



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:00 PM UTC

PDB ID : 5TUB / pdb_00005tub
Title : Crystal Structure of the Shark TBC1D15 GAP Domain
Authors : Chen, Y.-N.; Wang, W.; Cheng, D.; Ge, Y.; Gu, X.; Zhou, X.E.; Ye, F.; Xu, H.E.; Lv, Z.
Deposited on : 2016-11-05
Resolution : 2.85 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

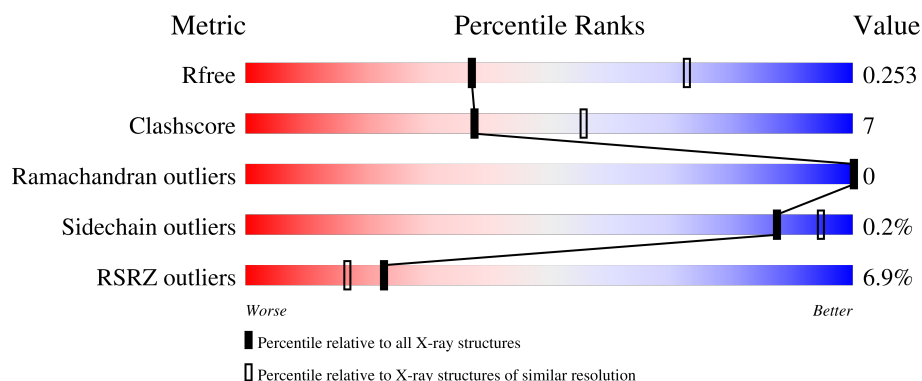
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	348	4% 76% 20% .
1	B	348	6% 82% 14% .
1	C	348	4% 76% 18% • 5%
1	D	348	12% 78% 17% • •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11231 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 Shark TBC1D15 GTPase-activating Protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2807	1811	466	505	25			
1	B	334	Total	C	N	O	S	0	0	0
			2798	1805	464	504	25			
1	C	330	Total	C	N	O	S	0	0	0
			2759	1779	458	497	25			
1	D	333	Total	C	N	O	S	0	0	0
			2784	1793	463	503	25			

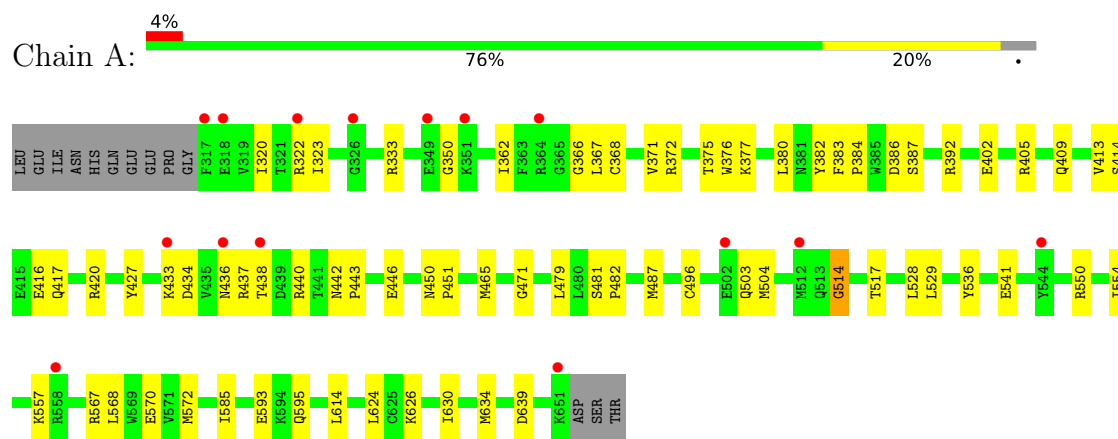
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	20	Total	O	0	0
			20	20		
2	B	21	Total	O	0	0
			21	21		
2	C	26	Total	O	0	0
			26	26		
2	D	16	Total	O	0	0
			16	16		

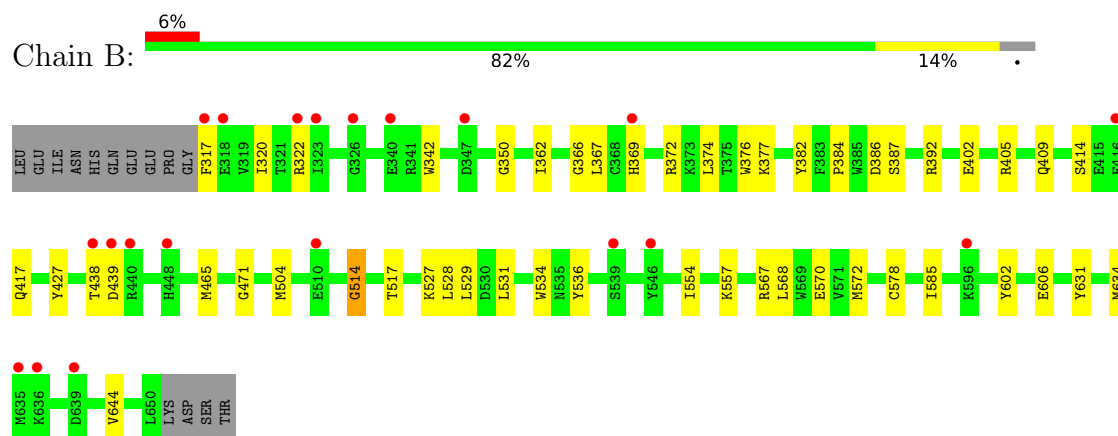
3 Residue-property plots [i](#)

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.

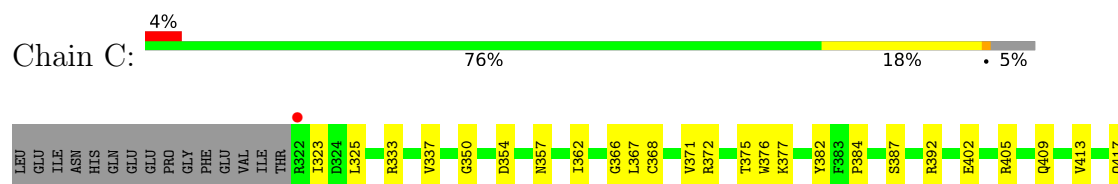
• Molecule 1: Shark TBC1D15 GTPase-activating Protein

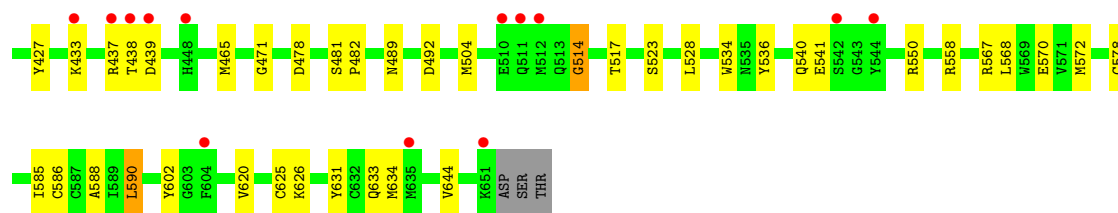


• Molecule 1: Shark TBC1D15 GTPase-activating Protein

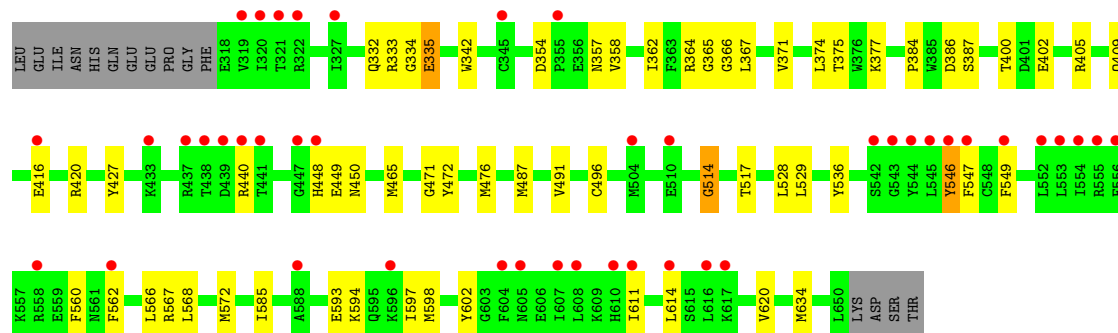
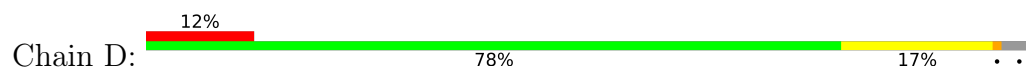


• Molecule 1: Shark TBC1D15 GTPase-activating Protein





● Molecule 1: Shark TBC1D15 GTPase-activating Protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	224.79Å 149.74Å 95.03Å 90.00° 108.93° 90.00°	Depositor
Resolution (Å)	47.26 – 2.85 47.26 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.26-2.85) 100.0 (47.26-2.85)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.215 , 0.248 0.225 , 0.253	Depositor DCC
R_{free} test set	4815 reflections (6.94%)	wwPDB-VP
Wilson B-factor (Å ²)	69.8	Xtriage
Anisotropy	0.492	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11231	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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

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	0.41	0/2872	0.80	1/3867 (0.0%)
1	B	0.40	0/2863	0.77	1/3856 (0.0%)
1	C	0.41	0/2823	0.78	1/3801 (0.0%)
1	D	0.36	0/2848	0.84	8/3836 (0.2%)
All	All	0.40	0/11406	0.80	11/15360 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	334	GLY	N-CA-C	7.89	131.87	113.18
1	D	514	GLY	N-CA-C	-7.06	106.68	115.08
1	C	514	GLY	N-CA-C	-6.99	106.77	115.08
1	A	514	GLY	N-CA-C	-6.59	107.23	115.08
1	D	546	TYR	N-CA-C	-6.14	105.82	113.38
1	D	450	ASN	CA-C-N	6.09	125.98	119.28
1	D	450	ASN	C-N-CA	6.09	125.98	119.28
1	D	440	ARG	N-CA-C	-5.99	105.73	113.16
1	D	332	GLN	N-CA-C	5.90	120.18	112.92
1	B	514	GLY	N-CA-C	-5.88	108.08	115.08
1	D	335	GLU	N-CA-C	5.40	118.94	109.48

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	2807	0	2789	50	0
1	B	2798	0	2776	31	0
1	C	2759	0	2736	46	0
1	D	2784	0	2758	35	0
2	A	20	0	0	0	0
2	B	21	0	0	0	0
2	C	26	0	0	1	0
2	D	16	0	0	0	0
All	All	11231	0	11059	156	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 7.

All (156) 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:D:384:PRO:HG2	1:D:387:SER:HB3	1.64	0.79
1:B:384:PRO:HG2	1:B:387:SER:HB3	1.64	0.77
1:C:384:PRO:HG2	1:C:387:SER:HB3	1.68	0.75
1:A:572:MET:HE2	1:A:585:ILE:HD12	1.71	0.70
1:B:572:MET:HE2	1:B:585:ILE:HG13	1.76	0.68
1:C:433:LYS:HE2	1:C:437:ARG:HH22	1.58	0.68
1:A:384:PRO:HG2	1:A:387:SER:HB3	1.76	0.67
1:D:335:GLU:O	1:D:365:GLY:HA3	1.95	0.67
1:C:438:THR:HG22	1:C:439:ASP:H	1.60	0.67
1:A:595:GLN:NE2	1:C:602:TYR:O	2.28	0.66
1:C:350:GLY:O	1:C:392:ARG:NH2	2.28	0.65
1:C:376:TRP:HE1	1:C:570:GLU:HG2	1.61	0.65
1:A:568:LEU:HG	1:A:572:MET:HE3	1.78	0.65
1:D:402:GLU:HG3	1:D:405:ARG:HH21	1.63	0.64
1:D:362:ILE:HG12	1:D:367:LEU:HD21	1.80	0.64
1:A:436:ASN:O	1:A:440:ARG:NH2	2.32	0.62
1:B:529:LEU:HD21	1:B:634:MET:HE3	1.82	0.62
1:A:514:GLY:HA2	1:A:517:THR:HB	1.80	0.62
1:B:402:GLU:HG3	1:B:405:ARG:HH21	1.65	0.61
1:B:427:TYR:CZ	1:B:471:GLY:HA3	2.36	0.61
1:C:514:GLY:HA2	1:C:517:THR:HB	1.83	0.61
1:C:572:MET:HE2	1:C:585:ILE:HD12	1.83	0.60
1:B:366:GLY:HA3	1:B:567:ARG:HH21	1.68	0.59
1:C:372:ARG:NE	1:C:570:GLU:OE2	2.28	0.59
1:A:409:GLN:HB3	1:A:465:MET:HE2	1.83	0.59
1:B:350:GLY:O	1:B:392:ARG:NH2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:GLN:HB3	1:B:465:MET:HE2	1.85	0.59
1:C:362:ILE:HG12	1:C:367:LEU:HD21	1.84	0.59
1:C:523:SER:HB2	1:C:534:TRP:HE1	1.68	0.59
1:A:322:ARG:HA	1:C:550:ARG:HD3	1.85	0.59
1:A:402:GLU:HG3	1:A:405:ARG:HH21	1.68	0.59
1:A:433:LYS:HE2	1:A:437:ARG:HH22	1.67	0.58
1:D:547:PHE:HB2	1:D:611:ILE:HD12	1.86	0.58
1:A:372:ARG:NE	1:A:570:GLU:OE2	2.28	0.57
1:B:438:THR:HG22	1:B:439:ASP:H	1.69	0.57
1:D:416:GLU:HG2	1:D:420:ARG:HH22	1.69	0.57
1:A:568:LEU:HD11	1:A:585:ILE:HD13	1.85	0.57
1:C:368:CYS:SG	1:C:371:VAL:HG23	2.45	0.57
1:C:409:GLN:HB3	1:C:465:MET:HE2	1.86	0.57
1:C:528:LEU:HD23	1:C:634:MET:HE2	1.87	0.56
1:C:568:LEU:HG	1:C:572:MET:HE3	1.87	0.56
1:A:416:GLU:HB3	1:A:420:ARG:HH22	1.70	0.55
1:C:402:GLU:HG3	1:C:405:ARG:NH2	2.22	0.55
1:D:568:LEU:HG	1:D:572:MET:HE3	1.89	0.55
1:A:593:GLU:HG3	1:A:614:LEU:HD11	1.88	0.55
1:C:433:LYS:HE2	1:C:437:ARG:NH2	2.21	0.54
1:D:409:GLN:HB3	1:D:465:MET:HE2	1.90	0.54
1:A:383:PHE:CD2	1:A:392:ARG:HD3	2.43	0.54
1:A:529:LEU:HD21	1:A:634:MET:HE3	1.88	0.54
1:D:400:THR:HG23	1:D:491:VAL:HG21	1.90	0.54
1:B:514:GLY:HA2	1:B:517:THR:HB	1.88	0.54
1:B:554:ILE:HG22	1:B:557:LYS:HB3	1.89	0.54
1:C:588:ALA:HB1	1:C:626:LYS:HB3	1.90	0.53
1:C:427:TYR:CZ	1:C:471:GLY:HA3	2.44	0.52
1:C:366:GLY:HA3	1:C:567:ARG:HH21	1.74	0.52
1:D:572:MET:HE2	1:D:585:ILE:HD12	1.91	0.52
1:A:376:TRP:HE1	1:A:570:GLU:HG2	1.74	0.52
1:A:550:ARG:HD3	1:B:322:ARG:HA	1.92	0.52
1:C:354:ASP:OD2	1:C:357:ASN:ND2	2.43	0.52
1:A:514:GLY:H	1:A:517:THR:H	1.57	0.51
1:C:514:GLY:H	1:C:517:THR:H	1.57	0.51
1:D:342:TRP:HE1	1:D:374:LEU:HD23	1.75	0.51
1:D:416:GLU:HG2	1:D:420:ARG:HH12	1.76	0.51
1:D:333:ARG:HB2	1:D:364:ARG:O	2.11	0.51
1:A:536:TYR:CD1	1:C:541:GLU:HG2	2.46	0.50
1:A:554:ILE:HG22	1:A:557:LYS:HB3	1.94	0.50
1:B:528:LEU:HD22	1:B:644:VAL:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:377:LYS:HG2	1:B:382:TYR:HD2	1.75	0.50
1:C:528:LEU:HD22	1:C:644:VAL:HG21	1.94	0.50
1:B:362:ILE:HG12	1:B:367:LEU:HD21	1.94	0.50
1:C:489:ASN:HD22	1:C:492:ASP:CG	2.20	0.49
1:D:547:PHE:HB2	1:D:611:ILE:CD1	2.42	0.49
1:A:434:ASP:O	1:A:438:THR:OG1	2.29	0.49
1:D:371:VAL:HG12	1:D:375:THR:HG23	1.94	0.49
1:C:620:VAL:HG23	2:C:704:HOH:O	2.13	0.49
1:D:472:TYR:CE1	1:D:476:MET:HB2	2.48	0.49
1:A:380:LEU:HD13	1:A:496:CYS:HB3	1.94	0.49
1:C:578:CYS:HB3	1:C:631:TYR:CE1	2.48	0.49
1:D:366:GLY:HA3	1:D:567:ARG:HH21	1.78	0.49
1:B:366:GLY:HA3	1:B:567:ARG:NH2	2.27	0.48
1:A:368:CYS:SG	1:A:371:VAL:HG23	2.54	0.48
1:C:413:VAL:HG13	1:C:417:GLN:HB3	1.94	0.48
1:A:320:ILE:O	1:A:323:ILE:HG22	2.14	0.48
1:A:366:GLY:HA3	1:A:567:ARG:NH2	2.29	0.48
1:B:320:ILE:HD11	1:B:531:LEU:HD13	1.96	0.48
1:B:369:HIS:HA	1:B:372:ARG:HD2	1.94	0.48
1:C:402:GLU:HG3	1:C:405:ARG:HH21	1.78	0.47
1:A:350:GLY:O	1:A:392:ARG:NH2	2.38	0.47
1:A:386:ASP:OD1	1:A:386:ASP:N	2.47	0.47
1:D:354:ASP:OD2	1:D:357:ASN:ND2	2.47	0.47
1:C:371:VAL:HG12	1:C:375:THR:HG23	1.96	0.47
1:B:342:TRP:HE1	1:B:374:LEU:HD23	1.79	0.47
1:D:487:MET:HE3	1:D:496:CYS:SG	2.54	0.47
1:C:376:TRP:NE1	1:C:570:GLU:HG2	2.30	0.47
1:D:448:HIS:CD2	1:D:449:GLU:HG3	2.50	0.47
1:D:386:ASP:OD1	1:D:386:ASP:N	2.44	0.47
1:B:528:LEU:HD23	1:B:634:MET:HE2	1.98	0.46
1:A:377:LYS:HG2	1:A:382:TYR:HD2	1.80	0.46
1:C:325:LEU:HB3	1:C:633:GLN:HG2	1.98	0.46
1:C:568:LEU:HD11	1:C:585:ILE:HD13	1.98	0.46
1:A:440:ARG:O	1:A:446:GLU:HB3	2.16	0.46
1:C:366:GLY:HA3	1:C:567:ARG:NH2	2.30	0.46
1:C:377:LYS:HG2	1:C:382:TYR:HD2	1.80	0.46
1:D:536:TYR:CZ	1:D:598:MET:HA	2.51	0.46
1:B:317:PHE:HB2	1:B:527:LYS:NZ	2.31	0.46
1:B:568:LEU:HG	1:B:572:MET:HE3	1.98	0.46
1:A:377:LYS:HE3	1:A:487:MET:SD	2.57	0.45
1:A:362:ILE:HG12	1:A:367:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:LEU:HD13	1:A:504:MET:HE1	1.98	0.45
1:C:333:ARG:HG2	1:C:625:CYS:SG	2.57	0.45
1:A:366:GLY:HA3	1:A:567:ARG:HH21	1.82	0.44
1:A:450:ASN:HA	1:A:451:PRO:HD3	1.89	0.44
1:C:481:SER:HB3	1:C:482:PRO:HD3	1.99	0.44
1:D:358:VAL:O	1:D:362:ILE:HG13	2.18	0.44
1:C:337:VAL:HB	1:C:367:LEU:HD23	1.99	0.44
1:A:376:TRP:HE1	1:A:570:GLU:CG	2.30	0.44
1:A:414:SER:OG	1:A:417:GLN:HB2	2.18	0.44
1:C:376:TRP:HE1	1:C:570:GLU:CG	2.30	0.44
1:B:372:ARG:NE	1:B:570:GLU:OE2	2.34	0.44
1:B:414:SER:OG	1:B:417:GLN:HB2	2.17	0.44
1:B:386:ASP:OD1	1:B:386:ASP:N	2.47	0.44
1:C:586:CYS:O	1:C:590:LEU:HB2	2.17	0.44
1:D:514:GLY:HA2	1:D:517:THR:HB	2.00	0.44
1:A:367:LEU:HB2	1:A:570:GLU:OE2	2.18	0.43
1:B:578:CYS:HB3	1:B:631:TYR:CE1	2.53	0.43
1:D:529:LEU:HD21	1:D:634:MET:HE3	2.00	0.43
1:D:562:PHE:O	1:D:566:LEU:HG	2.17	0.43
1:A:442:ASN:HA	1:A:443:PRO:HD3	1.89	0.43
1:B:504:MET:HE2	1:B:504:MET:HB3	1.77	0.43
1:A:626:LYS:O	1:A:630:ILE:HG13	2.19	0.42
1:A:481:SER:HB3	1:A:482:PRO:HD3	2.00	0.42
1:D:597:ILE:HA	1:D:602:TYR:CD2	2.54	0.42
1:A:371:VAL:HG12	1:A:375:THR:HG23	2.01	0.42
1:D:593:GLU:CD	1:D:614:LEU:HD11	2.44	0.42
1:D:427:TYR:CZ	1:D:471:GLY:HA3	2.53	0.42
1:C:536:TYR:OH	1:C:540:GLN:NE2	2.43	0.42
1:C:367:LEU:N	1:C:567:ARG:HH22	2.17	0.42
1:B:527:LYS:HG3	1:B:534:TRP:CD2	2.55	0.42
1:B:602:TYR:HB3	1:B:606:GLU:HB2	2.02	0.42
1:A:323:ILE:HD13	1:A:528:LEU:HD11	2.01	0.41
1:A:402:GLU:HG3	1:A:405:ARG:NH2	2.34	0.41
1:C:504:MET:HE3	1:C:504:MET:HB3	1.81	0.41
1:D:377:LYS:HE3	1:D:487:MET:SD	2.60	0.41
1:D:546:TYR:O	1:D:549:PHE:HB2	2.20	0.41
1:D:528:LEU:HD23	1:D:634:MET:HE2	2.03	0.41
1:A:639:ASP:CG	1:C:437:ARG:HD2	2.45	0.41
1:C:478:ASP:OD2	1:C:558:ARG:NH2	2.53	0.41
1:A:427:TYR:CZ	1:A:471:GLY:HA3	2.56	0.41
1:D:560:PHE:CD1	1:D:620:VAL:HG22	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:503:GLN:HG3	1:A:504:MET:HG3	2.03	0.41
1:D:402:GLU:HG3	1:D:405:ARG:NH2	2.32	0.41
1:A:333:ARG:HH21	1:A:624:LEU:HD13	1.87	0.40
1:A:413:VAL:HG13	1:A:417:GLN:HB3	2.04	0.40
1:B:376:TRP:HE1	1:B:570:GLU:HG2	1.85	0.40
1:A:541:GLU:HG2	1:B:536:TYR:CD1	2.57	0.40
1:D:594:LYS:O	1:D:598:MET:HG3	2.21	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	333/348 (96%)	326 (98%)	7 (2%)	0	100	100
1	B	332/348 (95%)	325 (98%)	7 (2%)	0	100	100
1	C	328/348 (94%)	323 (98%)	5 (2%)	0	100	100
1	D	331/348 (95%)	327 (99%)	4 (1%)	0	100	100
All	All	1324/1392 (95%)	1301 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	311/323 (96%)	311 (100%)	0	100	100
1	B	310/323 (96%)	310 (100%)	0	100	100
1	C	305/323 (94%)	303 (99%)	2 (1%)	76	87
1	D	308/323 (95%)	308 (100%)	0	100	100
All	All	1234/1292 (96%)	1232 (100%)	2 (0%)	87	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	323	ILE
1	C	590	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	580	ASN
1	A	633	GLN
1	B	563	GLN
1	C	474	GLN
1	D	600	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

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	335/348 (96%)	0.19	15 (4%) 38 29	48, 69, 103, 135	0
1	B	334/348 (95%)	0.30	20 (5%) 27 20	49, 73, 108, 139	0
1	C	330/348 (94%)	0.19	14 (4%) 40 32	46, 71, 112, 141	0
1	D	333/348 (95%)	0.83	43 (12%) 7 5	53, 98, 136, 152	0
All	All	1332/1392 (95%)	0.38	92 (6%) 23 17	46, 76, 121, 152	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	320	ILE	5.8
1	B	546	TYR	5.0
1	D	611	ILE	4.9
1	D	554	ILE	4.7
1	B	322	ARG	4.5
1	D	610	HIS	4.5
1	A	317	PHE	4.4
1	C	439	ASP	4.2
1	D	319	VAL	4.1
1	A	318	GLU	4.1
1	B	317	PHE	4.1
1	D	321	THR	4.0
1	D	614	LEU	4.0
1	A	322	ARG	3.9
1	A	433	LYS	3.7
1	D	616	LEU	3.7
1	D	439	ASP	3.6
1	C	544	TYR	3.6
1	D	547	PHE	3.5
1	D	545	LEU	3.4
1	B	369	HIS	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	437	ARG	3.3
1	B	340	GLU	3.3
1	D	546	TYR	3.3
1	B	326	GLY	3.3
1	A	651	LYS	3.2
1	A	544	TYR	3.1
1	D	440	ARG	3.1
1	C	448	HIS	3.1
1	D	542	SER	3.0
1	A	349	GLU	3.0
1	D	549	PHE	3.0
1	C	651	LYS	2.9
1	D	607	ILE	2.9
1	B	439	ASP	2.9
1	D	441	THR	2.9
1	D	544	TYR	2.9
1	A	326	GLY	2.8
1	C	433	LYS	2.8
1	D	605	ASN	2.8
1	B	438	THR	2.8
1	D	416	GLU	2.7
1	C	511	GLN	2.7
1	B	635	MET	2.6
1	C	437	ARG	2.6
1	B	448	HIS	2.5
1	C	322	ARG	2.5
1	D	617	LYS	2.5
1	D	543	GLY	2.5
1	D	322	ARG	2.5
1	D	604	PHE	2.5
1	C	438	THR	2.5
1	B	318	GLU	2.4
1	D	438	THR	2.4
1	B	636	LYS	2.4
1	A	512	MET	2.4
1	D	447	GLY	2.4
1	B	440	ARG	2.4
1	D	562	PHE	2.4
1	D	558	ARG	2.3
1	B	539	SER	2.3
1	A	558	ARG	2.3
1	D	327	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	510	GLU	2.2
1	B	347	ASP	2.2
1	A	436	ASN	2.2
1	D	504	MET	2.1
1	B	639	ASP	2.1
1	C	604	PHE	2.1
1	D	556	PHE	2.1
1	B	323	ILE	2.1
1	D	345	CYS	2.1
1	D	448	HIS	2.1
1	D	596	LYS	2.1
1	D	552	LEU	2.1
1	A	364	ARG	2.1
1	C	512	MET	2.1
1	B	416	GLU	2.1
1	B	510	GLU	2.1
1	A	351	LYS	2.0
1	B	596	LYS	2.0
1	D	433	LYS	2.0
1	D	355	PRO	2.0
1	D	555	ARG	2.0
1	A	438	THR	2.0
1	D	588	ALA	2.0
1	C	542	SER	2.0
1	D	553	LEU	2.0
1	D	608	LEU	2.0
1	A	502	GLU	2.0
1	D	510	GLU	2.0
1	C	635	MET	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 oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.