



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:22 AM UTC

PDB ID : 3U4Y / pdb_00003u4y
Title : The crystal structure of a functionally unknown protein (Dtox_1751) from Desulfotomaculum acetoxidans DSM 771.
Authors : Tan, K.; Bigelow, L.; Bearden, J.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2011-10-10
Resolution : 2.99 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

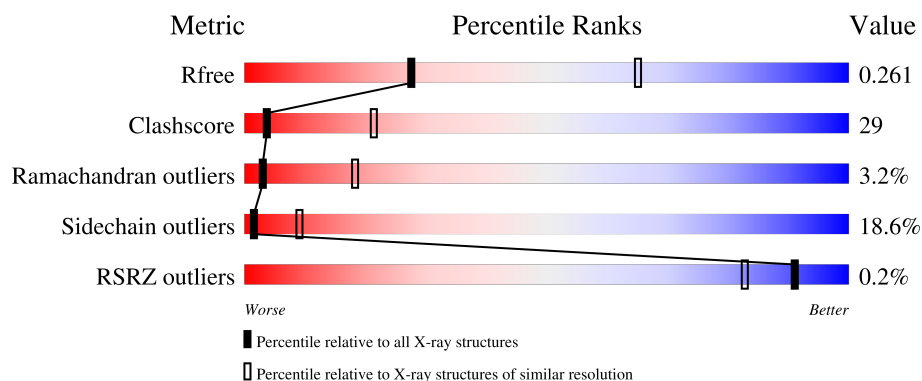
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	331	 51% 36% 8% . .
1	B	331	 37% 44% 14% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4862 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.

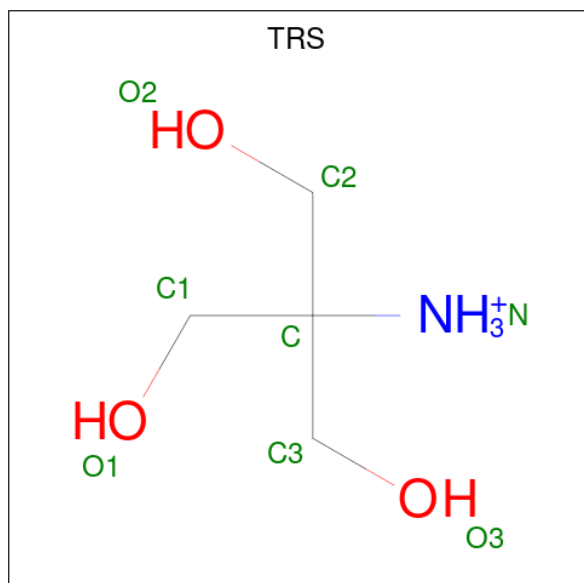
- Molecule 1 is a protein called uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	319	2425	1542	400	477	3	3	0	0	0
1	B	317	2413	1535	398	474	3	3	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP C8VX32
A	-1	ASN	-	expression tag	UNP C8VX32
A	0	ALA	-	expression tag	UNP C8VX32
B	-2	SER	-	expression tag	UNP C8VX32
B	-1	ASN	-	expression tag	UNP C8VX32
B	0	ALA	-	expression tag	UNP C8VX32

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			8	4	1	3		
2	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total	O	0	0
			7	7		
3	B	1	Total	O	0	0
			1	1		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	139.64Å 66.66Å 80.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.21 – 2.99 48.21 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.21-2.99) 98.5 (48.21-2.99)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.176 , 0.268 0.175 , 0.261	Depositor DCC
R_{free} test set	776 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	51.4	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4862	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: TRS

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	0.64	0/2467	0.98	1/3357 (0.0%)
1	B	0.51	0/2455	0.95	8/3340 (0.2%)
All	All	0.58	0/4922	0.97	9/6697 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	320	HIS	CA-C-N	7.11	127.15	119.89
1	B	320	HIS	C-N-CA	7.11	127.15	119.89
1	B	96	VAL	N-CA-C	6.21	116.81	107.75
1	B	192	LEU	N-CA-C	5.97	117.45	111.07
1	B	47	ASP	N-CA-C	-5.65	106.35	113.18
1	B	8	PHE	N-CA-C	5.46	115.24	108.19
1	A	45	THR	CB-CA-C	5.24	118.47	109.51
1	B	136	GLY	N-CA-C	-5.21	108.12	115.32
1	B	264	ILE	N-CA-C	5.09	115.25	108.27

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	2425	0	2397	113	0
1	B	2413	0	2388	168	0
2	A	16	0	24	3	0
3	A	7	0	0	0	0
3	B	1	0	0	0	0
All	All	4862	0	4809	280	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 29.

All (280) 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:280:THR:O	1:A:282:THR:HG23	1.55	1.05
1:B:99:THR:HG21	1:B:105:PHE:HA	1.41	1.01
1:A:29:ILE:HD11	1:A:308:ALA:O	1.60	0.99
1:A:227:ARG:HG2	1:A:281:GLU:OE1	1.73	0.89
1:B:190:ALA:HB2	1:B:223:ILE:HD11	1.56	0.87
1:B:109:SER:O	1:B:117:PHE:HD1	1.60	0.84
1:A:45:THR:CG2	1:A:47:ASP:HB3	2.07	0.84
1:B:222:THR:HG21	1:B:274:GLN:H	1.40	0.84
1:B:235:LEU:HB2	1:B:275:MSE:HE3	1.60	0.83
1:A:45:THR:HG23	1:A:47:ASP:HB3	1.62	0.81
1:A:240:VAL:HG22	1:A:275:MSE:HE1	1.61	0.81
1:A:29:ILE:HD12	1:A:29:ILE:H	1.44	0.80
1:A:236:THR:HG22	1:A:238:SER:H	1.46	0.80
1:B:41:ASP:OD2	1:B:42:THR:N	2.15	0.79
1:B:42:THR:HG22	1:B:53:VAL:HG22	1.64	0.78
1:B:298:THR:HG22	1:B:300:SER:H	1.46	0.78
1:B:225:VAL:HG12	1:B:232:VAL:HG22	1.67	0.77
1:B:192:LEU:HD22	1:B:219:LEU:HD12	1.68	0.76
1:B:279:LYS:H	1:B:279:LYS:CD	1.98	0.76
1:A:294:LEU:HB3	1:A:307:VAL:HG22	1.70	0.74
1:B:98:VAL:HG21	1:B:130:ILE:HB	1.70	0.72
1:B:265:ASP:O	1:B:289:ASN:ND2	2.23	0.72
1:A:69:GLU:CB	1:A:70:PRO:HD3	2.20	0.72
1:A:277:LEU:HD13	1:A:284:LEU:CD2	2.21	0.70
1:B:279:LYS:HE3	1:B:319:CYS:O	1.91	0.70
1:A:222:THR:HG21	1:A:274:GLN:H	1.55	0.70
1:B:135:ASN:HB2	1:B:137:ASN:HD22	1.57	0.70
1:B:277:LEU:HD13	1:B:284:LEU:HD23	1.73	0.69
1:A:114:LYS:HD3	1:A:116:LYS:NZ	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ASN:O	1:A:236:THR:HG23	1.92	0.69
1:B:144:ARG:HB2	1:B:149:THR:HG22	1.75	0.69
1:A:167:GLU:H	2:A:330:TRS:C1	2.07	0.68
1:A:240:VAL:CG2	1:A:275:MSE:HE1	2.24	0.67
1:A:236:THR:HB	1:A:239:THR:O	1.94	0.67
1:A:29:ILE:HD12	1:A:29:ILE:N	2.09	0.67
1:A:103:HIS:HB2	1:A:104:PRO:HA	1.76	0.66
1:A:107:MSE:HG2	1:A:161:LEU:HD13	1.78	0.66
1:A:265:ASP:O	1:A:289:ASN:ND2	2.29	0.65
1:B:38:ASP:HB3	1:B:55:SER:HB2	1.78	0.65
1:A:10:ILE:HD13	1:A:42:THR:HG21	1.78	0.65
1:A:277:LEU:HD13	1:A:284:LEU:HD23	1.79	0.64
1:A:21:PHE:CZ	1:A:64:ILE:HD11	2.33	0.64
1:B:265:ASP:OD1	1:B:267:ARG:HD2	1.97	0.64
1:B:69:GLU:HB3	1:B:70:PRO:HD3	1.80	0.64
1:B:245:PHE:CZ	1:B:250:GLY:HA2	2.33	0.63
1:A:69:GLU:HB3	1:A:70:PRO:HD3	1.81	0.63
1:B:45:THR:CG2	1:B:50:ASN:H	2.12	0.63
1:B:90:PRO:HG3	1:B:134:PRO:HA	1.81	0.63
1:B:135:ASN:HB2	1:B:137:ASN:ND2	2.13	0.63
1:B:69:GLU:HG2	1:B:70:PRO:HD3	1.80	0.63
1:A:197:ILE:CD1	1:A:216:THR:HG21	2.29	0.62
1:B:18:ARG:HD3	1:B:32:GLN:HB3	1.82	0.62
1:B:99:THR:CG2	1:B:106:ASN:H	2.13	0.61
1:B:135:ASN:HD21	1:B:184:GLY:H	1.47	0.61
1:B:183:ASP:O	1:B:185:ASN:N	2.29	0.61
1:A:114:LYS:O	1:A:116:LYS:HG3	2.00	0.61
1:A:262:LEU:HD13	1:A:288:ALA:HB2	1.83	0.61
1:B:260:HIS:ND1	1:B:262:LEU:HB2	2.16	0.60
1:B:135:ASN:CB	1:B:137:ASN:HD22	2.13	0.60
1:B:135:ASN:ND2	1:B:184:GLY:H	1.99	0.60
1:A:292:ARG:HG3	1:B:125:TYR:HB3	1.84	0.60
1:B:294:LEU:HD23	1:B:307:VAL:HG11	1.83	0.60
1:B:19:ILE:C	1:B:19:ILE:HD12	2.27	0.60
1:B:233:TYR:CD1	1:B:242:VAL:HG12	2.37	0.59
1:B:83:MSE:CG	1:B:97:THR:OG1	2.51	0.59
1:B:281:GLU:O	1:B:299:ILE:HD13	2.02	0.59
1:B:201:GLU:O	1:B:208:ILE:HG23	2.03	0.59
1:A:167:GLU:H	2:A:330:TRS:H12	1.67	0.59
1:B:263:LEU:HB3	1:B:290:ILE:HB	1.83	0.58
1:B:242:VAL:CG2	1:B:256:LYS:HB3	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:GLU:CB	1:B:70:PRO:HD3	2.33	0.58
1:A:172:GLY:H	1:A:191:ASN:ND2	2.02	0.57
1:B:262:LEU:HD22	1:B:288:ALA:HB2	1.87	0.57
1:B:29:ILE:HD11	1:B:32:GLN:OE1	2.04	0.57
1:B:47:ASP:OD2	1:B:47:ASP:N	2.36	0.57
1:A:145:SER:HA	1:A:175:PRO:HD2	1.87	0.57
1:B:277:LEU:HD13	1:B:284:LEU:CD2	2.34	0.57
1:B:81:SER:HB3	1:B:104:PRO:HG2	1.87	0.57
1:A:295:LYS:HD3	1:A:297:PHE:CZ	2.40	0.56
1:A:280:THR:O	1:A:281:GLU:C	2.47	0.56
1:B:228:ASP:OD1	1:B:230:SER:HB3	2.06	0.56
1:B:18:ARG:NH1	1:B:32:GLN:OE1	2.38	0.56
1:B:246:ASN:ND2	1:B:249:SER:OG	2.39	0.56
1:A:201:GLU:HG3	1:A:211:LEU:HD21	1.88	0.56
1:B:233:TYR:HD1	1:B:242:VAL:HG12	1.71	0.56
1:B:39:PHE:HA	1:B:54:THR:O	2.06	0.55
1:B:83:MSE:HG3	1:B:97:THR:OG1	2.05	0.55
1:A:149:THR:HG21	1:A:167:GLU:OE1	2.06	0.55
1:A:46:SER:HB2	1:A:92:ASP:OD2	2.06	0.55
1:A:29:ILE:HG22	1:A:30:LEU:N	2.21	0.55
1:A:169:ILE:HG22	1:A:171:GLY:H	1.72	0.55
1:A:222:THR:C	1:A:223:ILE:HD13	2.31	0.54
1:B:135:ASN:OD1	1:B:184:GLY:HA3	2.07	0.54
1:B:295:LYS:HD2	1:B:297:PHE:CE2	2.43	0.54
1:B:217:ASN:ND2	1:B:241:ASP:OD1	2.41	0.54
1:B:89:THR:O	1:B:92:ASP:N	2.33	0.54
1:A:148:ASN:HA	1:A:175:PRO:HD3	1.89	0.54
1:B:88:ILE:HD13	1:B:88:ILE:H	1.72	0.54
1:B:23:SER:OG	1:B:26:THR:HG23	2.08	0.54
1:A:265:ASP:O	1:A:268:PRO:HD2	2.08	0.53
1:B:61:LEU:C	1:B:61:LEU:HD23	2.33	0.53
1:B:279:LYS:CD	1:B:279:LYS:N	2.69	0.53
1:B:42:THR:CG2	1:B:53:VAL:HG22	2.38	0.53
1:B:151:ARG:NH1	1:B:163:ASP:OD2	2.41	0.53
1:A:277:LEU:HD13	1:A:284:LEU:HD21	1.90	0.53
1:A:166:GLN:HA	2:A:330:TRS:H11	1.91	0.53
1:B:96:VAL:HB	1:B:130:ILE:CD1	2.38	0.53
1:B:279:LYS:O	1:B:281:GLU:HG2	2.08	0.53
1:B:121:ILE:CD1	1:B:161:LEU:HB3	2.38	0.53
1:A:38:ASP:OD2	1:A:56:ASP:HB3	2.09	0.53
1:A:47:ASP:O	1:A:48:CYS:HB2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:ILE:HG13	1:B:317:ALA:N	2.24	0.53
1:B:195:ASN:OD1	1:B:218:ASN:HA	2.08	0.53
1:B:288:ALA:HB1	1:B:291:SER:HB2	1.91	0.52
1:B:185:ASN:O	1:B:202:THR:N	2.40	0.52
1:A:91:ASP:O	1:A:92:ASP:HB2	2.08	0.52
1:A:223:ILE:HD13	1:A:223:ILE:N	2.24	0.52
1:A:267:ARG:N	1:A:268:PRO:HD2	2.26	0.51
1:B:69:GLU:HB3	1:B:70:PRO:CD	2.40	0.51
1:B:69:GLU:CG	1:B:70:PRO:HD3	2.40	0.51
1:A:241:ASP:OD1	1:A:257:SER:HB3	2.10	0.51
1:A:298:THR:OG1	1:A:302:LYS:HB3	2.11	0.51
1:B:23:SER:N	1:B:30:LEU:HD13	2.24	0.51
1:A:307:VAL:HG21	1:A:310:ILE:HD12	1.91	0.51
1:B:307:VAL:HG23	1:B:308:ALA:H	1.76	0.51
1:A:21:PHE:HZ	1:A:64:ILE:HD11	1.72	0.51
1:B:142:ILE:HA	1:B:178:ILE:HD11	1.93	0.51
1:B:262:LEU:HD22	1:B:288:ALA:CB	2.40	0.51
1:A:43:ALA:HB3	1:A:88:ILE:HD11	1.93	0.51
1:B:243:PHE:HB3	1:B:252:LEU:HD22	1.93	0.51
1:A:69:GLU:CB	1:A:70:PRO:CD	2.89	0.51
1:A:69:GLU:HB2	1:A:70:PRO:HD3	1.92	0.51
1:A:43:ALA:CB	1:A:88:ILE:HD11	2.40	0.51
1:B:45:THR:HG22	1:B:50:ASN:H	1.75	0.51
1:B:227:ARG:NH1	1:B:320:HIS:HD2	2.08	0.51
1:A:114:LYS:HB2	1:A:116:LYS:HE2	1.93	0.51
1:B:219:LEU:HB2	1:B:237:GLU:HB2	1.93	0.51
1:B:238:SER:HA	1:B:260:HIS:CE1	2.46	0.51
1:B:262:LEU:O	1:B:263:LEU:HD23	2.11	0.51
1:B:279:LYS:H	1:B:279:LYS:HD2	1.75	0.51
1:A:29:ILE:H	1:A:29:ILE:CD1	2.19	0.50
1:A:280:THR:O	1:A:282:THR:CG2	2.45	0.50
1:A:114:LYS:HD3	1:A:116:LYS:HZ3	1.74	0.50
1:B:279:LYS:CE	1:B:319:CYS:O	2.59	0.50
1:A:128:VAL:O	1:A:143:ASP:HB2	2.12	0.50
1:B:139:LEU:HD12	1:B:140:ILE:H	1.77	0.50
1:B:51:VAL:CG1	1:B:52:VAL:N	2.75	0.50
1:B:195:ASN:OD1	1:B:219:LEU:N	2.43	0.49
1:A:16:LEU:N	1:A:16:LEU:HD23	2.28	0.49
1:B:279:LYS:N	1:B:279:LYS:HD2	2.28	0.49
1:A:280:THR:O	1:A:282:THR:N	2.46	0.49
1:B:315:GLY:C	1:B:316:ILE:HG22	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:SER:HB3	1:B:92:ASP:OD1	2.12	0.49
1:B:98:VAL:CG2	1:B:130:ILE:HB	2.39	0.49
1:A:33:ILE:HG22	1:A:35:LEU:HD12	1.95	0.49
1:A:41:ASP:OD2	1:A:315:GLY:HA3	2.14	0.48
1:B:68:LEU:HD11	1:B:72:LYS:HG3	1.95	0.48
1:A:114:LYS:CB	1:A:116:LYS:HE2	2.44	0.48
1:B:302:LYS:NZ	1:B:302:LYS:HB2	2.29	0.48
1:A:26:THR:O	1:A:27:LEU:HB2	2.13	0.48
1:B:10:ILE:HD12	1:B:11:VAL:H	1.79	0.48
1:A:173:THR:OG1	1:A:193:ILE:HD11	2.14	0.48
1:B:278:ASN:O	1:B:281:GLU:N	2.46	0.48
1:A:14:GLN:H	1:A:313:ASN:HB3	1.79	0.48
1:A:83:MSE:HB3	1:A:97:THR:HG21	1.96	0.48
1:B:121:ILE:HD11	1:B:161:LEU:HB3	1.96	0.48
1:A:33:ILE:HG22	1:A:35:LEU:CD1	2.45	0.47
1:B:84:ALA:O	1:B:85:ASP:HB2	2.12	0.47
1:A:174:ARG:HB2	1:A:193:ILE:HG12	1.97	0.47
1:A:51:VAL:CG1	1:A:52:VAL:N	2.78	0.47
1:A:83:MSE:HG2	1:A:97:THR:HG21	1.97	0.47
1:A:148:ASN:HA	1:A:175:PRO:CD	2.45	0.47
1:A:45:THR:HG22	1:A:48:CYS:H	1.80	0.47
1:B:45:THR:OG1	1:B:46:SER:N	2.48	0.47
1:B:130:ILE:HG12	1:B:131:ALA:N	2.29	0.47
1:B:278:ASN:O	1:B:279:LYS:C	2.58	0.47
1:B:33:ILE:HG22	1:B:35:LEU:HD21	1.97	0.47
1:B:217:ASN:O	1:B:218:ASN:HB2	2.14	0.47
1:B:242:VAL:HG22	1:B:256:LYS:O	2.14	0.47
1:B:29:ILE:HD11	1:B:32:GLN:CD	2.40	0.46
1:B:83:MSE:HG3	1:B:97:THR:CG2	2.45	0.46
1:B:139:LEU:HD12	1:B:140:ILE:N	2.30	0.46
1:B:235:LEU:HB2	1:B:275:MSE:CE	2.37	0.46
1:B:64:ILE:HD12	1:B:65:GLU:O	2.15	0.46
1:A:170:SER:OG	1:A:175:PRO:HG3	2.16	0.46
1:B:222:THR:HG21	1:B:274:GLN:N	2.21	0.46
1:B:310:ILE:O	1:B:310:ILE:HG22	2.16	0.46
1:B:83:MSE:HE3	1:B:83:MSE:HB2	1.91	0.46
1:B:152:ARG:HG2	1:B:164:THR:HG21	1.98	0.46
1:B:152:ARG:C	1:B:153:PHE:CD2	2.94	0.45
1:B:254:PHE:HZ	1:B:257:SER:OG	2.00	0.45
1:A:277:LEU:HG	1:A:281:GLU:HA	1.97	0.45
1:A:278:ASN:ND2	1:A:280:THR:OG1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:PHE:CD1	1:A:243:PHE:N	2.84	0.45
1:A:296:VAL:HB	1:A:304:VAL:HG22	1.99	0.45
1:B:99:THR:HG21	1:B:105:PHE:CA	2.29	0.45
1:B:109:SER:O	1:B:117:PHE:CD1	2.52	0.45
1:B:126:ASP:OD2	1:B:146:SER:HB2	2.17	0.45
1:B:135:ASN:HD21	1:B:184:GLY:N	2.12	0.45
1:B:149:THR:HG21	1:B:167:GLU:OE1	2.17	0.45
1:B:33:ILE:HG22	1:B:35:LEU:CD2	2.47	0.45
1:B:45:THR:HG21	1:B:50:ASN:H	1.80	0.45
1:B:132:ILE:O	1:B:133:SER:C	2.59	0.45
1:A:15:HIS:C	1:A:16:LEU:HD23	2.43	0.44
1:B:10:ILE:HD12	1:B:11:VAL:N	2.33	0.44
1:B:170:SER:OG	1:B:175:PRO:HG3	2.17	0.44
1:B:12:VAL:CG2	1:B:42:THR:HG23	2.47	0.44
1:B:64:ILE:HD12	1:B:65:GLU:C	2.41	0.44
1:A:150:VAL:HG11	1:A:189:VAL:HG21	2.00	0.44
1:B:155:ILE:HA	1:B:160:VAL:O	2.17	0.44
1:A:89:THR:HB	1:A:90:PRO:CD	2.48	0.44
1:B:70:PRO:O	1:B:71:PRO:C	2.60	0.44
1:B:218:ASN:O	1:B:236:THR:HB	2.17	0.44
1:A:30:LEU:HB3	1:A:31:ASN:ND2	2.32	0.44
1:B:143:ASP:HB3	1:B:175:PRO:HB2	1.99	0.44
1:B:17:ARG:HG3	1:B:36:GLY:HA2	1.99	0.43
1:B:29:ILE:HG22	1:B:308:ALA:CB	2.47	0.43
1:B:99:THR:HG21	1:B:106:ASN:H	1.83	0.43
1:A:236:THR:CG2	1:A:237:GLU:N	2.80	0.43
1:B:49:SER:O	1:B:66:THR:OG1	2.35	0.43
1:B:298:THR:C	1:B:300:SER:N	2.75	0.43
1:B:29:ILE:HG22	1:B:308:ALA:HB3	2.00	0.43
1:A:13:GLU:HG2	1:A:311:GLU:O	2.19	0.43
1:B:82:SER:HB3	1:B:102:ASN:CB	2.48	0.43
1:B:183:ASP:C	1:B:185:ASN:H	2.20	0.43
1:A:93:GLN:HG3	1:A:113:LEU:HD11	2.00	0.43
1:B:194:GLY:O	1:B:195:ASN:C	2.61	0.43
1:A:174:ARG:CB	1:A:193:ILE:HG12	2.48	0.43
1:B:306:TYR:HB3	1:B:307:VAL:H	1.66	0.43
1:B:40:VAL:HG12	1:B:41:ASP:N	2.32	0.43
1:A:265:ASP:C	1:A:289:ASN:HD22	2.26	0.43
1:B:18:ARG:HG3	1:B:34:THR:HB	2.01	0.43
1:B:287:SER:HB2	1:B:316:ILE:HG21	2.01	0.43
1:B:69:GLU:CB	1:B:70:PRO:CD	2.95	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:ALA:CB	1:B:291:SER:HB2	2.49	0.42
1:A:93:GLN:HE21	1:A:113:LEU:HD11	1.85	0.42
1:B:96:VAL:HB	1:B:130:ILE:HD11	1.99	0.42
1:A:10:ILE:CD1	1:A:42:THR:HG21	2.47	0.42
1:A:192:LEU:HD11	1:A:219:LEU:HG	2.01	0.42
1:B:174:ARG:HB2	1:B:193:ILE:HG12	2.01	0.42
1:B:19:ILE:HD12	1:B:20:SER:N	2.35	0.42
1:A:45:THR:HG22	1:A:48:CYS:N	2.35	0.42
1:A:286:ILE:O	1:A:294:LEU:HD12	2.20	0.42
1:B:163:ASP:OD1	1:B:163:ASP:C	2.63	0.42
1:A:224:VAL:HG11	1:A:277:LEU:HD22	2.01	0.42
1:A:294:LEU:HB3	1:A:307:VAL:CG2	2.46	0.42
1:B:280:THR:OG1	1:B:282:THR:OG1	2.37	0.42
1:B:94:PHE:CZ	1:B:159:GLY:HA3	2.55	0.42
1:A:29:ILE:CG2	1:A:30:LEU:N	2.83	0.42
1:A:285:PHE:CD1	1:A:296:VAL:HG22	2.55	0.42
1:B:58:CYS:O	1:B:59:GLN:C	2.62	0.42
1:B:252:LEU:HD23	1:B:252:LEU:HA	1.68	0.41
1:A:280:THR:HB	1:A:282:THR:HG23	2.01	0.41
1:B:82:SER:HB3	1:B:102:ASN:HB2	2.02	0.41
1:B:83:MSE:HG3	1:B:97:THR:HG21	2.02	0.41
1:B:85:ASP:OD1	1:B:129:GLY:HA2	2.20	0.41
1:A:144:ARG:HE	1:A:144:ARG:HB3	1.70	0.41
1:B:181:THR:O	1:B:182:PRO:C	2.63	0.41
1:A:276:ALA:HB3	1:A:318:ILE:HG13	2.02	0.41
1:B:217:ASN:HB2	1:B:236:THR:HG21	2.03	0.41
1:B:52:VAL:HG13	1:B:61:LEU:HD21	2.01	0.41
1:B:243:PHE:CD2	1:B:254:PHE:HA	2.56	0.41
1:A:276:ALA:CB	1:A:318:ILE:HG13	2.50	0.41
1:A:133:SER:HA	1:A:134:PRO:HD3	1.79	0.41
1:A:135:ASN:HB2	1:A:137:ASN:H	1.86	0.41
1:A:197:ILE:O	1:A:213:ALA:HA	2.20	0.41
1:A:212:ASN:HB2	1:A:213:ALA:H	1.70	0.41
1:B:103:HIS:CD2	1:B:104:PRO:HA	2.55	0.41
1:A:9:GLY:C	1:A:22:PHE:CE2	2.99	0.40
1:A:27:LEU:HD23	1:A:27:LEU:HA	1.77	0.40
1:B:121:ILE:H	1:B:121:ILE:HG12	1.59	0.40
1:B:133:SER:HA	1:B:134:PRO:HD3	1.78	0.40
1:B:202:THR:O	1:B:203:GLN:C	2.64	0.40
1:A:45:THR:HG22	1:A:49:SER:H	1.87	0.40
1:B:117:PHE:C	1:B:118:ILE:HG12	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:PHE:CD1	1:A:8:PHE:C	2.98	0.40
1:A:190:ALA:HB2	1:A:223:ILE:HD11	2.02	0.40
1:B:206:GLU:OE2	1:B:206:GLU:HA	2.22	0.40
1:B:263:LEU:CB	1:B:290:ILE:HB	2.51	0.40
1:B:265:ASP:H	1:B:289:ASN:HB3	1.87	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	317/331 (96%)	283 (89%)	27 (8%)	7 (2%)	5	26
1	B	315/331 (95%)	267 (85%)	35 (11%)	13 (4%)	2	13
All	All	632/662 (96%)	550 (87%)	62 (10%)	20 (3%)	3	18

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	ASP
1	A	281	GLU
1	A	289	ASN
1	B	59	GLN
1	B	118	ILE
1	B	184	GLY
1	A	70	PRO
1	B	38	ASP
1	B	39	PHE
1	B	70	PRO
1	B	84	ALA
1	A	59	GLN
1	B	69	GLU

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Mol	Chain	Res	Type
1	B	85	ASP
1	A	313	ASN
1	B	218	ASN
1	B	308	ALA
1	B	71	PRO
1	A	69	GLU
1	B	307	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	275/283 (97%)	226 (82%)	49 (18%)	2	10
1	B	274/283 (97%)	221 (81%)	53 (19%)	1	8
All	All	549/566 (97%)	447 (81%)	102 (19%)	1	9

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	10	ILE
1	A	19	ILE
1	A	23	SER
1	A	26	THR
1	A	29	ILE
1	A	30	LEU
1	A	42	THR
1	A	45	THR
1	A	48	CYS
1	A	51	VAL
1	A	53	VAL
1	A	62	VAL
1	A	64	ILE
1	A	68	LEU
1	A	73	VAL

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Mol	Chain	Res	Type
1	A	78	GLU
1	A	80	GLN
1	A	86	VAL
1	A	88	ILE
1	A	97	THR
1	A	98	VAL
1	A	101	LEU
1	A	113	LEU
1	A	116	LYS
1	A	118	ILE
1	A	141	LEU
1	A	150	VAL
1	A	154	LYS
1	A	173	THR
1	A	219	LEU
1	A	222	THR
1	A	223	ILE
1	A	225	VAL
1	A	227	ARG
1	A	242	VAL
1	A	247	GLN
1	A	253	SER
1	A	257	SER
1	A	264	ILE
1	A	277	LEU
1	A	279	LYS
1	A	280	THR
1	A	281	GLU
1	A	283	LYS
1	A	290	ILE
1	A	291	SER
1	A	303	VAL
1	A	304	VAL
1	B	7	ASN
1	B	10	ILE
1	B	11	VAL
1	B	16	LEU
1	B	23	SER
1	B	25	ASP
1	B	26	THR
1	B	29	ILE
1	B	34	THR

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Mol	Chain	Res	Type
1	B	47	ASP
1	B	62	VAL
1	B	64	ILE
1	B	65	GLU
1	B	73	VAL
1	B	74	VAL
1	B	88	ILE
1	B	96	VAL
1	B	97	THR
1	B	101	LEU
1	B	102	ASN
1	B	121	ILE
1	B	123	ILE
1	B	130	ILE
1	B	141	LEU
1	B	149	THR
1	B	152	ARG
1	B	169	ILE
1	B	173	THR
1	B	174	ARG
1	B	177	ASN
1	B	178	ILE
1	B	200	LEU
1	B	202	THR
1	B	207	ASN
1	B	219	LEU
1	B	222	THR
1	B	223	ILE
1	B	251	THR
1	B	252	LEU
1	B	253	SER
1	B	263	LEU
1	B	264	ILE
1	B	267	ARG
1	B	277	LEU
1	B	279	LYS
1	B	280	THR
1	B	281	GLU
1	B	302	LYS
1	B	303	VAL
1	B	304	VAL
1	B	307	VAL

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Mol	Chain	Res	Type
1	B	310	ILE
1	B	316	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
1	A	106	ASN
1	A	191	ASN
1	A	218	ASN
1	B	14	GLN
1	B	106	ASN
1	B	108	GLN
1	B	115	ASN
1	B	135	ASN
1	B	137	ASN
1	B	177	ASN
1	B	246	ASN
1	B	274	GLN
1	B	313	ASN
1	B	320	HIS

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](#)

2 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	TRS	A	330	-	7,7,7	0.37	0	9,9,9	0.42	0
2	TRS	A	329	-	7,7,7	0.27	0	9,9,9	0.32	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	TRS	A	330	-	-	3/9/9/9	-
2	TRS	A	329	-	-	9/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	329	TRS	C2-C-C1-O1
2	A	329	TRS	C1-C-C2-O2
2	A	329	TRS	C3-C-C2-O2
2	A	329	TRS	N-C-C2-O2
2	A	329	TRS	C1-C-C3-O3
2	A	329	TRS	C2-C-C3-O3
2	A	329	TRS	N-C-C3-O3
2	A	329	TRS	C3-C-C1-O1
2	A	330	TRS	C1-C-C2-O2
2	A	330	TRS	C3-C-C2-O2
2	A	329	TRS	N-C-C1-O1
2	A	330	TRS	N-C-C2-O2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	330	TRS	3	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	316/331 (95%)	-0.65	0	100 100	17, 38, 63, 98	0
1	B	314/331 (94%)	-0.07	1 (0%)	90 79	22, 67, 108, 153	0
All	All	630/662 (95%)	-0.36	1 (0%)	91 83	17, 49, 100, 153	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	248	LEU	2.2

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	TRS	A	330	8/8	0.91	0.12	65,74,76,81	0
2	TRS	A	329	8/8	0.94	0.10	75,81,83,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.