	B	43	HIS	5.2
1	A	48	ALA	5.1
1	C	135	VAL	4.8
1	C	41	ALA	4.7
1	B	60	LEU	4.7
1	D	45	ILE	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	243	HIS	4.4
1	A	131	LEU	4.4
1	B	242	ALA	4.3
1	D	48	ALA	4.3
1	C	193	MET	4.2
1	A	243	HIS	4.1
1	D	131	LEU	4.1
1	B	61	HIS	4.1
1	B	36	THR	3.8
1	C	106	TRP	3.8
1	D	47	ILE	3.7
1	A	133	GLY	3.7
1	A	39	SER	3.5
1	C	238	GLN	3.5
1	D	44	ALA	3.5
1	C	130	PRO	3.4
1	C	195	ARG	3.4
1	C	60	LEU	3.4
1	D	195	ARG	3.4
1	C	200	PHE	3.4
1	A	135	VAL	3.3
1	D	106	TRP	3.3
1	B	131	LEU	3.3
1	A	36	THR	3.2
1	D	54	TYR	3.2
1	A	132	ASN	3.2
1	D	49	HIS	3.2
1	C	61	HIS	3.2
1	D	46	THR	3.2
1	B	132	ASN	3.1
1	C	194	GLY	3.1
1	C	48	ALA	3.1
1	B	106	TRP	3.0
1	A	49	HIS	3.0
1	D	237	LEU	3.0
1	B	59	PRO	2.9
1	D	239	PRO	2.9
1	B	107	HIS	2.9
1	C	59	PRO	2.9
1	D	50	PRO	2.9
1	A	242	ALA	2.9
1	C	49	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	173	LEU	2.7
1	A	184	GLY	2.7
1	C	132	ASN	2.7
1	C	184	GLY	2.6
1	A	106	TRP	2.6
1	C	134	GLU	2.6
1	D	107	HIS	2.6
1	C	205	LEU	2.6
1	A	134	GLU	2.5
1	B	187	ILE	2.5
1	C	36	THR	2.5
1	C	107	HIS	2.5
1	D	206	LYS	2.5
1	D	86	GLY	2.4
1	D	134	GLU	2.3
1	D	135	VAL	2.3
1	A	61	HIS	2.3
1	A	205	LEU	2.3
1	B	50	PRO	2.3
1	D	192	PRO	2.3
1	C	133	GLY	2.3
1	D	35	ASP	2.2
1	C	203	ARG	2.2
1	C	190	GLU	2.2
1	C	62	ALA	2.2
1	A	60	LEU	2.2
1	D	132	ASN	2.2
1	B	193	MET	2.1
1	B	63	PRO	2.1
1	B	133	GLY	2.1
1	A	41	ALA	2.1
1	D	238	GLN	2.1
1	C	192	PRO	2.1
1	B	134	GLU	2.0

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

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
3	SO4	B	1402	5/5	0.69	0.15	87,89,91,94	0
3	SO4	A	404	5/5	0.71	0.19	82,84,88,92	0
4	GOL	B	1501	6/6	0.73	0.19	39,48,53,63	0
3	SO4	A	402	5/5	0.75	0.13	85,87,91,92	0
4	GOL	A	501	6/6	0.77	0.22	26,32,43,54	0
3	SO4	D	3402	5/5	0.81	0.12	81,84,84,86	0
3	SO4	A	403	5/5	0.85	0.14	67,72,72,78	0
2	MN	B	1301	1/1	0.95	0.14	48,48,48,48	0
2	MN	D	3301	1/1	0.97	0.10	42,42,42,42	0
2	MN	A	301	1/1	0.98	0.04	25,25,25,25	0
3	SO4	A	401	5/5	0.98	0.06	26,29,33,38	0
3	SO4	D	3401	5/5	0.98	0.07	31,35,37,45	0
2	MN	C	2301	1/1	0.99	0.02	24,24,24,24	0
3	SO4	C	2401	5/5	0.99	0.04	25,26,27,30	0
3	SO4	B	1401	5/5	0.99	0.04	21,24,27,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.