



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:48 AM UTC

PDB ID : 8GMF / pdb_00008gmf
Title : R153M variant of Citrate Synthase (CitA) in Mycobacterium tuberculosis
Authors : Pathirage, R.; Ronning, D.
Deposited on : 2023-03-25
Resolution : 2.96 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
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

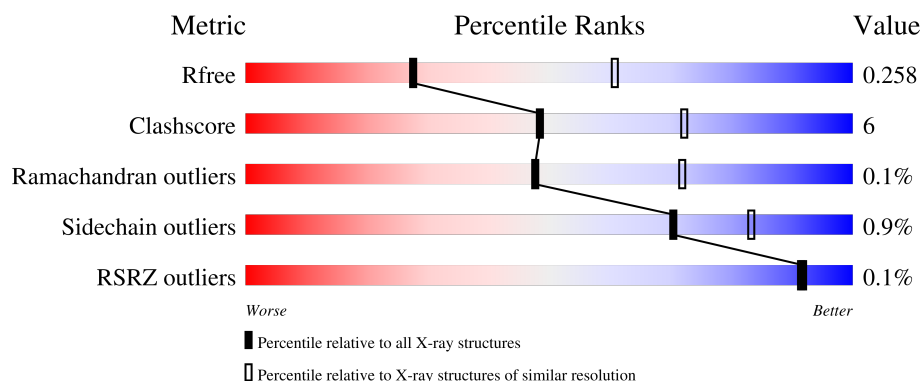
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	373	
1	B	373	
1	C	373	
1	D	373	
1	E	373	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	373	 86% 12% •
1	G	373	 81% 17% •
1	H	373	 80% 18% ••

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 22313 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 citrate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2780	1750	502	514	14			
1	B	369	Total	C	N	O	S	0	0	0
			2792	1758	504	516	14			
1	C	370	Total	C	N	O	S	0	0	0
			2801	1765	505	517	14			
1	D	370	Total	C	N	O	S	0	0	0
			2801	1765	505	517	14			
1	E	369	Total	C	N	O	S	0	0	0
			2794	1761	504	515	14			
1	F	366	Total	C	N	O	S	0	0	0
			2768	1744	500	510	14			
1	G	367	Total	C	N	O	S	0	0	0
			2780	1752	502	512	14			
1	H	370	Total	C	N	O	S	0	0	0
			2797	1764	502	516	15			

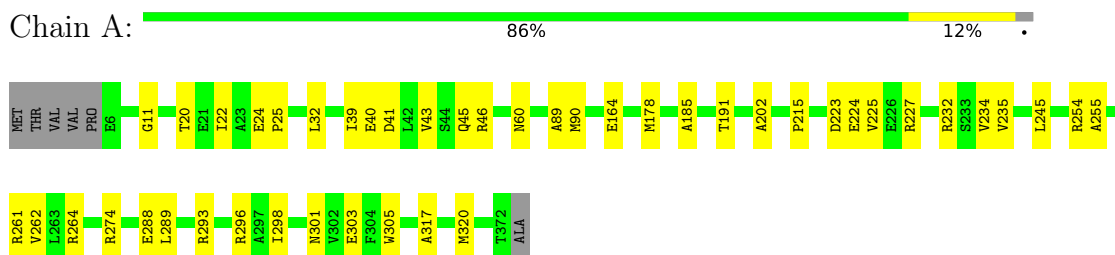
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	MET	ARG	engineered mutation	UNP A0A045JB88
B	153	MET	ARG	engineered mutation	UNP A0A045JB88
C	153	MET	ARG	engineered mutation	UNP A0A045JB88
D	153	MET	ARG	engineered mutation	UNP A0A045JB88
E	153	MET	ARG	engineered mutation	UNP A0A045JB88
F	153	MET	ARG	engineered mutation	UNP A0A045JB88
G	153	MET	ARG	engineered mutation	UNP A0A045JB88
H	153	MET	ARG	engineered mutation	UNP A0A045JB88

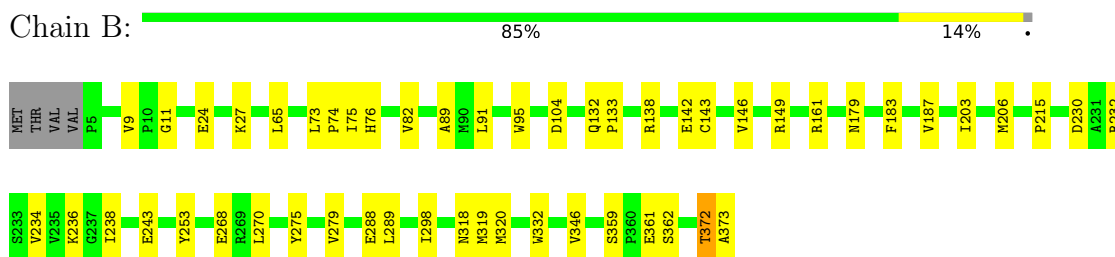
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

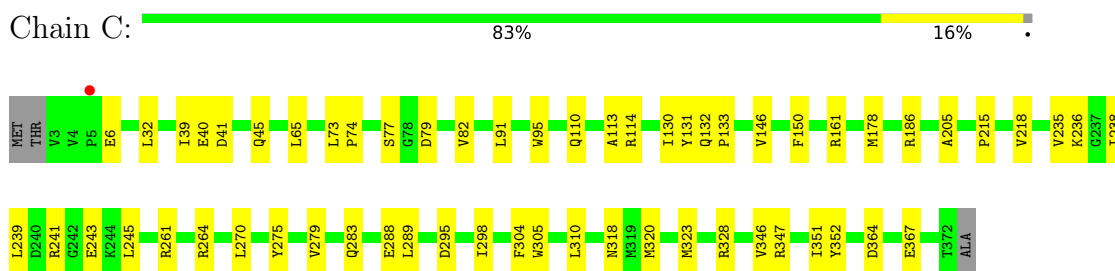
- Molecule 1: citrate synthase



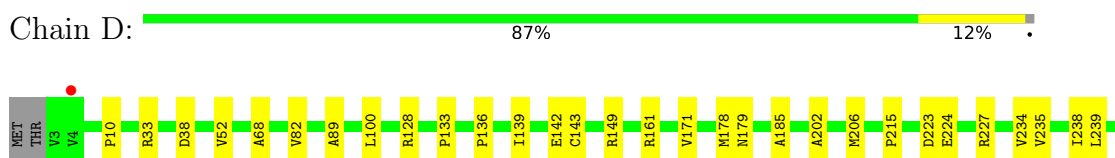
- Molecule 1: citrate synthase

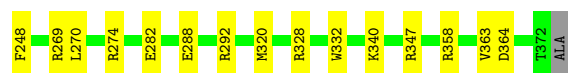


- Molecule 1: citrate synthase

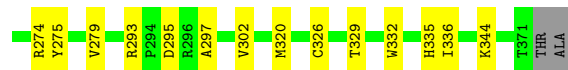
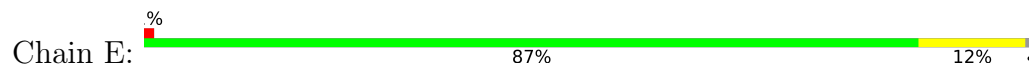


- Molecule 1: citrate synthase

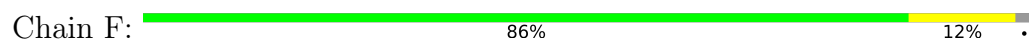




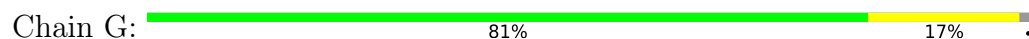
• Molecule 1: citrate synthase



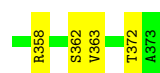
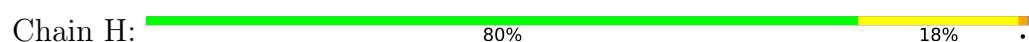
• Molecule 1: citrate synthase



• Molecule 1: citrate synthase



• Molecule 1: citrate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	129.91Å 129.91Å 256.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.83 – 2.96 91.83 – 2.96	Depositor EDS
% Data completeness (in resolution range)	99.2 (91.83-2.96) 89.6 (91.83-2.96)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.15 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158:000	Depositor
R, R_{free}	0.210 , 0.257 0.211 , 0.258	Depositor DCC
R_{free} test set	2005 reflections (1.93%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 84.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.185 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	22313	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.09	0/2843	0.23	0/3872
1	B	0.09	0/2856	0.24	0/3890
1	C	0.10	0/2865	0.25	0/3904
1	D	0.10	0/2865	0.23	0/3904
1	E	0.08	0/2858	0.22	0/3894
1	F	0.09	0/2831	0.23	0/3856
1	G	0.10	0/2844	0.24	0/3874
1	H	0.12	0/2860	0.27	0/3896
All	All	0.10	0/22822	0.24	0/31090

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 [i](#)

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	2780	0	2750	30	0
1	B	2792	0	2763	33	0
1	C	2801	0	2775	40	0
1	D	2801	0	2775	28	0
1	E	2794	0	2768	26	0
1	F	2768	0	2743	28	0
1	G	2780	0	2752	39	0
1	H	2797	0	2776	50	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	22313	0	22102	246	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 6.

All (246) 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:20:THR:HG22	1:A:22:ILE:H	1.48	0.78
1:B:179:ASN:HA	1:F:347:ARG:HE	1.48	0.77
1:H:48:THR:HG21	1:H:145:THR:HB	1.69	0.74
1:E:81:ARG:HD2	1:E:207:SER:HB2	1.68	0.73
1:D:100:LEU:HD22	1:D:340:LYS:HD2	1.71	0.71
1:F:241:ARG:HG3	1:F:243:GLU:HG3	1.71	0.71
1:A:232:ARG:NH1	1:A:288:GLU:OE1	2.23	0.71
1:G:232:ARG:HH12	1:G:288:GLU:HB2	1.54	0.71
1:H:223:ASP:OD1	1:H:274:ARG:NH2	2.24	0.71
1:D:68:ALA:H	1:D:149:ARG:HH22	1.37	0.70
1:H:39:ILE:HG13	1:H:262:VAL:HG21	1.72	0.70
1:B:232:ARG:NH1	1:B:288:GLU:OE1	2.25	0.69
1:G:100:LEU:HD22	1:G:340:LYS:HD2	1.77	0.67
1:A:224:GLU:OE2	1:A:227:ARG:NH2	2.27	0.67
1:B:318:ASN:ND2	1:C:131:TYR:O	2.27	0.66
1:A:223:ASP:OD1	1:A:274:ARG:NH2	2.28	0.66
1:G:236:LYS:NZ	1:G:288:GLU:OE1	2.27	0.66
1:E:143:CYS:HB2	1:E:149:ARG:HG2	1.77	0.65
1:C:40:GLU:OE2	1:C:261:ARG:NH1	2.30	0.64
1:D:82:VAL:HG13	1:E:89:ALA:HB1	1.81	0.63
1:A:235:VAL:HG13	1:A:245:LEU:HD21	1.81	0.63
1:D:223:ASP:OD1	1:D:274:ARG:NH2	2.31	0.63
1:A:317:ALA:HA	1:A:320:MET:HE3	1.81	0.62
1:G:288:GLU:OE2	1:G:292:ARG:NE	2.28	0.62
1:F:179:ASN:HD21	1:F:328:ARG:HH12	1.49	0.61
1:H:218:VAL:HG11	1:H:304:PHE:HD1	1.66	0.59
1:C:289:LEU:HB3	1:C:298:ILE:HD12	1.83	0.59
1:A:293:ARG:HD3	1:A:296:ARG:HG2	1.83	0.59
1:C:215:PRO:HB2	1:C:320:MET:HE3	1.85	0.58
1:F:40:GLU:OE2	1:F:261:ARG:NH1	2.37	0.57
1:A:40:GLU:OE2	1:A:261:ARG:NH1	2.37	0.57
1:F:293:ARG:HG2	1:F:296:ARG:HD2	1.85	0.57
1:D:143:CYS:HB2	1:D:149:ARG:HG2	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:121:SER:O	1:H:125:GLN:HG3	2.05	0.56
1:G:46:ARG:HB3	1:H:372:THR:HG22	1.87	0.56
1:H:65:LEU:HB2	1:H:146:VAL:HG21	1.88	0.56
1:G:89:ALA:HB1	1:H:82:VAL:HG12	1.87	0.56
1:G:326:CYS:O	1:G:329:THR:OG1	2.23	0.56
1:G:149:ARG:O	1:G:153:MET:HG3	2.06	0.56
1:F:244:LYS:N	1:F:244:LYS:HD2	2.21	0.55
1:E:215:PRO:HG2	1:E:320:MET:HB3	1.88	0.55
1:B:24:GLU:HB2	1:F:352:TYR:CG	2.41	0.55
1:C:73:LEU:HD12	1:C:74:PRO:HD2	1.89	0.55
1:D:89:ALA:HB1	1:E:82:VAL:HG13	1.88	0.55
1:H:40:GLU:OE2	1:H:261:ARG:NH1	2.40	0.54
1:A:90:MET:HE1	1:C:77:SER:HB3	1.88	0.54
1:B:143:CYS:HB2	1:B:149:ARG:HG2	1.88	0.54
1:F:158:PRO:HG2	1:F:163:ILE:HD11	1.90	0.54
1:E:332:TRP:O	1:E:336:ILE:HG13	2.07	0.54
1:B:215:PRO:HG2	1:B:320:MET:HB3	1.90	0.53
1:C:241:ARG:NH2	1:C:243:GLU:OE2	2.42	0.53
1:G:71:PHE:CE1	1:G:122:TYR:HB2	2.43	0.53
1:H:40:GLU:O	1:H:44:SER:OG	2.16	0.53
1:G:162:HIS:CD2	1:G:313:ALA:HA	2.44	0.53
1:G:218:VAL:HG11	1:G:304:PHE:HD1	1.74	0.53
1:C:161:ARG:NH1	1:C:270:LEU:O	2.42	0.53
1:E:73:LEU:HD12	1:E:74:PRO:HD2	1.91	0.53
1:C:295:ASP:OD1	1:C:295:ASP:N	2.40	0.52
1:D:347:ARG:HE	1:E:179:ASN:HA	1.75	0.52
1:B:346:VAL:HG22	1:F:11:GLY:HA2	1.92	0.52
1:B:234:VAL:O	1:B:238:ILE:HG13	2.09	0.52
1:B:76:HIS:CE1	1:C:130:ILE:HG21	2.44	0.52
1:B:268:GLU:HB2	1:B:275:TYR:CZ	2.45	0.52
1:C:41:ASP:O	1:C:45:GLN:HG3	2.10	0.52
1:C:236:LYS:NZ	1:C:288:GLU:OE1	2.43	0.52
1:G:235:VAL:O	1:G:239:LEU:HD12	2.10	0.52
1:G:65:LEU:HD12	1:G:146:VAL:HG21	1.92	0.51
1:C:238:ILE:HG23	1:C:243:GLU:HG3	1.93	0.51
1:H:25:PRO:O	1:H:27:LYS:N	2.44	0.51
1:E:223:ASP:OD1	1:E:274:ARG:NH2	2.44	0.51
1:G:11:GLY:HA2	1:H:346:VAL:HG22	1.93	0.51
1:G:20:THR:HG22	1:H:352:TYR:HA	1.92	0.51
1:G:359:SER:OG	1:G:361:GLU:OE1	2.27	0.51
1:B:138:ARG:O	1:B:142:GLU:HG3	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:VAL:HG22	1:A:234:VAL:HG21	1.93	0.51
1:G:85:GLN:NE2	1:G:200:SER:O	2.43	0.51
1:B:359:SER:OG	1:B:361:GLU:OE1	2.29	0.50
1:E:251:ARG:HD3	1:E:297:ALA:HB3	1.94	0.50
1:C:235:VAL:O	1:C:239:LEU:HD12	2.11	0.50
1:D:128:ARG:NH1	1:D:133:PRO:O	2.45	0.50
1:G:215:PRO:HG2	1:G:320:MET:HB3	1.94	0.50
1:D:161:ARG:NH1	1:D:270:LEU:O	2.45	0.50
1:B:289:LEU:HB3	1:B:298:ILE:HD13	1.93	0.50
1:F:275:TYR:O	1:F:279:VAL:HG23	2.12	0.50
1:H:277:VAL:O	1:H:281:VAL:HG23	2.12	0.50
1:A:32:LEU:HD23	1:A:39:ILE:HG21	1.93	0.49
1:D:234:VAL:O	1:D:238:ILE:HG13	2.12	0.49
1:D:68:ALA:H	1:D:149:ARG:NH2	2.10	0.49
1:B:230:ASP:C	1:B:232:ARG:H	2.20	0.49
1:F:235:VAL:HG11	1:F:285:ALA:HA	1.93	0.49
1:F:245:LEU:HD23	1:F:289:LEU:HD11	1.95	0.49
1:H:275:TYR:O	1:H:279:VAL:HG23	2.12	0.49
1:G:188:ILE:O	1:G:191:THR:OG1	2.30	0.49
1:H:347:ARG:HH12	1:H:348:PRO:C	2.21	0.49
1:E:259:ARG:HG3	1:E:302:VAL:HG21	1.95	0.48
1:G:24:GLU:HB2	1:H:352:TYR:CG	2.48	0.48
1:H:264:ARG:HA	1:H:305:TRP:CZ3	2.48	0.48
1:A:89:ALA:HB1	1:C:82:VAL:HG13	1.95	0.48
1:D:206:MET:HE2	1:D:332:TRP:CZ2	2.48	0.48
1:A:41:ASP:O	1:A:45:GLN:HG3	2.13	0.48
1:B:82:VAL:HG13	1:F:89:ALA:HB1	1.95	0.48
1:H:352:TYR:OH	1:H:355:PRO:O	2.28	0.48
1:B:236:LYS:NZ	1:B:288:GLU:OE2	2.47	0.48
1:H:218:VAL:HG11	1:H:304:PHE:CD1	2.46	0.48
1:D:215:PRO:HG2	1:D:320:MET:HB3	1.95	0.48
1:H:26:ASP:OD2	1:H:33:ARG:NH2	2.47	0.48
1:H:347:ARG:HH12	1:H:349:SER:HA	1.79	0.48
1:H:310:LEU:HD22	1:H:320:MET:HG2	1.95	0.47
1:H:245:LEU:HD22	1:H:289:LEU:HD11	1.95	0.47
1:H:259:ARG:HB2	1:H:302:VAL:HG11	1.95	0.47
1:C:279:VAL:O	1:C:283:GLN:HG2	2.14	0.47
1:E:326:CYS:O	1:E:329:THR:OG1	2.27	0.47
1:G:359:SER:O	1:G:362:SER:OG	2.32	0.47
1:A:25:PRO:HA	1:A:32:LEU:HD12	1.97	0.47
1:B:11:GLY:HA2	1:F:346:VAL:HG22	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:206:MET:HE1	1:F:325:THR:HA	1.97	0.47
1:G:4:VAL:N	1:G:351:ILE:HD13	2.30	0.47
1:H:128:ARG:HB2	1:H:154:TRP:HA	1.97	0.47
1:B:132:GLN:HG2	1:B:133:PRO:HD2	1.97	0.47
1:C:150:PHE:CE1	1:C:323:MET:HE1	2.50	0.47
1:H:286:LEU:O	1:H:290:ARG:HD3	2.15	0.47
1:A:43:VAL:HG21	1:A:262:VAL:HG13	1.97	0.47
1:A:90:MET:HE2	1:B:74:PRO:HG2	1.97	0.47
1:C:218:VAL:HG11	1:C:304:PHE:HD1	1.80	0.46
1:H:263:LEU:HG	1:H:309:VAL:HG21	1.98	0.46
1:C:32:LEU:HD23	1:C:39:ILE:HD13	1.97	0.46
1:D:224:GLU:OE2	1:D:227:ARG:NH2	2.44	0.46
1:E:185:ALA:HB2	1:E:202:ALA:HB2	1.96	0.46
1:F:52:VAL:HG21	1:F:171:VAL:HG22	1.97	0.46
1:G:22:ILE:HG22	1:G:56:LEU:HD23	1.98	0.46
1:D:33:ARG:HG2	1:D:38:ASP:HA	1.97	0.46
1:E:293:ARG:HG2	1:E:295:ASP:OD1	2.16	0.46
1:G:185:ALA:HB2	1:G:202:ALA:HB2	1.97	0.46
1:G:268:GLU:HB2	1:G:275:TYR:CZ	2.51	0.46
1:A:215:PRO:HG2	1:A:320:MET:HB3	1.97	0.46
1:G:128:ARG:NH1	1:G:133:PRO:O	2.49	0.46
1:G:179:ASN:HD21	1:G:328:ARG:NH1	2.13	0.46
1:G:241:ARG:NH1	1:G:243:GLU:OE2	2.49	0.46
1:F:69:GLU:OE2	1:F:114:ARG:NE	2.47	0.46
1:B:275:TYR:O	1:B:279:VAL:HG23	2.15	0.46
1:G:258:PRO:O	1:G:262:VAL:HG23	2.16	0.46
1:A:264:ARG:HG3	1:A:305:TRP:CZ2	2.51	0.46
1:C:91:LEU:HD22	1:C:95:TRP:CE3	2.51	0.46
1:C:178:MET:HE1	1:C:186:ARG:HD3	1.98	0.46
1:G:268:GLU:HB2	1:G:275:TYR:CE2	2.51	0.46
1:C:65:LEU:HD12	1:C:146:VAL:HG21	1.98	0.45
1:H:179:ASN:HD21	1:H:328:ARG:NH1	2.15	0.45
1:B:73:LEU:HG	1:B:75:ILE:HB	1.98	0.45
1:F:49:PHE:CD1	1:F:170:TRP:HB3	2.52	0.45
1:G:17:ALA:HB2	1:H:348:PRO:HB2	1.98	0.45
1:F:179:ASN:HD21	1:F:328:ARG:NH1	2.14	0.45
1:G:251:ARG:HD3	1:G:297:ALA:HB1	1.99	0.45
1:B:238:ILE:HG22	1:B:243:GLU:HB2	1.99	0.45
1:E:186:ARG:HD2	1:E:335:HIS:HB3	1.99	0.45
1:F:27:LYS:HA	1:F:253:TYR:CD2	2.52	0.45
1:A:191:THR:HG21	1:C:205:ALA:O	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:185:ALA:HB2	1:D:202:ALA:HB2	1.99	0.45
1:C:310:LEU:HD13	1:C:320:MET:HG2	1.99	0.45
1:E:88:LEU:HA	1:E:91:LEU:HG	1.98	0.45
1:H:5:PRO:HD3	1:H:351:ILE:HG21	1.99	0.45
1:H:68:ALA:H	1:H:149:ARG:HH22	1.65	0.45
1:A:11:GLY:HA2	1:C:346:VAL:HG22	1.99	0.44
1:H:264:ARG:HA	1:H:305:TRP:HZ3	1.80	0.44
1:A:245:LEU:HD12	1:A:245:LEU:HA	1.75	0.44
1:E:234:VAL:O	1:E:238:ILE:HG13	2.18	0.44
1:A:185:ALA:HB2	1:A:202:ALA:HB2	1.99	0.44
1:H:279:VAL:O	1:H:283:GLN:HG2	2.18	0.44
1:B:206:MET:HE2	1:B:332:TRP:CZ2	2.53	0.44
1:D:178:MET:HE2	1:D:178:MET:HB2	1.87	0.44
1:E:295:ASP:OD1	1:E:295:ASP:N	2.48	0.44
1:F:264:ARG:NH2	1:F:282:GLU:OE2	2.51	0.44
1:H:215:PRO:HG2	1:H:320:MET:HB3	2.00	0.44
1:H:358:ARG:CZ	1:H:363:VAL:HG22	2.47	0.44
1:E:73:LEU:HG	1:E:75:ILE:HB	2.00	0.44
1:E:178:MET:HE1	1:E:186:ARG:HD3	2.00	0.44
1:E:259:ARG:O	1:E:263:LEU:HG	2.17	0.44
1:F:30:GLY:HA2	1:F:253:TYR:HD2	1.83	0.44
1:F:32:LEU:HD23	1:F:39:ILE:HG21	2.00	0.44
1:H:261:ARG:O	1:H:264:ARG:HB3	2.18	0.44
1:E:27:LYS:HE2	1:E:252:VAL:HG12	1.99	0.43
1:A:24:GLU:HB2	1:C:352:TYR:CG	2.53	0.43
1:D:52:VAL:HG21	1:D:171:VAL:HG13	1.99	0.43
1:H:121:SER:HA	1:H:153:MET:HE1	2.00	0.43
1:H:304:PHE:CD2	1:H:305:TRP:CD1	3.06	0.43
1:B:91:LEU:HD22	1:B:95:TRP:CE3	2.53	0.43
1:D:235:VAL:O	1:D:239:LEU:HD12	2.18	0.43
1:H:143:CYS:HB2	1:H:149:ARG:HD2	2.00	0.43
1:A:254:ARG:HH11	1:A:255:ALA:HB2	1.83	0.43
1:C:215:PRO:HG2	1:C:320:MET:HB3	2.01	0.43
1:E:65:LEU:HB2	1:E:146:VAL:HG21	2.00	0.43
1:G:140:ILE:HA	1:G:143:CYS:SG	2.59	0.43
1:B:27:LYS:HA	1:B:253:TYR:CD2	2.54	0.43
1:B:161:ARG:NH1	1:B:270:LEU:O	2.51	0.43
1:H:112:LEU:O	1:H:116:SER:OG	2.31	0.43
1:A:178:MET:O	1:C:347:ARG:NH1	2.52	0.43
1:D:288:GLU:O	1:D:292:ARG:HG3	2.19	0.43
1:E:26:ASP:O	1:E:30:GLY:N	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:264:ARG:HG3	1:C:305:TRP:CZ2	2.54	0.43
1:H:295:ASP:OD1	1:H:295:ASP:N	2.45	0.42
1:A:46:ARG:HE	1:A:164:GLU:CD	2.27	0.42
1:C:328:ARG:HD3	1:C:328:ARG:HA	1.74	0.42
1:F:91:LEU:HD22	1:F:95:TRP:CE3	2.54	0.42
1:F:199:LEU:O	1:F:203:ILE:HG12	2.19	0.42
1:C:351:ILE:HD13	1:C:351:ILE:HA	1.77	0.42
1:H:347:ARG:HH12	1:H:349:SER:CA	2.32	0.42
1:A:60:ASN:HB2	1:C:364:ASP:O	2.19	0.42
1:H:27:LYS:HA	1:H:253:TYR:CD2	2.55	0.42
1:C:289:LEU:HD23	1:C:289:LEU:HA	1.78	0.42
1:D:139:ILE:O	1:D:142:GLU:HG2	2.20	0.42
1:A:301:ASN:HB3	1:A:303:GLU:OE1	2.19	0.42
1:C:110:GLN:O	1:C:113:ALA:N	2.52	0.42
1:D:52:VAL:HG11	1:D:171:VAL:HG13	2.01	0.42
1:D:179:ASN:HD21	1:D:328:ARG:NH1	2.17	0.42
1:B:65:LEU:HB2	1:B:146:VAL:HG21	2.01	0.42
1:F:215:PRO:HG2	1:F:320:MET:HB3	2.01	0.42
1:A:224:GLU:HG3	1:A:234:VAL:HG11	2.01	0.42
1:B:24:GLU:HB2	1:F:352:TYR:CD1	2.55	0.42
1:C:275:TYR:O	1:C:279:VAL:HG13	2.20	0.42
1:D:10:PRO:O	1:E:344:LYS:NZ	2.52	0.42
1:B:89:ALA:HB1	1:F:82:VAL:HG13	2.03	0.41
1:A:289:LEU:HB3	1:A:298:ILE:HD13	2.01	0.41
1:G:137:GLN:NE2	1:G:140:ILE:HD11	2.34	0.41
1:B:104:ASP:OD1	1:B:104:ASP:N	2.49	0.41
1:B:183:PHE:O	1:B:187:VAL:HG23	2.21	0.41
1:D:248:PHE:CZ	1:D:282:GLU:HA	2.55	0.41
1:C:6:GLU:O	1:C:6:GLU:HG2	2.21	0.41
1:C:110:GLN:OE1	1:C:114:ARG:HB2	2.21	0.41
1:D:136:PRO:HD2	1:D:139:ILE:HD12	2.03	0.41
1:D:358:ARG:NH1	1:D:363:VAL:HG13	2.35	0.41
1:E:275:TYR:O	1:E:279:VAL:HG13	2.19	0.41
1:G:73:LEU:HG	1:G:75:ILE:HB	2.03	0.41
1:G:234:VAL:O	1:G:238:ILE:HG13	2.20	0.41
1:H:242:GLY:O	1:H:244:LYS:N	2.53	0.41
1:B:372:THR:OG1	1:B:373:ALA:N	2.53	0.41
1:H:65:LEU:HD23	1:H:117:VAL:HG22	2.02	0.41
1:G:230:ASP:C	1:G:232:ARG:H	2.29	0.41
1:G:364:ASP:O	1:H:60:ASN:HB2	2.21	0.41
1:H:306:ALA:O	1:H:310:LEU:HD12	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:104:ASP:OD1	1:H:107:THR:OG1	2.30	0.40
1:B:319:MET:HE3	1:B:319:MET:HB2	1.97	0.40
1:C:79:ASP:HB3	1:C:82:VAL:HB	2.04	0.40
1:C:132:GLN:OE1	1:C:133:PRO:HD2	2.21	0.40
1:G:233:SER:HA	1:G:236:LYS:HB2	2.02	0.40
1:C:239:LEU:HD11	1:C:245:LEU:HD22	2.02	0.40
1:D:269:ARG:HG3	1:D:270:LEU:N	2.36	0.40
1:H:43:VAL:HG21	1:H:262:VAL:HG11	2.03	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	365/373 (98%)	349 (96%)	16 (4%)	0	100	100
1	B	367/373 (98%)	351 (96%)	16 (4%)	0	100	100
1	C	368/373 (99%)	350 (95%)	18 (5%)	0	100	100
1	D	368/373 (99%)	350 (95%)	18 (5%)	0	100	100
1	E	367/373 (98%)	352 (96%)	15 (4%)	0	100	100
1	F	364/373 (98%)	352 (97%)	12 (3%)	0	100	100
1	G	365/373 (98%)	349 (96%)	16 (4%)	0	100	100
1	H	366/373 (98%)	349 (95%)	14 (4%)	3 (1%)	16	37
All	All	2930/2984 (98%)	2802 (96%)	125 (4%)	3 (0%)	48	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	26	ASP
1	H	243	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	286	LEU

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	280/285 (98%)	280 (100%)	0	100	100
1	B	281/285 (99%)	277 (99%)	4 (1%)	59	77
1	C	283/285 (99%)	281 (99%)	2 (1%)	76	87
1	D	283/285 (99%)	282 (100%)	1 (0%)	84	92
1	E	282/285 (99%)	280 (99%)	2 (1%)	76	87
1	F	278/285 (98%)	276 (99%)	2 (1%)	76	87
1	G	280/285 (98%)	276 (99%)	4 (1%)	59	77
1	H	283/285 (99%)	278 (98%)	5 (2%)	51	72
All	All	2250/2280 (99%)	2230 (99%)	20 (1%)	70	83

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	9	VAL
1	B	203	ILE
1	B	362	SER
1	B	372	THR
1	C	318	ASN
1	C	367	GLU
1	D	364	ASP
1	E	9	VAL
1	E	101	LEU
1	F	12	LEU
1	F	15	VAL
1	G	16	VAL
1	G	19	THR
1	G	139	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	179	ASN
1	H	82	VAL
1	H	234	VAL
1	H	262	VAL
1	H	289	LEU
1	H	362	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	B	85	GLN
1	B	301	ASN
1	D	45	GLN
1	D	179	ASN
1	D	250	HIS
1	D	339	GLN
1	E	176	HIS
1	F	45	GLN
1	G	45	GLN
1	H	301	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	367/373 (98%)	-1.40	0 100 100	33, 51, 67, 109	103 (28%)
1	B	369/373 (98%)	-1.27	0 100 100	37, 55, 77, 143	96 (26%)
1	C	370/373 (99%)	-1.19	1 (0%) 90 88	36, 57, 85, 107	110 (29%)
1	D	370/373 (99%)	-1.21	1 (0%) 90 88	35, 61, 79, 112	157 (42%)
1	E	369/373 (98%)	-1.16	2 (0%) 87 83	34, 66, 89, 123	160 (43%)
1	F	366/373 (98%)	-1.34	0 100 100	23, 56, 78, 96	98 (26%)
1	G	367/373 (98%)	-1.13	0 100 100	40, 71, 96, 123	155 (42%)
1	H	370/373 (99%)	-0.95	0 100 100	42, 75, 120, 135	178 (48%)
All	All	2948/2984 (98%)	-1.20	4 (0%) 92 91	23, 61, 92, 143	1057 (35%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	4	VAL	4.0
1	E	7	ASN	2.1
1	E	4	VAL	2.1
1	C	5	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.