



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 08:18 AM GMT

PDB ID : 4D8T
Title : Crystal structure of D-Cysteine desulfhydrase from Salmonella typhimurium at 2.2 Å resolution
Authors : Bharath, S.R.; Shveta, B.; Rajesh, K.H.; Savithri, H.S.; Murthy, M.R.N.
Deposited on : 2012-01-11
Resolution : 2.28 Å (reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

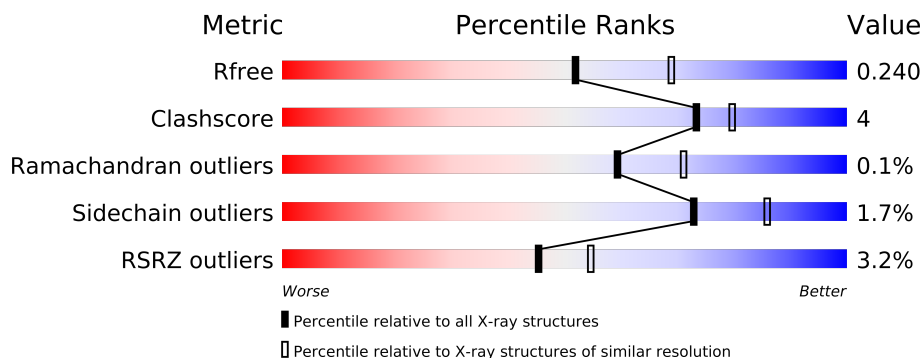
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.28 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}	66092	3861 (2.30-2.26)
Clashscore	79885	4801 (2.30-2.26)
Ramachandran outliers	78287	4729 (2.30-2.26)
Sidechain outliers	78261	4728 (2.30-2.26)
RSRZ outliers	66119	3864 (2.30-2.26)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	342	
1	B	342	
1	C	342	
1	D	342	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	CL	A	402	-	X
4	BEN	B	402	-	X
4	BEN	B	403	-	X
4	BEN	C	402	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10235 atoms, of which 0 are hydrogen and 0 are deuterium.

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 D-cysteine desulfhydrase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	P	S	0	1	0
			2468	1571	418	469	1	9			
1	B	318	Total	C	N	O	P	S	6	1	0
			2364	1507	396	451	1	9			
1	C	323	Total	C	N	O	P	S	0	4	0
			2436	1549	414	463	1	9			
1	D	328	Total	C	N	O	P	S	0	1	0
			2451	1565	412	464	1	9			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
A	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
A	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
A	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
A	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
A	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
A	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
A	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7
B	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
B	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
B	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
B	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
B	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
B	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
B	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
B	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7
C	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
C	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
C	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
C	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
C	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
C	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
C	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
C	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7
D	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
D	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
D	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
D	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
D	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
D	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
D	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
D	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7

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

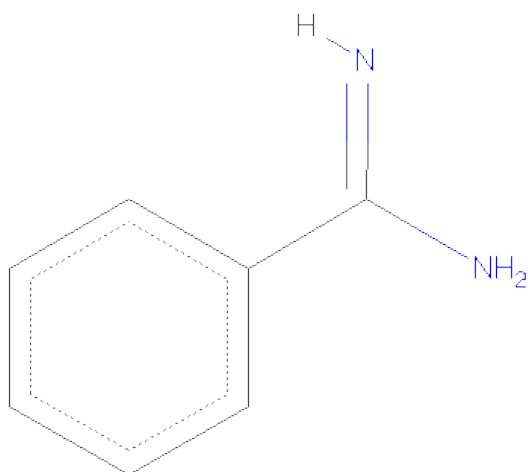


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is BENZAMIDINE (three-letter code: BEN) (formula: C₇H₈N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			9	7	2		
4	B	1	Total	C	N	0	0
			9	7	2		
4	B	1	Total	C	N	0	0
			9	7	2		
4	C	1	Total	C	N	0	0
			9	7	2		
4	D	1	Total	C	N	0	0
			9	7	2		

- Molecule 5 is water.

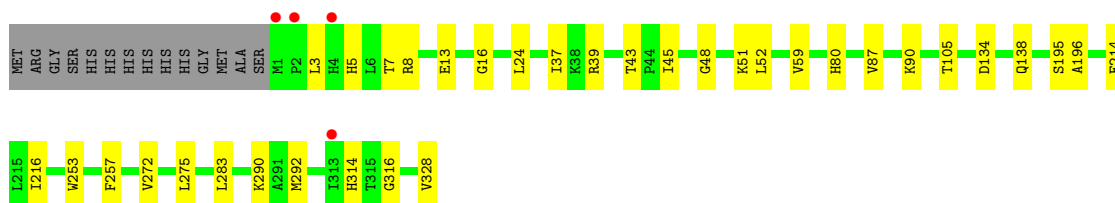
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	143	Total	O	0	0
			143	143		
5	B	90	Total	O	0	0
			90	90		
5	C	91	Total	O	0	0
			91	91		
5	D	126	Total	O	0	0
			126	126		

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.

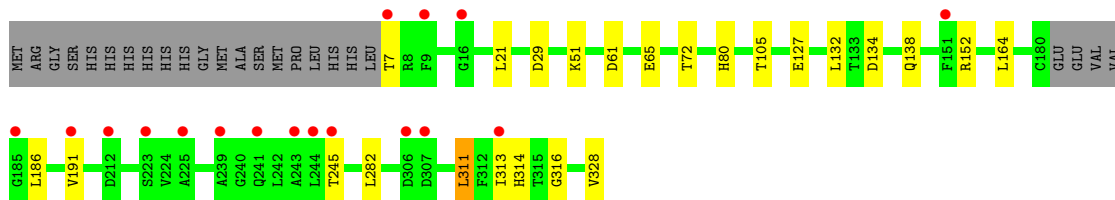
- Molecule 1: D-cysteine desulfhydrase

Chain A: 



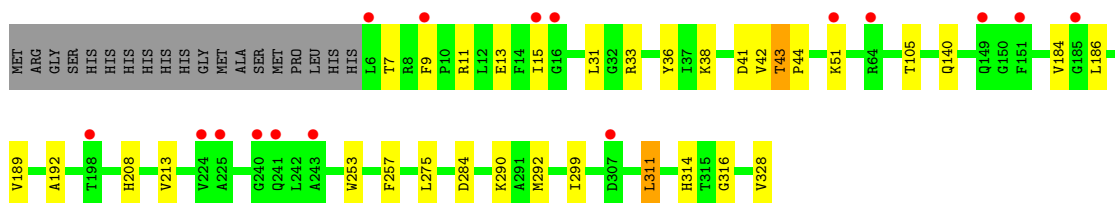
- Molecule 1: D-cysteine desulfhydrase

Chain B: 



- Molecule 1: D-cysteine desulfhydrase

Chain C: 



- Molecule 1: D-cysteine desulfhydrase

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.48Å 165.45Å 69.21Å 90.00° 119.01° 90.00°	Depositor
Resolution (Å)	29.19 – 2.28 29.20 – 2.28	Depositor EDS
% Data completeness (in resolution range)	97.6 (29.19-2.28) 97.7 (29.20-2.28)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.189 , 0.242 0.188 , 0.240	Depositor DCC
R_{free} test set	2926 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 33.6	EDS
Estimated twinning fraction	0.011 for l,k,-h-l 0.011 for -h-l,k,h 0.029 for h,-k,-h-l 0.028 for l,-k,h 0.044 for -h-l,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 57671 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10235	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, BEN, SO4, IT1

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	0.43	1/2494 (0.0%)	0.56	0/3399
1	B	0.44	0/2386	0.55	0/3252
1	C	0.41	1/2468 (0.0%)	0.54	0/3362
1	D	0.43	0/2477	0.56	0/3377
All	All	0.43	2/9825 (0.0%)	0.55	0/13390

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	253	TRP	CD2-CE2	5.31	1.47	1.41
1	A	253	TRP	CD2-CE2	5.08	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2468	0	2471	21	0
1	B	2364	0	2356	18	0
1	C	2436	0	2443	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2451	0	2452	18	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	1	0	0	0	0
4	A	9	0	7	0	0
4	B	18	0	14	0	0
4	C	9	0	7	0	0
4	D	9	0	7	0	0
5	A	143	0	0	1	0
5	B	90	0	0	0	0
5	C	91	0	0	1	0
5	D	126	0	0	2	0
All	All	10235	0	9757	82	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (82) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:33[B]:ARG:HG3	1:C:33[B]:ARG:HH11	1.15	1.08
1:C:33[B]:ARG:CG	1:C:33[B]:ARG:HH11	1.71	1.03
1:B:105:THR:OG1	1:B:328:VAL:HG12	1.77	0.84
1:C:33[B]:ARG:HG3	1:C:33[B]:ARG:NH1	1.86	0.83
1:C:105:THR:OG1	1:C:328:VAL:HG12	1.81	0.81
1:D:105:THR:OG1	1:D:328:VAL:HG12	1.82	0.79
1:D:90[B]:LYS:NZ	1:D:90[B]:LYS:HB2	2.00	0.75
1:C:42:VAL:O	1:C:42:VAL:HG12	1.90	0.71
1:C:33[B]:ARG:CB	1:C:33[B]:ARG:HH11	2.04	0.70
1:A:134:ASP:H	1:A:138:GLN:NE2	1.91	0.69
1:C:186:LEU:HD11	1:C:311:LEU:HD12	1.80	0.63
1:A:105:THR:OG1	1:A:328:VAL:HG12	1.99	0.62
1:C:43:THR:HG22	1:C:44:PRO:HD2	1.81	0.62
1:C:314:HIS:HD2	1:C:316:GLY:H	1.49	0.60
1:D:185:GLY:O	1:D:309:PRO:HD2	2.02	0.60
1:A:314:HIS:HD2	1:A:316:GLY:H	1.48	0.59
1:D:90[B]:LYS:HZ3	1:D:90[B]:LYS:HB2	1.67	0.59
1:B:314:HIS:HD2	1:B:316:GLY:H	1.51	0.57
1:C:33[B]:ARG:CG	1:C:33[B]:ARG:NH1	2.44	0.55
1:A:13:GLU:OE2	1:A:16:GLY:HA2	2.07	0.55
1:D:314:HIS:HD2	1:D:316:GLY:H	1.55	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:90[B]:LYS:HZ2	1:D:90[B]:LYS:HB2	1.73	0.54
1:A:90:LYS:NZ	5:A:636:HOH:O	2.40	0.54
1:C:15:ILE:HG12	1:C:43:THR:CG2	2.38	0.53
1:A:272:VAL:HG22	1:A:283:LEU:HB2	1.90	0.52
1:D:51:IT1:HEA	1:D:80:HIS:HB2	1.91	0.52
1:A:105:THR:CB	1:A:328:VAL:HG12	2.39	0.52
1:C:257:PHE:HA	1:C:290:LYS:HD3	1.92	0.52
1:A:51:IT1:HEA	1:A:80:HIS:HB2	1.90	0.52
1:C:189:VAL:HG23	1:C:213:VAL:HG11	1.92	0.51
1:C:42:VAL:O	1:C:42:VAL:CG1	2.58	0.49
1:A:5:HIS:O	1:A:8:ARG:HG2	2.12	0.49
1:C:11:ARG:HD2	5:C:511:HOH:O	2.13	0.49
1:D:266:ASP:O	1:D:270:GLU:HG2	2.13	0.49
1:D:251:HIS:HD2	5:D:619:HOH:O	1.97	0.48
1:A:314:HIS:CD2	1:A:316:GLY:H	2.30	0.48
1:A:257:PHE:HA	1:A:290:LYS:HD3	1.96	0.48
1:C:51:IT1:H6	1:C:192:ALA:HB3	1.96	0.48
1:D:94:HIS:HE1	1:D:125:GLN:HE21	1.61	0.48
1:C:15:ILE:HG12	1:C:43:THR:HG21	1.96	0.47
1:D:259:PRO:HG2	1:D:263:VAL:HG11	1.95	0.47
1:C:41:ASP:HB3	1:C:316:GLY:HA2	1.97	0.47
1:A:275:LEU:HD13	1:A:292:MET:HG2	1.97	0.47
1:D:51:IT1:H6	1:D:192:ALA:HB3	1.97	0.46
1:C:314:HIS:CD2	1:C:316:GLY:H	2.30	0.46
1:C:275:LEU:HD13	1:C:292:MET:HG2	1.97	0.46
1:B:186:LEU:HD11	1:B:311:LEU:HB2	1.98	0.46
1:D:71:ILE:HG12	1:D:96:VAL:HB	1.98	0.46
1:A:43:THR:OG1	1:A:48:GLY:HA2	2.17	0.45
1:C:33[B]:ARG:CB	1:C:33[B]:ARG:NH1	2.75	0.45
1:C:7:THR:HG23	1:C:9:PHE:HD1	1.82	0.45
1:B:51:IT1:HEA	1:B:80:HIS:HB2	1.99	0.45
1:A:134:ASP:H	1:A:138:GLN:HE21	1.64	0.45
1:D:94:HIS:HD2	5:D:538:HOH:O	2.00	0.44
1:B:72:THR:OG1	1:B:80:HIS:HE1	2.00	0.44
1:B:61:ASP:O	1:B:65:GLU:HG3	2.17	0.44
1:A:59:VAL:HG21	1:A:87:VAL:HG11	1.99	0.44
1:C:105:THR:HG1	1:C:328:VAL:HG12	1.82	0.44
1:B:282:LEU:O	1:B:314:HIS:HE1	2.00	0.44
1:A:195:SER:O	1:A:196:ALA:HB3	2.18	0.44
1:B:105:THR:HG1	1:B:328:VAL:HG12	1.80	0.44
1:A:105:THR:HB	1:A:328:VAL:HG12	1.99	0.43
1:B:132:LEU:HA	1:B:138:GLN:HE22	1.81	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:152:ARG:HH11	1:B:152:ARG:HB3	1.81	0.43
1:D:52:LEU:HB2	1:D:83:GLN:HE21	1.83	0.43
1:B:328:VAL:HG13	1:D:149:GLN:NE2	2.33	0.43
1:C:38:LYS:HB2	1:C:311:LEU:HD21	2.00	0.43
1:C:36:TYR:CE1	1:C:184:VAL:HG21	2.53	0.43
1:A:45:ILE:HD12	1:A:52:LEU:HD11	2.01	0.42
1:B:191:VAL:HG23	1:B:313:ILE:HB	2.01	0.42
1:B:21:LEU:HD11	1:B:311:LEU:HD21	2.02	0.42
1:A:37:ILE:HG12	1:A:39:ARG:HD2	2.02	0.42
1:D:94:HIS:HE1	1:D:125:GLN:NE2	2.17	0.42
1:A:214:GLU:CD	1:A:216:ILE:HD11	2.41	0.42
1:B:134:ASP:H	1:B:138:GLN:NE2	2.19	0.41
1:B:105:THR:CB	1:B:328:VAL:HG12	2.49	0.41
1:B:314:HIS:CD2	1:B:316:GLY:H	2.36	0.41
1:B:282:LEU:O	1:B:314:HIS:CE1	2.74	0.40
1:D:37:ILE:HD11	1:D:314:HIS:HB2	2.03	0.40
1:A:24:LEU:HD21	1:A:37:ILE:HG21	2.03	0.40
1:C:31:LEU:HD13	1:C:299:ILE:HD12	2.02	0.40
1:B:61:ASP:HB2	1:B:164:LEU:HD21	2.02	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	326/342 (95%)	317 (97%)	9 (3%)	0	100	100
1	B	314/342 (92%)	305 (97%)	9 (3%)	0	100	100
1	C	324/342 (95%)	316 (98%)	8 (2%)	0	100	100
1	D	326/342 (95%)	315 (97%)	10 (3%)	1 (0%)	50	59
All	All	1290/1368 (94%)	1253 (97%)	36 (3%)	1 (0%)	59	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	182	GLU

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	253/266 (95%)	251 (99%)	2 (1%)	89	96
1	B	240/266 (90%)	235 (98%)	5 (2%)	66	81
1	C	250/266 (94%)	244 (98%)	6 (2%)	61	77
1	D	249/266 (94%)	245 (98%)	4 (2%)	75	87
All	All	992/1064 (93%)	975 (98%)	17 (2%)	73	86

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	7	THR
1	B	7	THR
1	B	29	ASP
1	B	127	GLU
1	B	245	THR
1	B	311	LEU
1	C	13	GLU
1	C	43	THR
1	C	140	GLN
1	C	208	HIS
1	C	284	ASP
1	C	311	LEU
1	D	43	THR
1	D	140	GLN
1	D	147	GLU
1	D	186	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	138	GLN
1	A	208	HIS
1	A	314	HIS
1	A	325	HIS
1	B	80	HIS
1	B	83	GLN
1	B	138	GLN
1	B	314	HIS
1	B	325	HIS
1	C	80	HIS
1	C	83	GLN
1	C	125	GLN
1	C	138	GLN
1	C	178	GLN
1	C	314	HIS
1	C	325	HIS
1	D	80	HIS
1	D	83	GLN
1	D	94	HIS
1	D	125	GLN
1	D	138	GLN
1	D	140	GLN
1	D	149	GLN
1	D	178	GLN
1	D	208	HIS
1	D	251	HIS
1	D	314	HIS
1	D	325	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	IT1	A	51	1	24,24,25	4.00	2 (8%)	30,32,34	1.15	2 (6%)
1	IT1	B	51	1	24,24,25	4.01	2 (8%)	30,32,34	1.21	3 (10%)
1	IT1	C	51	1	24,24,25	3.81	2 (8%)	30,32,34	0.99	0
1	IT1	D	51	1	24,24,25	3.91	1 (4%)	30,32,34	1.14	2 (6%)

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
1	IT1	A	51	1	-	0/15/17/19	0/1/1/1
1	IT1	B	51	1	-	0/15/17/19	0/1/1/1
1	IT1	C	51	1	-	0/15/17/19	0/1/1/1
1	IT1	D	51	1	-	0/15/17/19	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	51	IT1	O-C	19.09	1.24	1.11
1	B	51	IT1	O-C	19.01	1.24	1.11
1	D	51	IT1	O-C	18.76	1.24	1.11
1	C	51	IT1	O-C	18.24	1.24	1.11
1	B	51	IT1	C3-C2	-3.63	1.38	1.40
1	A	51	IT1	C3-C2	-2.41	1.39	1.40
1	C	51	IT1	CA-C	2.12	1.52	1.48

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	51	IT1	C-CA-N	-3.42	110.41	113.83
1	B	51	IT1	CD-CE-NZ	-2.83	106.19	110.96
1	A	51	IT1	C-CA-N	-2.64	111.19	113.83
1	B	51	IT1	OP4-C5A-C5	2.63	114.60	109.26
1	D	51	IT1	C-CA-N	-2.44	111.39	113.83
1	A	51	IT1	CD-CE-NZ	-2.33	107.03	110.96
1	D	51	IT1	CD-CE-NZ	-2.31	107.06	110.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\# Z > 2$
2	SO4	A	401	-	4,4,4	0.27	0	6,6,6	0.28	0
4	BEN	A	403	-	9,9,9	0.76	0	11,11,11	0.63	0
2	SO4	B	401	-	4,4,4	0.40	0	6,6,6	0.25	0
4	BEN	B	402	-	9,9,9	0.77	0	11,11,11	0.74	0
4	BEN	B	403	-	9,9,9	0.68	0	11,11,11	0.55	0
2	SO4	C	401	-	4,4,4	0.30	0	6,6,6	0.25	0
4	BEN	C	402	-	9,9,9	0.65	0	11,11,11	0.72	0
2	SO4	D	401	-	4,4,4	0.35	0	6,6,6	0.29	0
4	BEN	D	402	-	9,9,9	0.90	1 (11%)	11,11,11	0.64	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	401	-	-	0/0/0/0	0/0/0/0
4	BEN	A	403	-	-	0/4/4/4	0/1/1/1
2	SO4	B	401	-	-	0/0/0/0	0/0/0/0
4	BEN	B	402	-	-	0/4/4/4	0/1/1/1
4	BEN	B	403	-	-	0/4/4/4	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	C	401	-	-	0/0/0/0	0/0/0/0
4	BEN	C	402	-	-	0/4/4/4	0/1/1/1
2	SO4	D	401	-	-	0/0/0/0	0/0/0/0
4	BEN	D	402	-	-	0/4/4/4	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	402	BEN	C1-C	2.23	1.51	1.49

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	328/342 (95%)	-0.23	4 (1%) 75 83	22, 28, 43, 57	0
1	B	318/342 (92%)	0.06	17 (5%) 25 34	25, 35, 52, 71	3 (0%)
1	C	323/342 (94%)	0.10	16 (4%) 28 36	23, 34, 51, 62	0
1	D	328/342 (95%)	-0.25	5 (1%) 70 78	23, 28, 46, 59	0
All	All	1297/1368 (94%)	-0.08	42 (3%) 45 54	22, 32, 50, 71	3 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	ALA	4.2
1	B	225	ALA	4.0
1	A	4	HIS	3.4
1	C	225	ALA	3.3
1	D	185	GLY	3.2
1	D	1	MET	3.1
1	D	7	THR	3.1
1	C	16	GLY	3.1
1	B	9	PHE	3.0
1	B	16	GLY	3.0
1	C	198	THR	3.0
1	D	184	VAL	2.9
1	B	306	ASP	2.9
1	B	245	THR	2.8
1	B	212	ASP	2.8
1	B	307	ASP	2.7
1	A	2	PRO	2.7
1	B	7	THR	2.6
1	B	244	LEU	2.6
1	C	15	ILE	2.5
1	B	239	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	313	ILE	2.5
1	B	185	GLY	2.4
1	C	51	IT1	2.4
1	C	151	PHE	2.4
1	C	9	PHE	2.4
1	A	313	ILE	2.3
1	D	4	HIS	2.2
1	C	240	GLY	2.2
1	B	223	SER	2.2
1	C	243	ALA	2.2
1	C	6	LEU	2.1
1	B	191	VAL	2.1
1	C	241	GLN	2.1
1	B	241	GLN	2.1
1	B	151	PHE	2.1
1	C	149	GLN	2.1
1	C	224	VAL	2.1
1	C	64	ARG	2.1
1	C	307	ASP	2.0
1	C	185	GLY	2.0
1	A	1	MET	2.0

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

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	IT1	B	51	24/25	0.19	1.56	30,31,32,32	0
1	IT1	C	51	24/25	0.21	1.29	28,29,32,33	0
1	IT1	A	51	24/25	0.17	0.45	22,24,25,27	0
1	IT1	D	51	24/25	0.15	0.41	23,25,27,27	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	CL	A	402	1/1	0.17	8.23	51,51,51,51	0
4	BEN	B	403	9/9	0.18	4.99	47,48,52,53	0
4	BEN	C	402	9/9	0.16	3.33	39,40,41,41	0
4	BEN	B	402	9/9	0.15	2.55	40,41,42,42	0
2	SO4	C	401	5/5	0.15	0.72	37,39,41,42	0
2	SO4	A	401	5/5	0.11	0.29	33,33,34,35	0
4	BEN	D	402	9/9	0.08	-0.34	23,23,24,24	0
2	SO4	B	401	5/5	0.11	-0.54	39,39,42,44	0
4	BEN	A	403	9/9	0.08	-0.55	24,24,25,26	0
2	SO4	D	401	5/5	0.08	-0.83	29,29,31,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.