



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 01:19 AM UTC

PDB ID : 7EP9 / pdb_00007ep9
Title : The structure of carboxypeptidase from Fusobacterium nucleatum
Authors : Wang, X.; Jiang, Y.L.
Deposited on : 2021-04-26
Resolution : 2.60 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

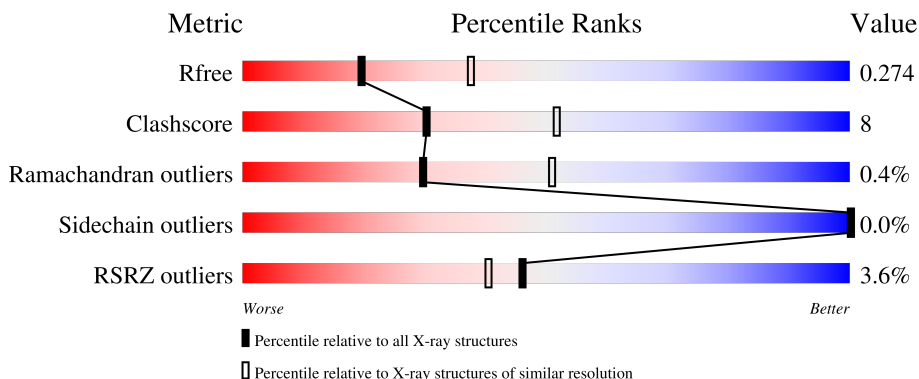
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	660	2% 81% 19%
1	B	660	% 82% 18%
1	C	660	10% 77% 22%
1	G	660	% 84% 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22126 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 S9 family peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	660	Total	C	N	O	S	0	0	0
			5409	3460	891	1042	16			
1	A	660	Total	C	N	O	S	0	0	0
			5409	3460	891	1042	16			
1	B	660	Total	C	N	O	S	0	0	0
			5409	3460	891	1042	16			
1	C	660	Total	C	N	O	S	0	0	0
			5409	3460	891	1042	16			

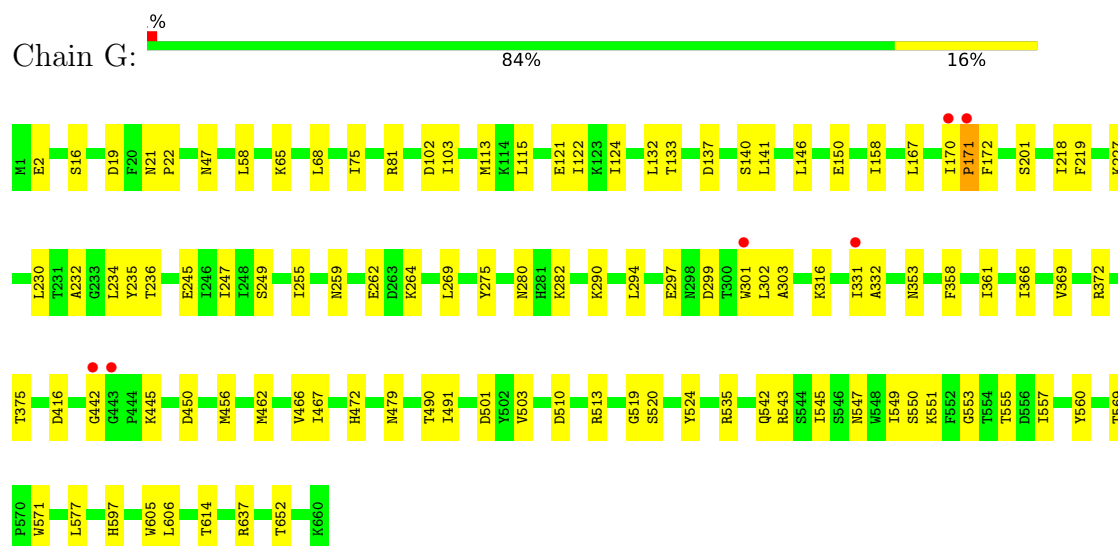
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	164	Total	O	0	0
			164	164		
2	A	122	Total	O	0	0
			122	122		
2	B	118	Total	O	0	0
			118	118		
2	C	86	Total	O	0	0
			86	86		

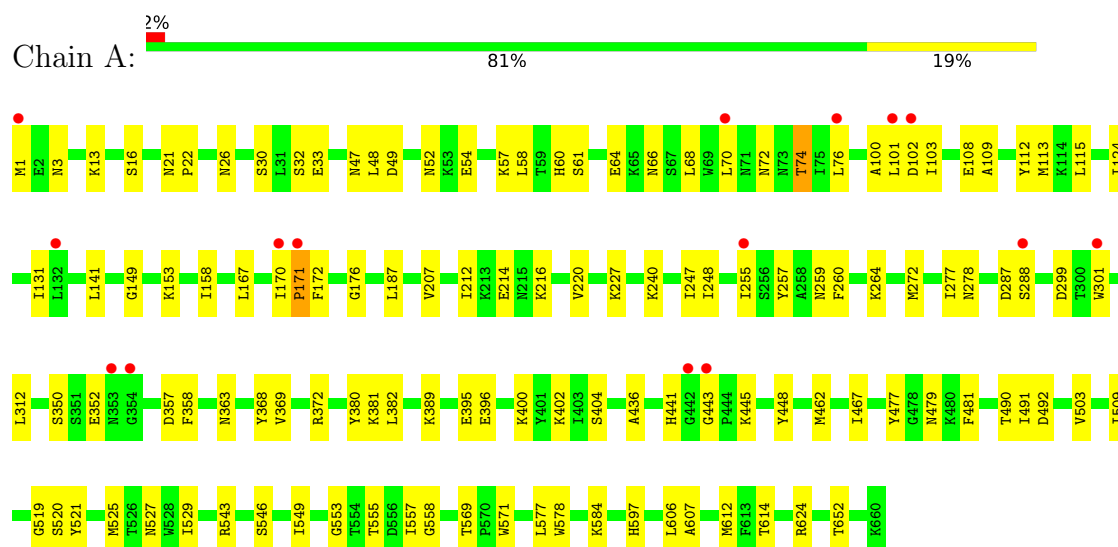
3 Residue-property plots

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.

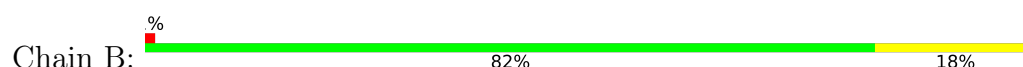
- Molecule 1: S9 family peptidase

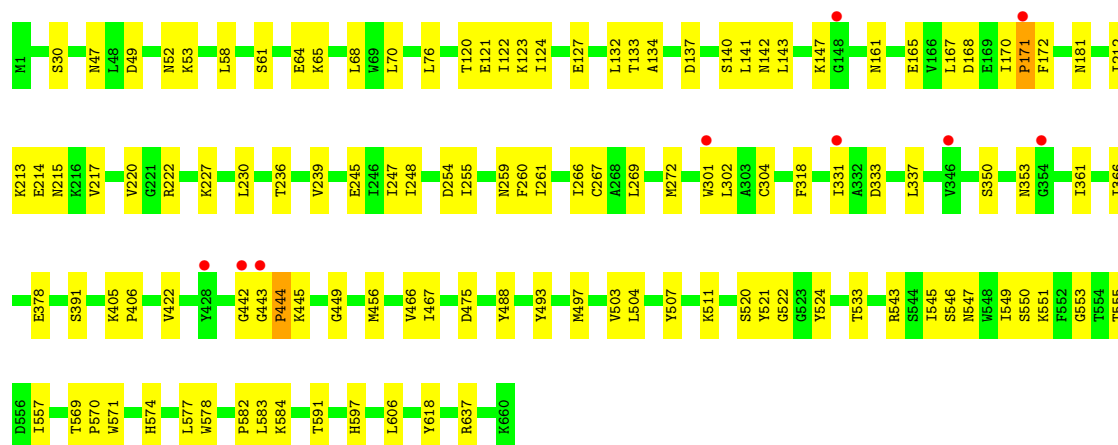


- Molecule 1: S9 family peptidase

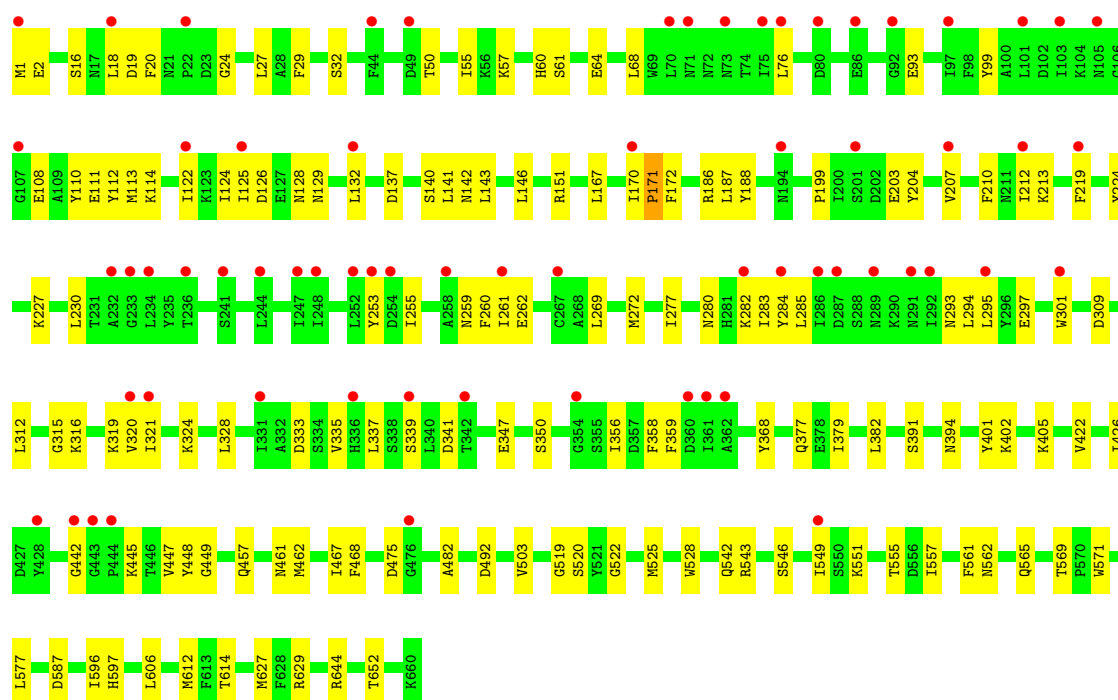
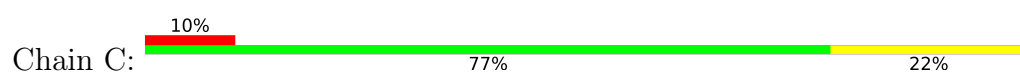


- Molecule 1: S9 family peptidase





• Molecule 1: S9 family peptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	192.00Å 124.80Å 128.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.83 – 2.60 44.83 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.83-2.60) 99.6 (44.83-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.90 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.14_3228	Depositor
R, R_{free}	0.229 , 0.274 0.233 , 0.274	Depositor DCC
R_{free} test set	4944 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.048 for -h,l,k	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	22126	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% 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	0.12	0/5538	0.34	0/7478
1	B	0.10	0/5538	0.31	0/7478
1	C	0.13	0/5538	0.35	0/7478
1	G	0.10	0/5538	0.31	0/7478
All	All	0.11	0/22152	0.33	0/29912

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	5409	0	5236	89	0
1	B	5409	0	5236	85	0
1	C	5409	0	5236	122	0
1	G	5409	0	5236	72	0
2	A	122	0	0	9	0
2	B	118	0	0	8	0
2	C	86	0	0	4	0
2	G	164	0	0	7	0
All	All	22126	0	20944	356	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 8.

All (356) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:ILE:HD12	1:B:132:LEU:HB3	1.46	0.96
1:C:146:LEU:O	1:C:151:ARG:NH2	1.99	0.95
1:A:1:MET:HE2	1:A:402:LYS:HG2	1.49	0.92
1:B:267:CYS:SG	1:B:269:LEU:HD21	2.17	0.83
1:G:569:THR:HG22	1:G:571:TRP:H	1.47	0.80
1:C:122:ILE:HD12	1:C:132:LEU:HD21	1.65	0.78
1:C:137:ASP:HB3	1:C:140:SER:HB2	1.66	0.77
1:G:113:MET:HE2	1:G:115:LEU:HD11	1.66	0.77
1:C:520:SER:H	1:C:543:ARG:HG3	1.49	0.75
1:C:230:LEU:HB3	1:C:272:MET:HE1	1.68	0.75
1:G:501:ASP:OD1	1:G:535:ARG:NH1	2.19	0.74
1:A:74:THR:OG1	1:A:102:ASP:OD1	2.06	0.74
1:A:264:LYS:HG2	1:A:287:ASP:HA	1.69	0.74
1:C:68:LEU:HD13	1:C:122:ILE:HG23	1.70	0.74
1:A:441:HIS:HB3	1:A:448:TYR:CE2	2.22	0.74
1:G:467:ILE:HG21	1:G:503:VAL:HG11	1.69	0.73
1:A:441:HIS:HB3	1:A:448:TYR:CD2	2.24	0.72
1:G:637:ARG:NH2	2:G:701:HOH:O	2.22	0.72
1:A:520:SER:H	1:A:543:ARG:HG3	1.55	0.72
1:A:381:LYS:NZ	2:A:707:HOH:O	2.23	0.72
1:C:282:LYS:HD3	1:C:297:GLU:HG2	1.72	0.72
1:B:504:LEU:HB3	1:B:511:LYS:HE2	1.70	0.71
1:C:122:ILE:HD12	1:C:132:LEU:CD2	2.20	0.71
1:C:122:ILE:CD1	1:C:132:LEU:HD21	2.21	0.70
1:C:285:LEU:HG	1:C:295:LEU:HD22	1.72	0.70
1:C:126:ASP:OD1	1:C:129:ASN:N	2.25	0.69
1:A:247:ILE:HG22	1:A:248:ILE:HG13	1.74	0.69
1:C:18:LEU:HD11	1:C:27:LEU:HD13	1.74	0.69
1:C:546:SER:HB2	1:C:612:MET:HG2	1.74	0.69
1:B:569:THR:HG22	1:B:571:TRP:H	1.56	0.68
1:C:542:GLN:HB3	1:C:596:ILE:HB	1.74	0.67
1:C:68:LEU:CD1	1:C:122:ILE:HG23	2.25	0.67
1:B:267:CYS:SG	1:B:269:LEU:CD2	2.84	0.66
1:A:467:ILE:HG21	1:A:503:VAL:HG11	1.76	0.66
1:A:108:GLU:HG2	1:C:108:GLU:HG2	1.79	0.65
1:A:569:THR:HG22	1:A:571:TRP:H	1.61	0.65
1:B:467:ILE:HG21	1:B:503:VAL:HG11	1.78	0.65
1:C:457:GLN:O	1:C:461:ASN:ND2	2.24	0.65
1:C:467:ILE:HG21	1:C:503:VAL:HG11	1.79	0.64
1:G:555:THR:HG22	1:G:557:ILE:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:75:ILE:HG13	1:G:103:ILE:HD11	1.80	0.64
1:B:170:ILE:HG22	1:B:227:LYS:HA	1.79	0.64
1:B:574:HIS:NE2	2:B:709:HOH:O	2.30	0.64
1:C:187:LEU:HB2	1:C:207:VAL:HG21	1.80	0.63
1:B:61:SER:OG	1:B:64:GLU:OE2	2.17	0.63
1:G:115:LEU:HD22	1:G:132:LEU:HD21	1.81	0.62
1:C:606:LEU:HD22	1:C:627:MET:HE3	1.80	0.62
1:C:324:LYS:HG2	1:C:341:ASP:HB3	1.82	0.62
1:A:22:PRO:HD2	1:A:72:ASN:OD1	1.99	0.62
1:A:61:SER:OG	1:A:64:GLU:OE2	2.15	0.62
1:A:389:LYS:NZ	1:A:395:GLU:OE1	2.29	0.62
1:A:70:LEU:HB2	1:A:76:LEU:HD13	1.83	0.61
1:A:555:THR:HG22	1:A:557:ILE:H	1.64	0.61
1:C:339:SER:HB3	1:C:347:GLU:HG2	1.82	0.61
1:B:70:LEU:HB2	1:B:76:LEU:HD13	1.81	0.61
1:A:170:ILE:HG22	1:A:227:LYS:HA	1.83	0.61
1:A:58:LEU:HB3	1:A:101:LEU:HD21	1.83	0.61
1:A:167:LEU:HD22	1:A:172:PHE:HB2	1.83	0.60
1:C:132:LEU:O	1:C:188:TYR:N	2.28	0.60
1:A:68:LEU:HD21	1:A:124:ILE:HB	1.83	0.60
1:G:16:SER:HA	1:G:358:PHE:CZ	2.37	0.60
1:C:569:THR:HG22	1:C:571:TRP:H	1.66	0.60
1:A:58:LEU:HD11	1:A:103:ILE:HD11	1.82	0.60
1:B:524:TYR:HB2	1:B:545:ILE:HB	1.83	0.60
1:G:219:PHE:CE1	1:G:235:TYR:HB2	2.37	0.60
1:C:122:ILE:HD12	1:C:132:LEU:CG	2.32	0.59
1:B:255:ILE:CG2	1:B:269:LEU:HD22	2.32	0.59
1:G:170:ILE:HG22	1:G:227:LYS:HA	1.84	0.59
1:G:262:GLU:OE1	1:G:264:LYS:NZ	2.33	0.59
1:A:16:SER:HA	1:A:358:PHE:CZ	2.37	0.59
1:B:442:GLY:HA2	1:B:521:TYR:HD2	1.66	0.59
1:G:490:THR:OG1	1:G:491:ILE:N	2.35	0.59
1:C:405:LYS:NZ	2:C:711:HOH:O	2.35	0.59
1:C:269:LEU:HB2	1:C:284:TYR:CE2	2.38	0.59
1:G:456:MET:HG2	1:G:466:VAL:HG11	1.84	0.59
1:A:70:LEU:HB3	1:A:74:THR:HG22	1.84	0.59
1:B:549:ILE:HG22	1:B:577:LEU:HD23	1.84	0.59
1:A:624:ARG:NH1	2:A:704:HOH:O	2.21	0.58
1:C:112:TYR:CD2	1:C:113:MET:HG3	2.39	0.58
1:B:247:ILE:HG13	1:B:248:ILE:HG13	1.85	0.58
1:C:549:ILE:HG22	1:C:577:LEU:HD23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:333:ASP:HB2	1:C:449:GLY:HA2	1.86	0.58
1:A:278:ASN:O	1:A:445:LYS:NZ	2.35	0.58
1:B:361:ILE:HG12	1:B:366:ILE:HG12	1.86	0.58
1:B:213:LYS:HG3	1:B:214:GLU:HG3	1.84	0.58
1:A:220:VAL:HG22	1:A:255:ILE:HD11	1.85	0.57
1:A:264:LYS:HE3	1:A:288:SER:H	1.69	0.57
1:G:547:ASN:HB3	1:G:550:SER:HB3	1.86	0.57
1:C:61:SER:OG	1:C:64:GLU:OE2	2.21	0.57
1:C:606:LEU:CD2	1:C:627:MET:HE3	2.35	0.57
1:C:280:ASN:HD22	1:C:301:TRP:CD1	2.23	0.57
1:G:146:LEU:HD13	1:G:150:GLU:HG2	1.87	0.56
1:A:113:MET:HE2	1:A:115:LEU:HD11	1.87	0.56
1:B:49:ASP:HB3	1:B:52:ASN:HB3	1.87	0.56
1:B:70:LEU:HG	1:B:127:GLU:HG2	1.86	0.56
1:B:555:THR:HG22	1:B:557:ILE:H	1.72	0.55
1:A:462:MET:HE1	1:A:652:THR:HG21	1.89	0.55
1:B:68:LEU:HD22	1:B:124:ILE:HG22	1.88	0.55
1:G:282:LYS:NZ	2:G:721:HOH:O	2.39	0.55
1:A:57:LYS:HE3	1:A:60:HIS:CD2	2.42	0.55
1:C:112:TYR:HD2	1:C:113:MET:HG3	1.71	0.55
1:B:497:MET:HE1	1:B:533:THR:HG21	1.89	0.54
1:A:176:GLY:N	2:A:723:HOH:O	2.31	0.54
1:C:269:LEU:HB2	1:C:284:TYR:HE2	1.72	0.54
1:B:161:ASN:ND2	2:B:707:HOH:O	2.27	0.54
1:G:255:ILE:HG22	1:G:269:LEU:HG	1.90	0.53
1:C:269:LEU:HD13	1:C:284:TYR:HD2	1.72	0.53
1:C:555:THR:HG22	1:C:557:ILE:H	1.74	0.53
1:B:222:ARG:NH1	1:B:254:ASP:OD1	2.41	0.53
1:G:219:PHE:HE1	1:G:235:TYR:HB2	1.73	0.53
1:B:591:THR:N	2:B:724:HOH:O	2.41	0.53
1:A:3:ASN:HB2	2:A:717:HOH:O	2.09	0.53
1:B:547:ASN:HB3	1:B:550:SER:HB3	1.89	0.53
1:A:30:SER:OG	1:A:66:ASN:OD1	2.26	0.53
1:C:20:PHE:HE1	1:C:50:THR:HG21	1.73	0.53
1:A:100:ALA:O	1:A:109:ALA:HA	2.09	0.52
1:A:214:GLU:HA	2:A:759:HOH:O	2.08	0.52
1:G:361:ILE:HG12	1:G:366:ILE:HG12	1.90	0.52
1:C:283:ILE:HG22	1:C:295:LEU:HD21	1.90	0.52
1:A:396:GLU:O	1:A:400:LYS:N	2.42	0.52
1:B:170:ILE:HG21	1:B:227:LYS:HG3	1.92	0.52
1:C:93:GLU:HG3	1:C:143:LEU:HD23	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:PHE:CZ	1:C:55:ILE:HD11	2.44	0.52
1:B:68:LEU:HD21	1:B:123:LYS:HA	1.91	0.52
1:C:379:ILE:H	1:C:391:SER:HG	1.56	0.52
1:C:68:LEU:CD2	1:C:124:ILE:HB	2.40	0.52
1:B:236:THR:HG22	1:B:245:GLU:HB3	1.91	0.52
1:G:19:ASP:OD1	1:G:316:LYS:NZ	2.40	0.51
1:B:597:HIS:CD2	1:B:606:LEU:HA	2.46	0.51
1:C:319:LYS:HG3	1:C:320:VAL:N	2.24	0.51
1:C:525:MET:HE1	1:C:528:TRP:CD1	2.45	0.51
1:B:637:ARG:NH1	2:B:713:HOH:O	2.32	0.51
1:C:261:ILE:HG23	1:C:262:GLU:H	1.75	0.51
1:C:551:LYS:HG2	1:C:562:ASN:HD21	1.75	0.51
1:G:167:LEU:HD22	1:G:172:PHE:HB2	1.92	0.51
1:G:280:ASN:ND2	1:G:299:ASP:OD1	2.42	0.51
1:A:13:LYS:NZ	1:A:33:GLU:OE1	2.39	0.51
1:G:372:ARG:O	1:G:375:THR:OG1	2.23	0.51
1:C:122:ILE:HD12	1:C:132:LEU:HG	1.93	0.51
1:B:220:VAL:HG22	1:B:255:ILE:HD11	1.93	0.51
1:C:125:ILE:HG12	1:C:212:ILE:HD11	1.93	0.51
1:C:32:SER:HB3	1:C:312:LEU:HD23	1.93	0.51
1:C:167:LEU:HD22	1:C:172:PHE:HB2	1.92	0.51
1:A:546:SER:HB2	1:A:612:MET:HG2	1.92	0.51
1:B:520:SER:H	1:B:543:ARG:HG3	1.74	0.51
1:A:555:THR:HB	1:A:558:GLY:HA3	1.93	0.50
1:G:122:ILE:HD12	1:G:132:LEU:HG	1.92	0.50
1:C:280:ASN:HD22	1:C:301:TRP:HD1	1.58	0.50
1:A:1:MET:HE2	1:A:402:LYS:CG	2.32	0.50
1:C:16:SER:HA	1:C:358:PHE:CZ	2.45	0.50
1:C:335:VAL:HB	1:C:356:ILE:H	1.76	0.50
1:B:65:LYS:NZ	2:B:717:HOH:O	2.34	0.50
1:C:141:LEU:O	1:C:143:LEU:N	2.45	0.50
1:G:121:GLU:HB3	1:G:133:THR:HG22	1.93	0.50
1:A:60:HIS:CD2	1:C:110:TYR:HB3	2.47	0.50
1:A:350:SER:HB2	1:A:382:LEU:HD21	1.94	0.50
1:G:16:SER:HA	1:G:358:PHE:HZ	1.77	0.49
1:G:301:TRP:CD1	1:G:445:LYS:HZ3	2.30	0.49
1:G:462:MET:HE1	1:G:652:THR:HG21	1.94	0.49
1:G:520:SER:H	1:G:543:ARG:HG3	1.77	0.49
1:G:358:PHE:CZ	1:G:369:VAL:HG11	2.47	0.49
1:A:141:LEU:HD12	1:A:158:ILE:HG13	1.95	0.49
1:C:442:GLY:O	1:C:520:SER:HB3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:170:ILE:HG21	1:C:227:LYS:HG3	1.94	0.49
1:G:247:ILE:HG22	1:G:290:LYS:HE2	1.95	0.49
1:G:218:ILE:HG21	1:G:259:ASN:HA	1.94	0.49
1:A:112:TYR:CD2	1:A:113:MET:HG3	2.48	0.49
1:G:524:TYR:HB2	1:G:545:ILE:HB	1.95	0.48
1:A:357:ASP:HB2	1:A:369:VAL:HG13	1.95	0.48
1:G:170:ILE:HG21	1:G:227:LYS:HG3	1.94	0.48
1:B:259:ASN:OD1	1:B:260:PHE:N	2.46	0.48
1:G:294:LEU:HD21	1:G:297:GLU:HG3	1.95	0.48
1:A:187:LEU:HB2	1:A:207:VAL:HG21	1.96	0.48
1:C:319:LYS:HE2	1:C:321:ILE:HD11	1.96	0.48
1:B:304:CYS:HB3	2:B:712:HOH:O	2.13	0.48
1:A:49:ASP:HB3	1:A:52:ASN:HB3	1.94	0.48
1:B:165:GLU:HG2	1:C:629:ARG:HH12	1.78	0.48
1:B:553:GLY:HA2	1:C:614:THR:HG21	1.95	0.48
1:B:618:TYR:O	1:C:227:LYS:NZ	2.45	0.48
1:C:126:ASP:CG	1:C:128:ASN:H	2.21	0.48
1:G:81:ARG:NH1	2:G:711:HOH:O	2.29	0.48
1:A:101:LEU:CD1	1:C:108:GLU:HG3	2.44	0.48
1:A:259:ASN:OD1	1:A:260:PHE:N	2.47	0.48
1:A:264:LYS:HE3	1:A:288:SER:N	2.29	0.48
1:B:493:TYR:O	1:B:497:MET:HG2	2.14	0.47
1:A:358:PHE:CZ	1:A:369:VAL:HG11	2.49	0.47
1:G:21:ASN:HB2	1:G:22:PRO:HD2	1.95	0.47
1:G:542:GLN:NE2	2:G:705:HOH:O	2.26	0.47
1:B:546:SER:HA	1:B:582:PRO:HD2	1.96	0.47
1:G:102:ASP:HB3	2:G:784:HOH:O	2.14	0.47
1:B:212:ILE:HG22	1:B:217:VAL:HG22	1.96	0.47
1:C:20:PHE:CD1	1:C:24:GLY:HA2	2.48	0.47
1:G:47:ASN:HB2	1:G:58:LEU:HD11	1.96	0.47
1:G:170:ILE:HG13	1:A:614:THR:HG23	1.96	0.47
1:A:352:GLU:HB3	1:A:372:ARG:NH1	2.30	0.47
1:A:363:ASN:OD1	1:A:363:ASN:N	2.47	0.47
1:B:488:TYR:HB3	1:B:524:TYR:OH	2.14	0.47
1:C:170:ILE:HG22	1:C:171:PRO:HD3	1.97	0.47
1:G:442:GLY:HA2	1:G:519:GLY:O	2.15	0.47
1:C:315:GLY:HA3	1:C:358:PHE:CD2	2.50	0.47
1:C:333:ASP:OD1	1:C:333:ASP:N	2.46	0.47
1:G:141:LEU:HD22	1:G:158:ILE:HG13	1.96	0.47
1:A:54:GLU:OE1	2:A:701:HOH:O	2.21	0.46
1:G:232:ALA:HB3	1:G:255:ILE:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:262:GLU:HB2	1:G:264:LYS:HZ3	1.81	0.46
1:G:353:ASN:ND2	1:G:450:ASP:OD2	2.46	0.46
1:B:170:ILE:HG22	1:B:171:PRO:HD3	1.98	0.46
1:C:442:GLY:HA2	1:C:522:GLY:H	1.81	0.46
1:C:259:ASN:OD1	1:C:260:PHE:N	2.48	0.46
1:C:519:GLY:HA3	1:C:543:ARG:CZ	2.46	0.46
1:C:597:HIS:CD2	1:C:606:LEU:HA	2.50	0.46
1:B:47:ASN:HB2	1:B:58:LEU:HD11	1.98	0.46
1:G:549:ILE:HG22	1:G:577:LEU:HD23	1.97	0.46
1:A:131:ILE:HG13	1:A:212:ILE:HG21	1.98	0.46
1:A:216:LYS:NZ	2:A:710:HOH:O	2.25	0.46
1:A:527:ASN:HB3	1:A:612:MET:HE2	1.97	0.46
1:B:301:TRP:CD1	1:B:445:LYS:HZ2	2.34	0.46
1:A:549:ILE:HG13	1:A:577:LEU:HD23	1.98	0.46
1:B:337:LEU:HB3	1:B:350:SER:HB3	1.98	0.46
1:G:234:LEU:HG	1:G:247:ILE:HD11	1.98	0.45
1:G:553:GLY:HA2	1:A:614:THR:HG21	1.97	0.45
1:C:2:GLU:O	1:C:401:TYR:HA	2.16	0.45
1:G:301:TRP:O	1:G:303:ALA:N	2.48	0.45
1:B:443:GLY:O	1:B:445:LYS:N	2.49	0.45
1:B:442:GLY:HA3	1:B:522:GLY:H	1.82	0.45
1:C:55:ILE:HD12	1:C:55:ILE:HA	1.87	0.45
1:G:170:ILE:CG2	1:G:171:PRO:HD3	2.47	0.45
1:B:443:GLY:O	1:B:444:PRO:C	2.59	0.45
1:G:597:HIS:CD2	1:G:606:LEU:HA	2.51	0.45
1:A:301:TRP:CZ2	1:A:445:LYS:HD3	2.51	0.45
1:C:301:TRP:CD1	1:C:445:LYS:HZ1	2.34	0.45
1:A:272:MET:SD	1:A:277:ILE:HA	2.57	0.45
1:C:210:PHE:HA	1:C:219:PHE:HA	1.99	0.45
1:C:301:TRP:CD2	1:C:445:LYS:HE2	2.51	0.45
1:C:350:SER:HB2	1:C:382:LEU:HD21	1.99	0.45
1:B:213:LYS:HB2	1:B:260:PHE:CD2	2.52	0.45
1:C:19:ASP:HA	1:C:316:LYS:HZ1	1.80	0.45
1:G:68:LEU:HD22	1:G:124:ILE:HG22	1.98	0.45
1:C:1:MET:HE3	1:C:402:LYS:HG3	1.97	0.45
1:B:333:ASP:HB2	1:B:449:GLY:HA2	1.99	0.45
1:B:570:PRO:O	2:B:701:HOH:O	2.21	0.45
1:C:447:VAL:HG23	1:C:475:ASP:HB3	1.99	0.45
1:B:141:LEU:O	1:B:143:LEU:N	2.50	0.45
1:A:525:MET:O	1:A:529:ILE:N	2.42	0.44
1:G:115:LEU:CD2	1:G:132:LEU:HD21	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ILE:HG21	1:A:227:LYS:HG3	1.99	0.44
1:A:519:GLY:HA3	1:A:543:ARG:CZ	2.47	0.44
1:C:125:ILE:HG12	1:C:212:ILE:CD1	2.47	0.44
1:C:525:MET:HE1	1:C:528:TRP:HD1	1.82	0.44
1:C:93:GLU:OE1	1:C:151:ARG:NH1	2.50	0.44
1:C:204:TYR:HB3	1:C:224:TYR:O	2.18	0.44
1:A:21:ASN:HD21	1:A:26:ASN:HD22	1.66	0.44
1:B:121:GLU:HB3	1:B:133:THR:HG22	1.99	0.44
1:B:165:GLU:HG2	1:C:629:ARG:NH1	2.33	0.44
1:C:57:LYS:HG3	1:C:60:HIS:NE2	2.32	0.44
1:A:492:ASP:OD2	1:A:521:TYR:OH	2.34	0.44
1:B:122:ILE:HD12	1:B:132:LEU:CB	2.33	0.44
1:G:605:TRP:HZ3	1:A:607:ALA:HB2	1.82	0.44
1:B:147:LYS:HD3	1:B:147:LYS:HA	1.82	0.44
1:B:578:TRP:CD1	1:B:584:LYS:HD2	2.52	0.44
1:A:299:ASP:OD1	1:A:479:ASN:ND2	2.51	0.43
1:B:68:LEU:HD13	1:B:124:ILE:HB	2.00	0.43
1:B:215:ASN:HB3	1:B:239:VAL:HG22	2.00	0.43
1:B:583:LEU:HD21	2:C:726:HOH:O	2.17	0.43
1:C:253:TYR:CD2	1:C:269:LEU:HD23	2.52	0.43
1:C:448:TYR:CD2	1:C:468:PHE:HB2	2.53	0.43
1:C:492:ASP:N	1:C:492:ASP:OD1	2.51	0.43
1:C:170:ILE:HG22	1:C:227:LYS:HA	1.99	0.43
1:C:186:ARG:NH1	1:C:203:GLU:HA	2.34	0.43
1:A:170:ILE:CG2	1:A:171:PRO:HD3	2.48	0.43
1:A:257:TYR:HA	2:A:730:HOH:O	2.18	0.43
1:C:76:LEU:HA	1:C:99:TYR:O	2.18	0.43
1:C:359:PHE:HA	1:C:368:TYR:HA	2.00	0.43
1:G:2:GLU:HB3	2:G:720:HOH:O	2.18	0.43
1:G:551:LYS:NZ	1:G:555:THR:HG21	2.33	0.43
1:A:21:ASN:ND2	1:A:26:ASN:HD22	2.16	0.43
1:B:302:LEU:HB3	1:B:318:PHE:CZ	2.53	0.43
1:C:319:LYS:HG2	1:C:321:ILE:HG13	2.00	0.43
1:C:462:MET:HE1	1:C:652:THR:HG21	1.99	0.43
1:G:416:ASP:OD2	1:G:472:HIS:NE2	2.52	0.43
1:A:441:HIS:N	1:A:448:TYR:CE2	2.87	0.43
1:A:578:TRP:CD1	1:A:584:LYS:HD2	2.54	0.43
1:G:137:ASP:HB3	1:G:140:SER:HB2	2.01	0.43
1:C:132:LEU:HD23	1:C:132:LEU:HA	1.70	0.43
1:C:561:PHE:CE2	1:C:565:GLN:HG3	2.54	0.43
1:C:587:ASP:OD2	2:C:701:HOH:O	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:331:ILE:HD13	1:G:331:ILE:HA	1.83	0.43
1:G:519:GLY:HA2	1:G:542:GLN:O	2.19	0.43
1:C:445:LYS:HD2	1:C:482:ALA:HB1	2.00	0.43
1:C:146:LEU:HA	2:C:738:HOH:O	2.18	0.42
1:G:65:LYS:HB3	1:G:65:LYS:HE2	1.80	0.42
1:B:422:VAL:HG21	1:B:507:TYR:CE2	2.55	0.42
1:C:272:MET:HE3	1:C:272:MET:HB2	1.91	0.42
1:C:309:ASP:O	1:C:644:ARG:NH2	2.52	0.42
1:A:22:PRO:CD	1:A:72:ASN:OD1	2.66	0.42
1:B:230:LEU:HB3	1:B:272:MET:HE1	2.02	0.42
1:C:16:SER:HA	1:C:358:PHE:HZ	1.84	0.42
1:C:186:ARG:HE	1:C:199:PRO:HB3	1.84	0.42
1:G:301:TRP:NE1	1:G:445:LYS:HZ3	2.17	0.42
1:A:32:SER:HB3	1:A:312:LEU:HD23	2.01	0.42
1:A:112:TYR:HD2	1:A:113:MET:HG3	1.85	0.42
1:A:597:HIS:CD2	1:A:606:LEU:HA	2.55	0.42
1:B:551:LYS:NZ	1:B:555:THR:HG21	2.34	0.42
1:C:27:LEU:HD23	1:C:27:LEU:HA	1.81	0.42
1:C:272:MET:SD	1:C:277:ILE:HA	2.58	0.42
1:B:167:LEU:HD22	1:B:172:PHE:HB2	2.00	0.42
1:C:519:GLY:O	1:C:522:GLY:N	2.52	0.42
1:B:120:THR:OG1	1:B:133:THR:HG23	2.20	0.42
1:C:213:LYS:HB2	1:C:260:PHE:HD2	1.85	0.42
1:G:614:THR:HG21	1:A:553:GLY:HA2	2.02	0.42
1:A:404:SER:OG	2:A:702:HOH:O	2.21	0.42
1:B:333:ASP:OD1	1:B:333:ASP:N	2.50	0.42
1:B:445:LYS:HG2	1:B:475:ASP:HB2	2.02	0.42
1:C:280:ASN:ND2	1:C:301:TRP:CD1	2.87	0.42
1:G:510:ASP:OD2	1:G:513:ARG:NH1	2.48	0.42
1:A:149:GLY:O	1:A:153:LYS:HD3	2.20	0.42
1:B:137:ASP:HB3	1:B:140:SER:HB2	2.02	0.42
1:G:249:SER:O	2:G:702:HOH:O	2.22	0.41
1:C:261:ILE:HG13	1:C:262:GLU:HG3	2.02	0.41
1:A:48:LEU:HA	1:A:54:GLU:O	2.20	0.41
1:B:547:ASN:OD1	1:B:549:ILE:HG12	2.21	0.41
1:C:29:PHE:CE1	1:C:55:ILE:HD11	2.54	0.41
1:C:68:LEU:HD13	1:C:122:ILE:CG2	2.47	0.41
1:G:280:ASN:OD1	1:G:301:TRP:HD1	2.04	0.41
1:A:436:ALA:HB2	1:A:509:ILE:HD13	2.01	0.41
1:G:230:LEU:HD21	1:G:560:TYR:HB2	2.01	0.41
1:A:368:TYR:CE1	1:A:380:TYR:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:456:MET:HG2	1:B:466:VAL:HG11	2.03	0.41
1:C:377:GLN:O	1:C:394:ASN:ND2	2.54	0.41
1:A:26:ASN:HB3	1:A:47:ASN:OD1	2.21	0.41
1:B:331:ILE:HD13	1:B:331:ILE:HA	1.90	0.41
1:G:236:THR:HG22	1:G:245:GLU:HB3	2.02	0.41
1:A:477:TYR:HB2	1:A:481:PHE:CB	2.51	0.41
1:A:492:ASP:N	1:A:492:ASP:OD1	2.54	0.41
1:B:168:ASP:OD1	1:B:181:ASN:ND2	2.42	0.41
1:B:378:GLU:OE1	1:B:391:SER:OG	2.28	0.41
1:B:405:LYS:HA	1:B:406:PRO:HD3	1.95	0.41
1:B:549:ILE:HD11	1:C:549:ILE:HD11	2.03	0.41
1:C:111:GLU:OE2	1:C:114:LYS:HE3	2.21	0.41
1:G:201:SER:HB3	1:G:219:PHE:HE2	1.86	0.41
1:B:353:ASN:HB2	2:B:811:HOH:O	2.21	0.41
1:C:328:LEU:HD23	1:C:337:LEU:HD13	2.03	0.41
1:B:30:SER:OG	1:B:65:LYS:HG3	2.20	0.40
1:B:49:ASP:O	1:B:53:LYS:N	2.49	0.40
1:B:551:LYS:HZ3	1:B:555:THR:HG21	1.85	0.40
1:A:240:LYS:HA	1:A:240:LYS:HD3	1.84	0.40
1:B:132:LEU:HD12	1:B:134:ALA:HB2	2.03	0.40
1:C:255:ILE:HG22	1:C:269:LEU:HG	2.03	0.40
1:C:422:VAL:HG22	1:C:467:ILE:HG22	2.02	0.40
1:C:426:ILE:HD13	1:C:426:ILE:HA	1.87	0.40
1:C:284:TYR:HE1	1:C:294:LEU:HD12	1.87	0.40
1:C:301:TRP:NE1	1:C:445:LYS:HZ1	2.20	0.40
1:G:275:TYR:CD1	1:G:479:ASN:HB3	2.57	0.40
1:B:261:ILE:HG21	1:B:266:ILE:HB	2.02	0.40
1:B:504:LEU:HD23	1:B:504:LEU:HA	1.90	0.40
1:A:490:THR:OG1	1:A:491:ILE:N	2.54	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	658/660 (100%)	620 (94%)	36 (6%)	2 (0%)	36	58
1	B	658/660 (100%)	620 (94%)	35 (5%)	3 (0%)	24	46
1	C	658/660 (100%)	597 (91%)	58 (9%)	3 (0%)	24	46
1	G	658/660 (100%)	621 (94%)	34 (5%)	3 (0%)	24	46
All	All	2632/2640 (100%)	2458 (93%)	163 (6%)	11 (0%)	30	51

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	142	ASN
1	C	142	ASN
1	G	332	ALA
1	C	171	PRO
1	G	302	LEU
1	B	171	PRO
1	G	171	PRO
1	B	444	PRO
1	C	293	ASN
1	A	171	PRO
1	A	443	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	591/591 (100%)	590 (100%)	1 (0%)	87	95
1	B	591/591 (100%)	591 (100%)	0	100	100
1	C	591/591 (100%)	591 (100%)	0	100	100
1	G	591/591 (100%)	591 (100%)	0	100	100
All	All	2364/2364 (100%)	2363 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	3	ASN
1	G	17	ASN
1	G	26	ASN
1	G	105	ASN
1	G	129	ASN
1	G	139	ASN
1	G	291	ASN
1	G	364	ASN
1	A	17	ASN
1	A	26	ASN
1	A	60	HIS
1	A	157	GLN
1	A	291	ASN
1	A	336	HIS
1	A	364	ASN
1	B	60	HIS
1	B	293	ASN
1	B	298	ASN
1	B	363	ASN
1	B	398	ASN
1	B	567	GLN
1	C	128	ASN
1	C	144	ASN
1	C	211	ASN
1	C	280	ASN
1	C	562	ASN
1	C	574	HIS

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 [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 ⓘ

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	660/660 (100%)	0.27	15 (2%) 61 55	22, 36, 58, 73	0
1	B	660/660 (100%)	0.24	9 (1%) 73 69	20, 38, 53, 73	0
1	C	660/660 (100%)	0.73	66 (10%) 12 9	24, 45, 66, 80	0
1	G	660/660 (100%)	0.01	6 (0%) 81 78	20, 31, 45, 63	0
All	All	2640/2640 (100%)	0.32	96 (3%) 46 40	20, 37, 60, 80	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	443	GLY	7.2
1	G	442	GLY	6.6
1	A	354	GLY	6.0
1	B	443	GLY	4.4
1	C	354	GLY	4.4
1	C	442	GLY	4.1
1	A	301	TRP	4.0
1	G	301	TRP	3.7
1	B	442	GLY	3.4
1	C	321	ILE	3.4
1	A	442	GLY	3.4
1	A	132	LEU	3.4
1	B	354	GLY	3.4
1	C	71	ASN	3.3
1	C	292	ILE	3.3
1	C	443	GLY	3.2
1	C	212	ILE	3.2
1	C	258	ALA	3.2
1	C	342	THR	3.1
1	A	101	LEU	3.1
1	A	170	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	339	SER	3.0
1	C	170	ILE	3.0
1	C	232	ALA	2.9
1	A	288	SER	2.9
1	C	92	GLY	2.9
1	C	73	ASN	2.8
1	C	70	LEU	2.8
1	C	247	ILE	2.8
1	C	76	LEU	2.7
1	A	1	MET	2.7
1	G	331	ILE	2.6
1	G	171	PRO	2.6
1	C	44	PHE	2.6
1	C	254	ASP	2.6
1	A	171	PRO	2.6
1	C	289	ASN	2.6
1	C	261	ILE	2.5
1	C	320	VAL	2.5
1	C	248	ILE	2.5
1	B	148	GLY	2.5
1	C	241	SER	2.5
1	C	132	LEU	2.5
1	C	1	MET	2.5
1	G	170	ILE	2.4
1	C	75	ILE	2.4
1	C	125	ILE	2.4
1	C	444	PRO	2.4
1	C	97	ILE	2.4
1	C	252	LEU	2.4
1	C	360	ASP	2.4
1	B	301	TRP	2.3
1	C	105	ASN	2.3
1	C	244	LEU	2.3
1	C	361	ILE	2.3
1	C	207	VAL	2.3
1	A	70	LEU	2.3
1	C	18	LEU	2.3
1	C	234	LEU	2.3
1	A	255	ILE	2.3
1	B	331	ILE	2.3
1	C	86	GLU	2.3
1	C	291	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	201	SER	2.3
1	C	295	LEU	2.3
1	C	107	GLY	2.2
1	A	76	LEU	2.2
1	C	103	ILE	2.2
1	C	194	ASN	2.2
1	C	22	PRO	2.2
1	A	102	ASP	2.2
1	B	346	VAL	2.2
1	A	443	GLY	2.2
1	C	549	ILE	2.2
1	C	331	ILE	2.2
1	C	362	ALA	2.1
1	C	267	CYS	2.1
1	C	253	TYR	2.1
1	C	49	ASP	2.1
1	C	287	ASP	2.1
1	C	101	LEU	2.1
1	C	428	TYR	2.1
1	C	122	ILE	2.1
1	C	286	ILE	2.1
1	A	353	ASN	2.1
1	C	476	GLY	2.1
1	C	301	TRP	2.1
1	C	336	HIS	2.1
1	C	284	TYR	2.1
1	C	219	PHE	2.1
1	C	282	LYS	2.0
1	C	233	GLY	2.0
1	C	80	ASP	2.0
1	B	171	PRO	2.0
1	C	236	THR	2.0
1	B	428	TYR	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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.