



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:16 AM GMT

PDB ID : 3OKG
Title : Crystal structure of HsdS subunit from *Thermoanaerobacter tengcongensis*
Authors : Liang, D.; Gao, P.; Tang, Q.; An, X.; Yan, X.
Deposited on : 2010-08-24
Resolution : 1.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

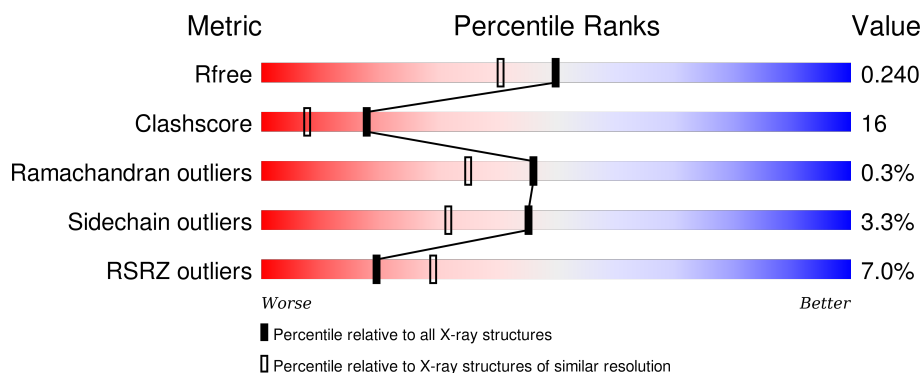
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	412	<div> <div>5%</div> <div>74%</div> <div>19%</div> <div>• 5%</div> </div>
1	B	412	<div> <div>8%</div> <div>73%</div> <div>21%</div> <div>• 5%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	406	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7061 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 Restriction endonuclease S subunits.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	1	0	0
			3096	1973	550	560	13			
1	B	391	Total	C	N	O	S	1	0	0
			3104	1978	551	561	14			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q8R9Q6
A	-12	SER	-	EXPRESSION TAG	UNP Q8R9Q6
A	-11	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
A	-10	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
A	-9	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
A	-8	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
A	-7	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
A	-6	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
A	-5	SER	-	EXPRESSION TAG	UNP Q8R9Q6
A	-4	MET	-	EXPRESSION TAG	UNP Q8R9Q6
A	-3	ASP	-	EXPRESSION TAG	UNP Q8R9Q6
A	-2	ILE	-	EXPRESSION TAG	UNP Q8R9Q6
A	-1	GLU	-	EXPRESSION TAG	UNP Q8R9Q6
A	0	PHE	-	EXPRESSION TAG	UNP Q8R9Q6
B	-13	MET	-	EXPRESSION TAG	UNP Q8R9Q6
B	-12	SER	-	EXPRESSION TAG	UNP Q8R9Q6
B	-11	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
B	-10	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
B	-9	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
B	-8	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
B	-7	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
B	-6	HIS	-	EXPRESSION TAG	UNP Q8R9Q6
B	-5	SER	-	EXPRESSION TAG	UNP Q8R9Q6
B	-4	MET	-	EXPRESSION TAG	UNP Q8R9Q6
B	-3	ASP	-	EXPRESSION TAG	UNP Q8R9Q6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	ILE	-	EXPRESSION TAG	UNP Q8R9Q6
B	-1	GLU	-	EXPRESSION TAG	UNP Q8R9Q6
B	0	PHE	-	EXPRESSION TAG	UNP Q8R9Q6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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

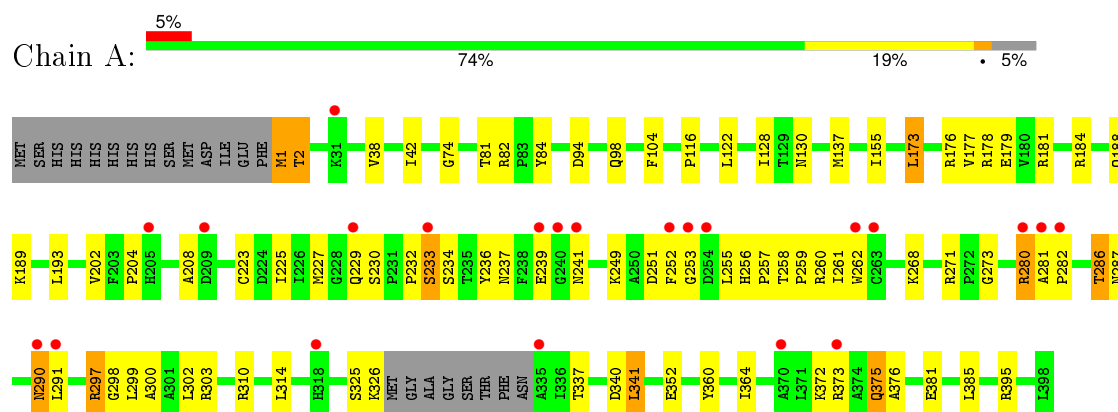
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	397	Total	O	0	0
			397	397		
3	B	389	Total	O	0	0
			389	389		

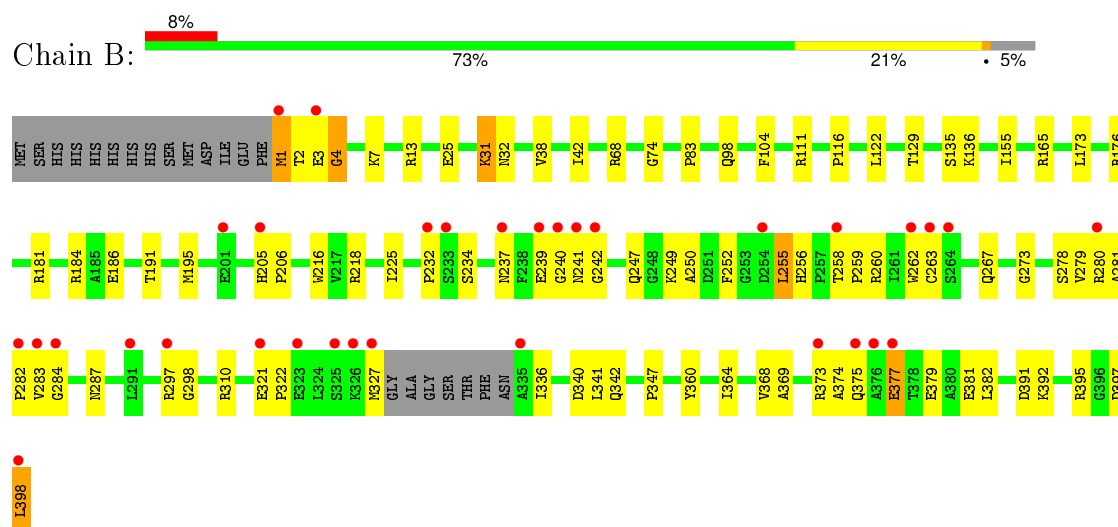
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Restriction endonuclease S subunits



- Molecule 1: Restriction endonuclease S subunits



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.99Å 137.80Å 142.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.95 10.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (10.00-1.95) 99.7 (10.00-1.95)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.55 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.197 , 0.240 0.205 , 0.240	Depositor DCC
R_{free} test set	4371 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 62.0	EDS
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 87286 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7061	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 66.19 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.2913e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.49	0/3170	0.65	0/4309
1	B	0.47	0/3178	0.61	0/4319
All	All	0.48	0/6348	0.63	0/8628

There are no bond length outliers.

There are no bond angle outliers.

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	3096	0	3131	109	0
1	B	3104	0	3140	103	0
2	A	35	0	0	2	0
2	B	40	0	0	1	0
3	A	397	0	0	9	0
3	B	389	0	0	15	0
All	All	7061	0	6271	198	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 16.

All (198) 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:281:ALA:HB3	1:B:282:PRO:CD	1.73	1.18
1:B:281:ALA:CB	1:B:282:PRO:HD3	1.71	1.18
1:A:281:ALA:HB3	1:A:282:PRO:HD3	1.30	1.12
1:A:281:ALA:CB	1:A:282:PRO:HD3	1.81	1.10
1:A:130:ASN:HB3	3:A:567:HOH:O	1.50	1.08
1:A:280:ARG:CG	1:A:280:ARG:HH11	1.68	1.07
1:A:280:ARG:NH1	1:A:280:ARG:HG3	1.64	1.05
1:A:281:ALA:HB3	1:A:282:PRO:CD	1.87	1.04
1:B:165:ARG:HH12	1:B:398:LEU:HD11	1.22	1.02
1:B:283:VAL:HG21	1:B:336:ILE:HG22	1.39	1.01
1:B:281:ALA:HB3	1:B:282:PRO:HD3	1.30	1.00
1:B:165:ARG:HH22	1:B:398:LEU:HD21	1.21	0.98
1:A:280:ARG:HH11	1:A:280:ARG:HG3	0.83	0.97
1:B:279:VAL:HG13	1:B:336:ILE:HG23	1.46	0.94
1:B:321:GLU:HB3	1:B:322:PRO:HD3	1.49	0.93
1:B:283:VAL:CG2	1:B:336:ILE:HG22	2.01	0.89
1:B:281:ALA:HB3	1:B:282:PRO:HD2	1.57	0.84
1:B:281:ALA:HB1	1:B:282:PRO:HD3	1.58	0.83
1:B:281:ALA:CB	1:B:282:PRO:CD	2.33	0.82
1:A:234:SER:HB2	1:B:234:SER:HB2	1.59	0.82
1:A:237:ASN:HD22	1:A:239:GLU:H	1.24	0.80
1:A:81:THR:HG23	2:A:399:SO4:O3	1.82	0.80
1:A:280:ARG:NH2	1:A:297:ARG:HD3	1.97	0.79
1:B:165:ARG:HH22	1:B:398:LEU:CD2	1.95	0.79
1:B:369:ALA:O	1:B:373:ARG:HD3	1.82	0.78
1:B:242:GLY:HA3	1:B:263:CYS:O	1.82	0.78
1:B:280:ARG:HG3	1:B:298:GLY:HA2	1.66	0.78
1:B:283:VAL:O	1:B:283:VAL:HG22	1.83	0.77
1:A:376:ALA:HB2	1:B:374:ALA:HB2	1.66	0.77
1:A:280:ARG:HG2	1:A:298:GLY:HA2	1.66	0.77
1:A:122:LEU:HD21	1:A:155:ILE:HB	1.65	0.77
1:B:397:ASP:O	1:B:398:LEU:HB2	1.83	0.76
1:A:179:GLU:HG2	3:A:767:HOH:O	1.84	0.76
1:A:249:LYS:HD3	1:A:282:PRO:HB2	1.65	0.76
1:B:205:HIS:CD2	1:B:206:PRO:HD2	2.20	0.76
1:A:225:ILE:HD13	1:A:341:LEU:HB3	1.69	0.74
1:A:271:ARG:HG3	1:A:303:ARG:NH2	2.03	0.74
1:A:281:ALA:CB	1:A:282:PRO:CD	2.51	0.74
1:B:283:VAL:CG2	1:B:336:ILE:CG2	2.67	0.73
1:B:279:VAL:HA	1:B:283:VAL:HG23	1.70	0.73
1:B:255:LEU:HD22	1:B:256:HIS:CE1	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:ARG:HG2	1:A:375:GLN:HG2	1.71	0.72
1:A:237:ASN:HD21	1:A:241:ASN:H	1.35	0.72
1:A:188:GLN:NE2	1:A:372:LYS:HA	2.04	0.72
1:A:337:THR:HG23	1:A:340:ASP:H	1.55	0.70
1:B:395:ARG:HD3	3:B:614:HOH:O	1.91	0.70
1:A:234:SER:CB	1:B:234:SER:HB2	2.22	0.69
1:A:286:THR:HG21	1:A:314:LEU:HD11	1.73	0.69
1:A:273:GLY:O	1:A:310:ARG:HD2	1.93	0.69
1:B:4:GLY:N	3:B:781:HOH:O	2.24	0.68
1:B:68:ARG:NE	3:B:787:HOH:O	2.26	0.68
1:B:237:ASN:ND2	1:B:241:ASN:HB3	2.09	0.68
1:A:337:THR:HG22	1:A:340:ASP:CG	2.14	0.67
1:A:184:ARG:HD3	1:B:381:GLU:OE1	1.95	0.66
1:B:181:ARG:HD2	1:B:382:LEU:HD21	1.77	0.66
1:B:283:VAL:HG21	1:B:336:ILE:CG2	2.23	0.65
1:B:360:TYR:CZ	1:B:364:ILE:HD11	2.31	0.65
1:B:165:ARG:NH2	1:B:398:LEU:HD21	2.04	0.65
1:B:38:VAL:H	1:B:98:GLN:NE2	1.94	0.64
1:A:280:ARG:HH22	1:A:297:ARG:HH11	1.43	0.64
1:A:42:ILE:HG12	2:A:400:SO4:O2	1.97	0.64
1:A:337:THR:CG2	1:A:340:ASP:H	2.10	0.64
1:B:3:GLU:HG3	3:B:781:HOH:O	1.98	0.64
1:B:237:ASN:ND2	1:B:239:GLU:O	2.31	0.63
1:A:42:ILE:HD13	1:A:104:PHE:CZ	2.33	0.63
1:A:188:GLN:HE21	1:A:372:LYS:HA	1.61	0.63
1:A:230:SER:HB3	3:A:665:HOH:O	1.99	0.62
1:B:129:THR:HG23	3:B:790:HOH:O	2.00	0.62
1:B:377:GLU:CG	1:B:377:GLU:O	2.47	0.61
1:A:225:ILE:HG22	1:A:227:MET:HE3	1.83	0.61
1:A:178:ARG:NH1	3:A:490:HOH:O	2.34	0.60
1:A:286:THR:CG2	1:A:314:LEU:HD11	2.31	0.60
1:B:38:VAL:H	1:B:98:GLN:HE21	1.50	0.60
1:B:68:ARG:CZ	3:B:787:HOH:O	2.50	0.59
1:B:278:SER:O	1:B:283:VAL:HA	2.03	0.59
1:B:249:LYS:CD	1:B:282:PRO:HG2	2.33	0.59
1:B:232:PRO:HD3	1:B:267:GLN:NE2	2.18	0.58
1:B:321:GLU:HB3	1:B:322:PRO:CD	2.28	0.58
1:B:184:ARG:CZ	1:B:374:ALA:HB1	2.34	0.57
1:B:165:ARG:NH1	1:B:398:LEU:HD11	2.06	0.57
1:B:184:ARG:HG2	1:B:375:GLN:HG3	1.87	0.57
1:B:31:LYS:N	1:B:31:LYS:HD2	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:VAL:H	1:A:98:GLN:NE2	2.02	0.57
1:A:239:GLU:HB2	1:A:241:ASN:ND2	2.19	0.57
1:A:271:ARG:HG3	1:A:303:ARG:HH21	1.68	0.56
1:A:376:ALA:HB2	1:B:374:ALA:CB	2.34	0.56
1:A:286:THR:HG21	1:A:314:LEU:CD1	2.35	0.56
1:B:379:GLU:HB2	3:B:659:HOH:O	2.05	0.56
1:B:249:LYS:HD3	1:B:282:PRO:HG2	1.88	0.56
1:B:239:GLU:HA	1:B:239:GLU:OE1	2.05	0.56
1:A:290:ASN:H	1:A:290:ASN:HD22	1.52	0.56
1:A:249:LYS:CD	1:A:282:PRO:HB2	2.36	0.55
1:A:375:GLN:HE21	1:A:375:GLN:HA	1.71	0.55
1:A:176:ARG:HD3	1:B:176:ARG:HD3	1.88	0.55
1:A:38:VAL:H	1:A:98:GLN:HE21	1.53	0.55
1:A:281:ALA:HB1	1:A:282:PRO:HD3	1.81	0.55
1:B:336:ILE:HD11	1:B:341:LEU:HG	1.87	0.55
1:A:360:TYR:CZ	1:A:364:ILE:HD11	2.42	0.55
1:A:253:GLY:H	1:A:287:ASN:HD21	1.56	0.54
1:A:251:ASP:OD1	1:B:260:ARG:HG2	2.07	0.54
1:A:202:VAL:C	1:A:204:PRO:HD3	2.29	0.53
1:A:290:ASN:H	1:A:290:ASN:ND2	2.06	0.53
1:A:237:ASN:HD22	1:A:239:GLU:N	2.02	0.53
1:B:218:ARG:NH2	3:B:478:HOH:O	2.42	0.53
1:A:252:PHE:CZ	1:A:299:LEU:HD22	2.43	0.53
1:A:280:ARG:HH22	1:A:297:ARG:NH1	2.07	0.52
1:A:290:ASN:O	1:A:291:LEU:HD13	2.09	0.52
1:A:173:LEU:CD1	1:A:176:ARG:HH11	2.23	0.52
1:B:392:LYS:HE3	3:B:712:HOH:O	2.09	0.52
1:B:3:GLU:CD	1:B:7:LYS:HB2	2.30	0.52
1:A:395:ARG:HD2	3:A:797:HOH:O	2.10	0.52
1:A:251:ASP:O	1:A:257:PRO:HB3	2.11	0.51
1:B:377:GLU:HG3	1:B:377:GLU:O	2.10	0.51
1:A:325:SER:O	1:A:325:SER:OG	2.24	0.51
1:A:260:ARG:NH2	1:B:260:ARG:HH12	2.08	0.51
1:A:233:SER:O	1:A:234:SER:OG	2.27	0.51
1:A:227:MET:HE2	1:A:300:ALA:HB1	1.92	0.51
1:A:281:ALA:HB3	1:A:282:PRO:HD2	1.82	0.51
1:A:303:ARG:HD3	3:A:518:HOH:O	2.10	0.51
1:A:252:PHE:CZ	1:A:299:LEU:CD2	2.95	0.50
1:A:236:TYR:HB3	1:A:261:ILE:HD11	1.93	0.50
1:B:135:SER:HB2	3:B:694:HOH:O	2.12	0.49
1:B:247:GLN:NE2	1:B:297:ARG:HG2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:ILE:HG13	1:B:340:ASP:HB2	1.93	0.49
1:A:381:GLU:O	1:A:385:LEU:HG	2.12	0.49
1:B:273:GLY:O	1:B:310:ARG:HD3	2.13	0.48
1:B:42:ILE:HD13	1:B:104:PHE:CZ	2.47	0.48
1:B:391:ASP:O	1:B:395:ARG:HG3	2.13	0.48
1:B:32:ASN:ND2	3:B:487:HOH:O	2.36	0.48
1:B:184:ARG:HE	1:B:375:GLN:HE21	1.60	0.48
1:A:286:THR:HG22	3:A:720:HOH:O	2.13	0.48
1:B:284:GLY:O	1:B:321:GLU:OE2	2.32	0.48
1:B:122:LEU:HD21	1:B:155:ILE:HB	1.94	0.47
1:A:325:SER:O	1:A:326:LYS:C	2.53	0.47
1:A:280:ARG:CG	1:A:280:ARG:NH1	2.40	0.47
1:B:3:GLU:OE1	1:B:7:LYS:HB2	2.14	0.47
1:A:177:VAL:O	1:A:181:ARG:HG3	2.15	0.47
1:B:68:ARG:NH2	3:B:787:HOH:O	2.48	0.47
1:A:251:ASP:HA	1:B:260:ARG:HD3	1.96	0.47
1:A:290:ASN:HD22	1:A:290:ASN:N	2.12	0.47
1:B:327:MET:CE	1:B:336:ILE:HD12	2.45	0.47
1:A:237:ASN:ND2	1:A:241:ASN:H	2.08	0.46
1:A:373:ARG:O	1:B:374:ALA:HA	2.15	0.46
1:B:1:MET:HA	3:B:700:HOH:O	2.15	0.46
1:B:237:ASN:HD21	1:B:241:ASN:HB3	1.80	0.46
1:B:186:GLU:HG2	3:B:431:HOH:O	2.15	0.46
1:A:229:GLN:OE1	1:A:268:LYS:HE2	2.16	0.46
1:A:128:ILE:HD11	1:A:155:ILE:HG22	1.97	0.46
1:A:236:TYR:HA	1:A:262:TRP:O	2.16	0.45
1:B:279:VAL:O	1:B:279:VAL:HG12	2.17	0.45
1:B:216:TRP:CZ3	1:B:347:PRO:HD3	2.52	0.45
1:B:83:PRO:HB2	1:B:129:THR:HG22	1.97	0.45
1:A:173:LEU:HD13	1:A:176:ARG:HH11	1.82	0.45
1:A:1:MET:HB2	1:A:2:THR:H	1.58	0.45
1:B:321:GLU:CB	1:B:322:PRO:HD3	2.31	0.45
1:B:191:THR:HG22	1:B:368:VAL:HG23	1.98	0.45
1:B:195:MET:HE2	3:B:601:HOH:O	2.16	0.45
1:A:260:ARG:NH2	1:B:260:ARG:NH1	2.65	0.44
1:A:1:MET:HE2	1:A:2:THR:H	1.83	0.44
1:A:227:MET:HE2	1:A:300:ALA:CB	2.47	0.44
1:B:42:ILE:HG12	2:B:400:SO4:O1	2.18	0.44
1:A:375:GLN:HA	1:A:375:GLN:NE2	2.31	0.44
1:A:204:PRO:HB2	1:A:208:ALA:HB3	1.99	0.44
1:B:249:LYS:O	1:B:252:PHE:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:GLY:HA2	1:B:262:TRP:CD1	2.53	0.43
1:B:249:LYS:HD2	1:B:282:PRO:HG2	2.00	0.43
1:A:232:PRO:C	1:A:233:SER:O	2.53	0.43
1:A:225:ILE:HG22	1:A:227:MET:CE	2.47	0.43
1:B:184:ARG:HG2	1:B:375:GLN:CG	2.49	0.43
1:B:205:HIS:CG	1:B:206:PRO:HD2	2.53	0.43
1:B:225:ILE:HD12	1:B:342:GLN:HG3	2.00	0.43
1:A:258:THR:HA	1:A:259:PRO:HD3	1.72	0.43
1:B:74:GLY:O	1:B:116:PRO:HB3	2.20	0.42
1:A:252:PHE:HZ	1:A:299:LEU:HD22	1.84	0.42
1:A:260:ARG:NH1	1:B:250:ALA:O	2.53	0.42
1:A:137:MET:HG3	1:A:137:MET:H	1.61	0.42
1:A:181:ARG:NE	1:A:381:GLU:OE2	2.43	0.42
1:A:189:LYS:NZ	1:A:189:LYS:HB3	2.34	0.42
1:A:341:LEU:HA	1:A:341:LEU:HD12	1.93	0.42
1:B:1:MET:SD	1:B:2:THR:N	2.83	0.41
1:A:234:SER:HA	1:B:234:SER:HA	2.01	0.41
1:A:280:ARG:NH2	1:A:297:ARG:CD	2.75	0.41
1:B:258:THR:HA	1:B:259:PRO:HD3	1.86	0.41
1:A:82:ARG:O	1:A:84:TYR:N	2.54	0.41
1:A:74:GLY:O	1:A:116:PRO:HB3	2.21	0.41
1:A:255:LEU:HB2	1:A:256:HIS:CD2	2.56	0.41
1:A:280:ARG:HA	1:A:280:ARG:HD2	1.55	0.41
1:A:239:GLU:HB2	1:A:241:ASN:HD21	1.86	0.41
1:A:372:LYS:HD3	3:A:668:HOH:O	2.21	0.41
1:A:1:MET:CE	1:A:2:THR:H	2.34	0.41
1:B:111:ARG:CD	1:B:116:PRO:HD3	2.51	0.41
1:B:283:VAL:O	1:B:283:VAL:CG2	2.55	0.41
1:B:247:GLN:HE21	1:B:297:ARG:HG2	1.85	0.40
1:A:223:CYS:SG	1:A:302:LEU:HB3	2.61	0.40
1:B:206:PRO:HA	1:B:216:TRP:CH2	2.56	0.40
1:A:1:MET:HG2	3:A:691:HOH:O	2.20	0.40
1:A:273:GLY:O	1:A:310:ARG:CD	2.68	0.40
1:A:176:ARG:CD	1:B:176:ARG:HD3	2.50	0.40

There are no symmetry-related clashes.

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	386/412 (94%)	372 (96%)	13 (3%)	1 (0%)	46	35
1	B	387/412 (94%)	365 (94%)	21 (5%)	1 (0%)	46	35
All	All	773/824 (94%)	737 (95%)	34 (4%)	2 (0%)	46	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	297	ARG
1	B	4	GLY

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	335/354 (95%)	323 (96%)	12 (4%)	42	28
1	B	336/354 (95%)	326 (97%)	10 (3%)	48	36
All	All	671/708 (95%)	649 (97%)	22 (3%)	45	32

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	THR
1	A	94	ASP
1	A	173	LEU

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Mol	Chain	Res	Type
1	A	193	LEU
1	A	233	SER
1	A	280	ARG
1	A	286	THR
1	A	290	ASN
1	A	341	LEU
1	A	352	GLU
1	A	375	GLN
1	B	1	MET
1	B	13	ARG
1	B	25	GLU
1	B	31	LYS
1	B	136	LYS
1	B	173	LEU
1	B	255	LEU
1	B	287	ASN
1	B	377	GLU
1	B	398	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	ASN
1	A	98	GLN
1	A	188	GLN
1	A	237	ASN
1	A	241	ASN
1	A	287	ASN
1	A	290	ASN
1	A	363	GLN
1	A	375	GLN
1	B	87	ASN
1	B	98	GLN
1	B	148	ASN
1	B	205	HIS
1	B	237	ASN
1	B	241	ASN
1	B	366	GLN
1	B	375	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

15 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	399	-	4,4,4	0.19	0	6,6,6	0.24	0
2	SO4	A	400	-	4,4,4	0.38	0	6,6,6	0.27	0
2	SO4	A	401	-	4,4,4	0.14	0	6,6,6	0.19	0
2	SO4	A	402	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	403	-	4,4,4	0.14	0	6,6,6	0.25	0
2	SO4	A	404	-	4,4,4	0.11	0	6,6,6	0.12	0
2	SO4	A	405	-	4,4,4	0.22	0	6,6,6	0.23	0
2	SO4	B	399	-	4,4,4	0.20	0	6,6,6	0.13	0
2	SO4	B	400	-	4,4,4	0.38	0	6,6,6	0.21	0
2	SO4	B	401	-	4,4,4	0.13	0	6,6,6	0.40	0
2	SO4	B	402	-	4,4,4	0.13	0	6,6,6	0.32	0
2	SO4	B	403	-	4,4,4	0.11	0	6,6,6	0.09	0
2	SO4	B	404	-	4,4,4	0.13	0	6,6,6	0.08	0
2	SO4	B	405	-	4,4,4	0.16	0	6,6,6	0.18	0
2	SO4	B	406	-	4,4,4	0.18	0	6,6,6	0.34	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	399	-	-	0/0/0/0	0/0/0/0
2	SO4	A	400	-	-	0/0/0/0	0/0/0/0
2	SO4	A	401	-	-	0/0/0/0	0/0/0/0
2	SO4	A	402	-	-	0/0/0/0	0/0/0/0
2	SO4	A	403	-	-	0/0/0/0	0/0/0/0
2	SO4	A	404	-	-	0/0/0/0	0/0/0/0
2	SO4	A	405	-	-	0/0/0/0	0/0/0/0
2	SO4	B	399	-	-	0/0/0/0	0/0/0/0
2	SO4	B	400	-	-	0/0/0/0	0/0/0/0
2	SO4	B	401	-	-	0/0/0/0	0/0/0/0
2	SO4	B	402	-	-	0/0/0/0	0/0/0/0
2	SO4	B	403	-	-	0/0/0/0	0/0/0/0
2	SO4	B	404	-	-	0/0/0/0	0/0/0/0
2	SO4	B	405	-	-	0/0/0/0	0/0/0/0
2	SO4	B	406	-	-	0/0/0/0	0/0/0/0

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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	399	SO4	1	0
2	A	400	SO4	1	0
2	B	400	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	390/412 (94%)	0.29	22 (5%)	28 39	16, 31, 62, 90	1 (0%)
1	B	391/412 (94%)	0.38	33 (8%)	14 22	17, 33, 69, 96	1 (0%)
All	All	781/824 (94%)	0.33	55 (7%)	19 29	16, 32, 65, 96	2 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	ALA	7.3
1	B	233	SER	6.4
1	A	233	SER	6.1
1	B	283	VAL	5.8
1	B	284	GLY	5.8
1	B	377	GLU	5.4
1	B	239	GLU	5.3
1	A	252	PHE	5.1
1	B	240	GLY	4.6
1	B	398	LEU	4.5
1	B	376	ALA	4.4
1	B	262	TRP	3.9
1	B	241	ASN	3.9
1	A	280	ARG	3.8
1	B	282	PRO	3.7
1	B	263	CYS	3.6
1	B	373	ARG	3.4
1	A	335	ALA	3.3
1	B	325	SER	3.2
1	B	242	GLY	3.1
1	B	326	LYS	3.1
1	A	254	ASP	3.1
1	B	254	ASP	3.0
1	B	3	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	258	THR	2.7
1	A	253	GLY	2.7
1	A	262	TRP	2.7
1	B	297	ARG	2.5
1	A	263	CYS	2.5
1	B	323	GLU	2.5
1	A	370	ALA	2.5
1	A	205	HIS	2.4
1	B	232	PRO	2.4
1	B	280	ARG	2.4
1	A	229	GLN	2.4
1	B	335	ALA	2.4
1	A	373	ARG	2.4
1	B	291	LEU	2.4
1	A	240	GLY	2.3
1	A	291	LEU	2.3
1	A	290	ASN	2.3
1	B	327	MET	2.3
1	B	264	SER	2.2
1	A	31	LYS	2.2
1	A	241	ASN	2.2
1	B	237	ASN	2.2
1	B	321	GLU	2.2
1	B	375	GLN	2.2
1	A	239	GLU	2.1
1	B	201	GLU	2.1
1	A	282	PRO	2.1
1	A	318	HIS	2.0
1	B	205	HIS	2.0
1	B	1	MET	2.0
1	A	209	ASP	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	B	406	5/5	0.95	0.20	2.28	49,53,63,68	0
2	SO4	B	403	5/5	0.95	0.20	1.77	46,54,78,83	0
2	SO4	A	404	5/5	0.93	0.15	0.77	46,57,83,93	0
2	SO4	A	399	5/5	0.98	0.12	0.41	36,37,42,62	0
2	SO4	A	400	5/5	0.99	0.09	-1.07	35,37,39,61	0
2	SO4	B	400	5/5	0.98	0.09	-1.22	37,37,45,56	0
2	SO4	A	401	5/5	0.92	0.17	-	59,60,93,94	0
2	SO4	B	399	5/5	0.97	0.19	-	47,48,62,64	0
2	SO4	A	403	5/5	0.93	0.19	-	73,79,80,109	0
2	SO4	B	401	5/5	0.96	0.18	-	37,41,51,57	0
2	SO4	A	405	5/5	0.94	0.19	-	41,49,64,68	0
2	SO4	B	405	5/5	0.92	0.30	-	53,73,93,94	0
2	SO4	B	402	5/5	0.86	0.23	-	63,67,97,103	0
2	SO4	A	402	5/5	0.96	0.29	-	43,44,69,90	0
2	SO4	B	404	5/5	0.91	0.24	-	67,68,85,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.