



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:13 PM UTC

PDB ID : 5HEW / pdb_00005hew
Title : Pentameric ligand-gated ion channel ELIC mutant T28D
Authors : Engeler, S.; Dutzler, R.
Deposited on : 2016-01-06
Resolution : 4.50 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

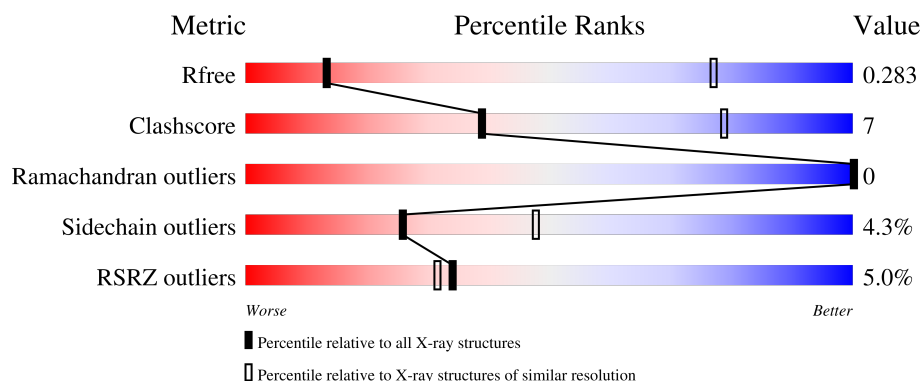
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 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	1127 (5.10-3.90)
Clashscore	190562	1002 (5.06-3.94)
Ramachandran outliers	187476	1060 (5.10-3.90)
Sidechain outliers	187428	1043 (5.10-3.90)
RSRZ outliers	180081	1122 (5.10-3.90)

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	322	6% 78% 17% 5%
1	B	322	7% 75% 18% • 5%
1	C	322	5% 73% 21% • 5%
1	D	322	5% 78% 16% • 5%
1	E	322	5% 76% 19% • 5%

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Mol	Chain	Length	Quality of chain
1	F	322	2% 75% 20% 5%
1	G	322	5% 73% 21% • 5%
1	H	322	4% 72% 22% • 5%
1	I	322	6% 74% 20% • 5%
1	J	322	4% 75% 19% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25060 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 Gamma-aminobutyric-acid receptor subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	B	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	C	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	D	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	E	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	F	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	G	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	H	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	I	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			
1	J	307	Total	C	N	O	S	0	0	0
			2506	1633	416	451	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ASP	THR	engineered mutation	UNP E0SJQ4
B	28	ASP	THR	engineered mutation	UNP E0SJQ4
C	28	ASP	THR	engineered mutation	UNP E0SJQ4
D	28	ASP	THR	engineered mutation	UNP E0SJQ4
E	28	ASP	THR	engineered mutation	UNP E0SJQ4
F	28	ASP	THR	engineered mutation	UNP E0SJQ4
G	28	ASP	THR	engineered mutation	UNP E0SJQ4
H	28	ASP	THR	engineered mutation	UNP E0SJQ4
I	28	ASP	THR	engineered mutation	UNP E0SJQ4

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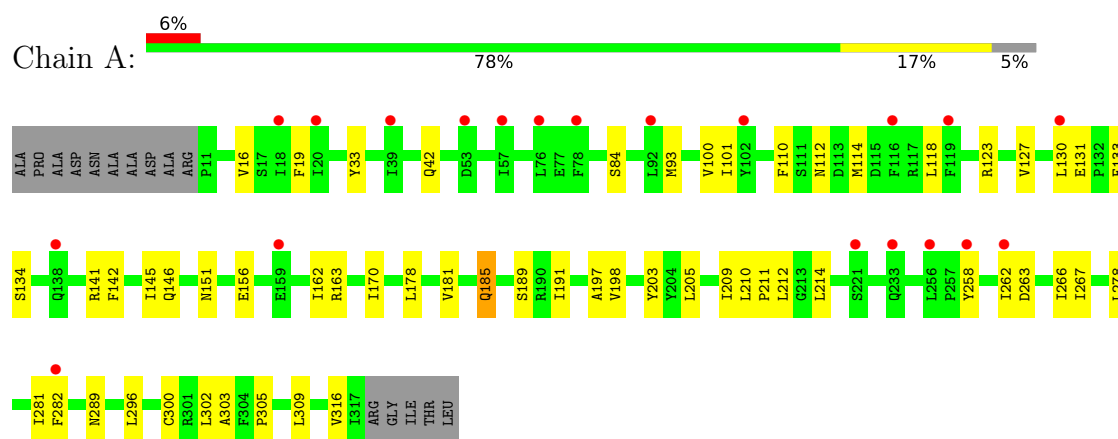
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Chain	Residue	Modelled	Actual	Comment	Reference
J	28	ASP	THR	engineered mutation	UNP E0SJQ4

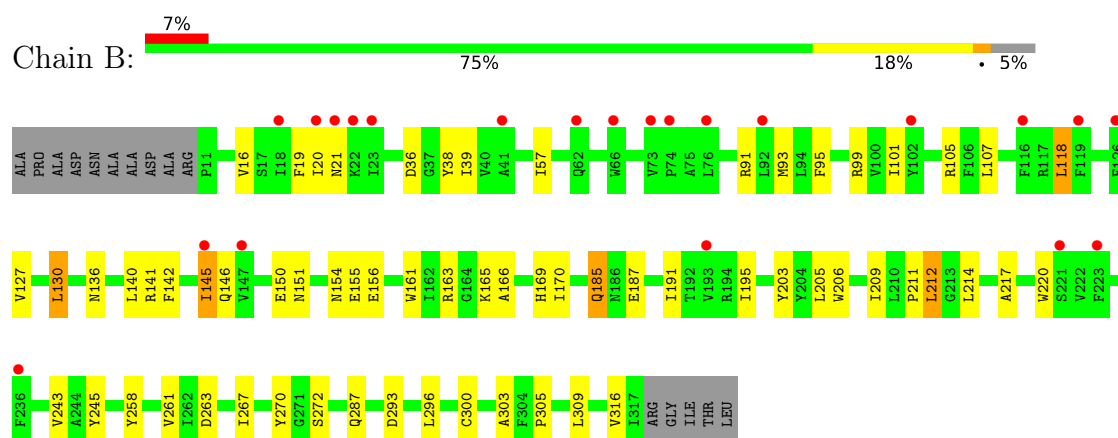
3 Residue-property plots [i](#)

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.

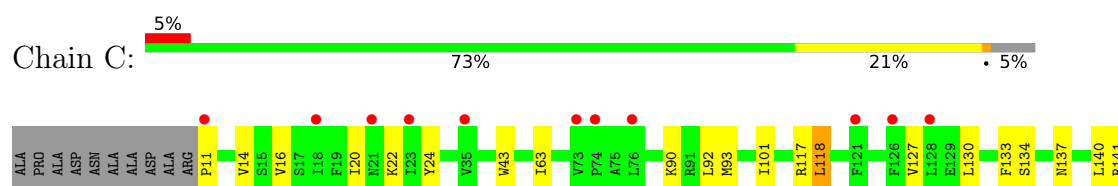
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

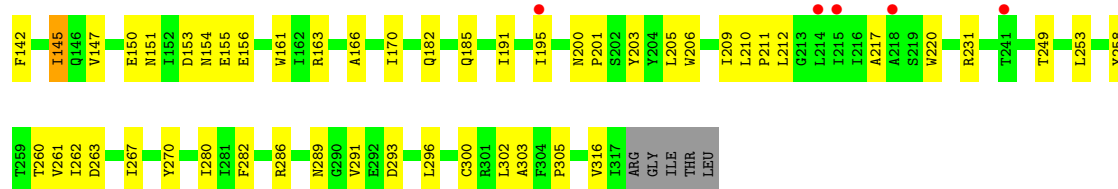


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



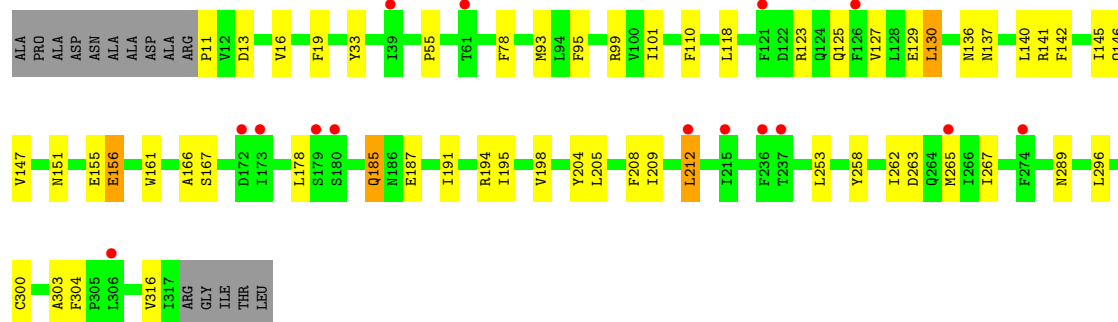
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1





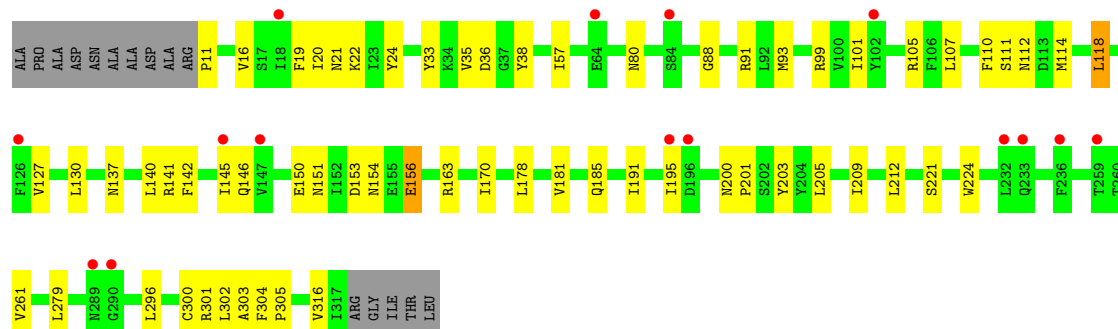
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain D: 5% 78% 16% 5%



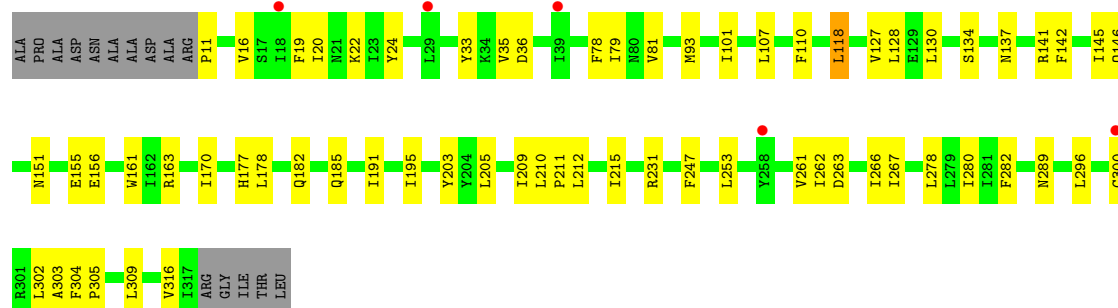
- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain E: 5% 76% 19% 5%

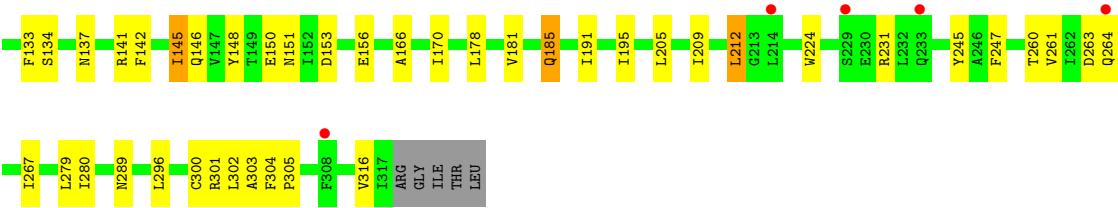


- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1

Chain F: 2% 75% 20% 5%



- Molecule 1: Gamma-aminobutyric-acid receptor subunit beta-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.45Å 266.96Å 110.20Å 90.00° 110.50° 90.00°	Depositor
Resolution (Å)	29.93 – 4.50 29.93 – 4.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.93-4.50) 99.6 (29.93-4.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 3.12Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.237 , 0.271 (Not available) , 0.283	Depositor DCC
R_{free} test set	4335 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	216.4	Xtriage
Anisotropy	0.542	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 155.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.043 for l,-k,h	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	25060	wwPDB-VP
Average B, all atoms (Å ²)	288.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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	0.15	0/2574	0.35	0/3508
1	B	0.16	0/2574	0.37	0/3508
1	C	0.15	0/2574	0.36	0/3508
1	D	0.15	0/2574	0.36	0/3508
1	E	0.15	0/2574	0.35	0/3508
1	F	0.15	0/2574	0.34	0/3508
1	G	0.15	0/2574	0.36	0/3508
1	H	0.15	0/2574	0.34	0/3508
1	I	0.15	0/2574	0.36	0/3508
1	J	0.16	0/2574	0.37	0/3508
All	All	0.15	0/25740	0.36	0/35080

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	2506	0	2475	30	0
1	B	2506	0	2475	39	0
1	C	2506	0	2475	39	0
1	D	2506	0	2475	31	0
1	E	2506	0	2475	37	0
1	F	2506	0	2475	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	2506	0	2475	40	0
1	H	2506	0	2475	43	0
1	I	2506	0	2475	44	0
1	J	2506	0	2475	38	0
All	All	25060	0	24750	339	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 (339) 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:J:170:ILE:HG12	1:J:191:ILE:HG12	1.72	0.71
1:I:93:MET:HB3	1:I:101:ILE:HB	1.75	0.69
1:G:170:ILE:HG12	1:G:191:ILE:HG12	1.76	0.67
1:B:170:ILE:HG12	1:B:191:ILE:HG12	1.76	0.67
1:B:300:CYS:HA	1:B:303:ALA:HB3	1.77	0.66
1:B:165:LYS:HG3	1:I:163:ARG:HB3	1.78	0.65
1:A:170:ILE:HG12	1:A:191:ILE:HG12	1.79	0.65
1:E:36:ASP:HB2	1:E:107:LEU:HD13	1.79	0.65
1:G:300:CYS:HA	1:G:303:ALA:HB3	1.80	0.63
1:I:300:CYS:HA	1:I:303:ALA:HB3	1.79	0.63
1:F:300:CYS:HA	1:F:303:ALA:HB3	1.79	0.62
1:F:93:MET:HB3	1:F:101:ILE:HB	1.81	0.61
1:A:281:ILE:HD11	1:E:221:SER:HB2	1.82	0.61
1:F:170:ILE:HG12	1:F:191:ILE:HG12	1.82	0.61
1:A:300:CYS:HA	1:A:303:ALA:HB3	1.84	0.59
1:D:300:CYS:HA	1:D:303:ALA:HB3	1.83	0.59
1:J:300:CYS:HA	1:J:303:ALA:HB3	1.85	0.58
1:C:300:CYS:HA	1:C:303:ALA:HB3	1.85	0.58
1:H:93:MET:HB3	1:H:101:ILE:HB	1.84	0.58
1:J:39:ILE:HD11	1:J:130:LEU:HD11	1.85	0.58
1:B:93:MET:HB3	1:B:101:ILE:HB	1.85	0.58
1:C:11:PRO:HA	1:C:137:ASN:O	2.04	0.58
1:E:205:LEU:HD23	1:E:209:ILE:HD12	1.84	0.58
1:G:57:ILE:HD13	1:H:134:SER:HB3	1.86	0.57
1:D:205:LEU:HD23	1:D:209:ILE:HD12	1.86	0.57
1:G:205:LEU:HD23	1:G:209:ILE:HD12	1.86	0.57
1:I:140:LEU:HD13	1:I:191:ILE:HG13	1.87	0.57
1:D:93:MET:HB3	1:D:101:ILE:HB	1.86	0.56
1:I:91:ARG:HB3	1:J:133:PHE:HE2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:36:ASP:HB2	1:F:107:LEU:HD13	1.87	0.56
1:G:33:TYR:CE1	1:G:110:PHE:HB2	2.40	0.56
1:G:93:MET:HB3	1:G:101:ILE:HB	1.87	0.56
1:H:205:LEU:HD23	1:H:209:ILE:HD12	1.87	0.56
1:F:205:LEU:HD23	1:F:209:ILE:HD12	1.88	0.56
1:H:63:ILE:HD12	1:H:90:LYS:HG3	1.88	0.55
1:H:300:CYS:HA	1:H:303:ALA:HB3	1.86	0.55
1:B:205:LEU:HD23	1:B:209:ILE:HD12	1.87	0.55
1:C:118:LEU:HA	1:C:261:VAL:HG23	1.88	0.55
1:B:140:LEU:HD13	1:B:191:ILE:HG13	1.89	0.55
1:B:169:HIS:HA	1:I:168:THR:O	2.07	0.55
1:E:300:CYS:HA	1:E:303:ALA:HB3	1.87	0.54
1:B:166:ALA:HB2	1:B:195:ILE:HG12	1.89	0.54
1:A:205:LEU:HD23	1:A:209:ILE:HD12	1.88	0.54
1:J:36:ASP:HB2	1:J:107:LEU:HD13	1.89	0.54
1:I:150:GLU:HG3	1:I:154:ASN:H	1.73	0.54
1:B:150:GLU:HG3	1:B:154:ASN:H	1.73	0.54
1:E:150:GLU:HG3	1:E:154:ASN:H	1.72	0.54
1:D:33:TYR:CE1	1:D:110:PHE:HB2	2.43	0.53
1:C:14:VAL:HG22	1:C:43:TRP:HB3	1.89	0.53
1:I:205:LEU:HD23	1:I:209:ILE:HD12	1.90	0.53
1:F:305:PRO:O	1:F:309:LEU:HG	2.10	0.52
1:B:19:PHE:CE2	1:B:146:GLN:HG3	2.44	0.52
1:I:63:ILE:HD12	1:I:90:LYS:HG3	1.91	0.52
1:E:150:GLU:HG3	1:E:153:ASP:HB3	1.92	0.52
1:J:19:PHE:CE2	1:J:146:GLN:HG3	2.45	0.52
1:C:93:MET:HB3	1:C:101:ILE:HB	1.91	0.51
1:C:170:ILE:HG12	1:C:191:ILE:HG12	1.92	0.51
1:E:33:TYR:CE1	1:E:110:PHE:HB2	2.46	0.51
1:F:11:PRO:HA	1:F:137:ASN:O	2.11	0.51
1:H:118:LEU:HA	1:H:261:VAL:HG23	1.92	0.51
1:A:134:SER:HB3	1:E:57:ILE:HD13	1.93	0.51
1:I:44:THR:HA	1:I:99:ARG:HA	1.93	0.51
1:G:36:ASP:HB2	1:G:107:LEU:HD13	1.93	0.50
1:A:93:MET:HB3	1:A:101:ILE:HB	1.94	0.50
1:I:136:ASN:HB2	1:I:187:GLU:O	2.12	0.50
1:J:141:ARG:HG3	1:J:142:PHE:CD2	2.47	0.50
1:B:36:ASP:HB2	1:B:107:LEU:HD13	1.93	0.49
1:J:33:TYR:CE1	1:J:110:PHE:HB2	2.47	0.49
1:D:140:LEU:HD13	1:D:191:ILE:HG13	1.94	0.49
1:G:141:ARG:HG3	1:G:142:PHE:CD2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:33:TYR:CE1	1:H:110:PHE:HB2	2.47	0.49
1:H:206:TRP:O	1:H:211:PRO:HD3	2.13	0.49
1:G:287:GLN:HG3	1:G:293:ASP:HB2	1.94	0.49
1:E:141:ARG:HG3	1:E:142:PHE:CD2	2.48	0.49
1:H:170:ILE:HG12	1:H:191:ILE:HG12	1.93	0.49
1:D:136:ASN:HB2	1:D:187:GLU:O	2.12	0.49
1:D:147:VAL:HG21	1:D:195:ILE:HD13	1.95	0.48
1:E:19:PHE:CE2	1:E:146:GLN:HG3	2.48	0.48
1:H:221:SER:HA	1:H:224:TRP:HD1	1.78	0.48
1:J:205:LEU:HD23	1:J:209:ILE:HD12	1.94	0.48
1:J:20:ILE:HD12	1:J:195:ILE:HD11	1.95	0.48
1:D:166:ALA:HB2	1:D:195:ILE:HG12	1.95	0.48
1:E:38:TYR:CZ	1:E:105:ARG:HD3	2.49	0.48
1:F:215:ILE:HG12	1:G:239:MET:HE3	1.94	0.48
1:F:253:LEU:HD21	1:F:262:ILE:HD12	1.94	0.48
1:G:212:LEU:HD12	1:G:265:MET:HB3	1.95	0.48
1:F:19:PHE:CE2	1:F:146:GLN:HG3	2.48	0.48
1:B:145:ILE:HG13	1:B:166:ALA:HB3	1.96	0.48
1:G:212:LEU:CD1	1:G:265:MET:HB3	2.44	0.48
1:I:19:PHE:CE2	1:I:146:GLN:HG3	2.48	0.48
1:B:21:ASN:HD21	1:B:38:TYR:HE1	1.60	0.48
1:C:150:GLU:HG3	1:C:154:ASN:H	1.79	0.48
1:E:224:TRP:CE2	1:E:301:ARG:HG2	2.49	0.48
1:D:263:ASP:O	1:D:267:ILE:HG12	2.14	0.47
1:H:287:GLN:HB2	1:H:291:VAL:HB	1.96	0.47
1:G:221:SER:HA	1:G:224:TRP:HD1	1.79	0.47
1:H:253:LEU:HD21	1:H:262:ILE:HD12	1.96	0.47
1:I:263:ASP:O	1:I:267:ILE:HG12	2.14	0.47
1:B:305:PRO:O	1:B:309:LEU:HG	2.15	0.47
1:B:185:GLN:H	1:B:185:GLN:HG3	1.50	0.47
1:G:91:ARG:HB3	1:H:133:PHE:HE2	1.78	0.47
1:H:141:ARG:HG3	1:H:142:PHE:CD2	2.49	0.47
1:H:150:GLU:HG3	1:H:154:ASN:H	1.79	0.47
1:J:150:GLU:HG3	1:J:153:ASP:HB3	1.95	0.47
1:H:203:TYR:HB2	1:I:258:TYR:HA	1.97	0.47
1:A:19:PHE:CE2	1:A:146:GLN:HG3	2.50	0.47
1:A:203:TYR:HB2	1:B:258:TYR:HA	1.97	0.47
1:B:170:ILE:HB	1:I:169:HIS:ND1	2.29	0.47
1:F:141:ARG:HG3	1:F:142:PHE:CD2	2.49	0.47
1:H:22:LYS:HE3	1:H:24:TYR:CD1	2.50	0.47
1:H:204:TYR:O	1:H:208:PHE:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:57:ILE:HD13	1:J:134:SER:HB3	1.97	0.47
1:D:141:ARG:HG3	1:D:142:PHE:CD2	2.50	0.47
1:C:205:LEU:HD23	1:C:209:ILE:HD12	1.97	0.47
1:F:33:TYR:CE1	1:F:110:PHE:HB2	2.50	0.47
1:I:99:ARG:CZ	1:J:181:VAL:HG21	2.45	0.47
1:G:178:LEU:HD12	1:G:178:LEU:HA	1.76	0.46
1:C:203:TYR:HB2	1:D:258:TYR:HA	1.97	0.46
1:D:19:PHE:CE2	1:D:146:GLN:HG3	2.51	0.46
1:E:20:ILE:HD12	1:E:195:ILE:HD11	1.96	0.46
1:E:22:LYS:HE3	1:E:24:TYR:CD1	2.51	0.46
1:H:302:LEU:C	1:H:305:PRO:HD2	2.40	0.46
1:A:163:ARG:HD3	1:A:163:ARG:HA	1.70	0.46
1:B:203:TYR:HB2	1:C:258:TYR:HA	1.96	0.46
1:H:178:LEU:HD12	1:H:178:LEU:HA	1.78	0.46
1:H:300:CYS:O	1:H:304:PHE:HB2	2.15	0.46
1:I:141:ARG:HG3	1:I:142:PHE:CD2	2.50	0.46
1:I:305:PRO:O	1:I:309:LEU:HG	2.16	0.46
1:J:11:PRO:HA	1:J:137:ASN:O	2.16	0.46
1:J:22:LYS:HE3	1:J:24:TYR:CD1	2.51	0.46
1:C:166:ALA:HB2	1:C:195:ILE:HG12	1.97	0.46
1:C:302:LEU:C	1:C:305:PRO:HD2	2.40	0.46
1:I:155:GLU:O	1:I:161:TRP:NE1	2.49	0.46
1:A:141:ARG:HG3	1:A:142:PHE:CD2	2.51	0.46
1:A:281:ILE:CD1	1:E:221:SER:HB2	2.46	0.46
1:A:263:ASP:O	1:A:267:ILE:HG12	2.16	0.46
1:G:216:ILE:HD13	1:G:308:PHE:CZ	2.51	0.46
1:B:20:ILE:HD12	1:B:195:ILE:HD11	1.97	0.46
1:B:141:ARG:HG3	1:B:142:PHE:CD2	2.51	0.46
1:I:178:LEU:HD12	1:I:178:LEU:HA	1.79	0.46
1:B:39:ILE:HD11	1:B:130:LEU:HD11	1.97	0.46
1:E:178:LEU:HD12	1:E:178:LEU:HA	1.80	0.46
1:H:140:LEU:HD13	1:H:191:ILE:HG13	1.98	0.46
1:I:91:ARG:HB3	1:J:133:PHE:CE2	2.48	0.46
1:I:145:ILE:HG13	1:I:166:ALA:HB3	1.97	0.46
1:J:300:CYS:O	1:J:304:PHE:HB2	2.16	0.46
1:C:217:ALA:HA	1:C:220:TRP:CE3	2.51	0.46
1:C:140:LEU:HD13	1:C:191:ILE:HG13	1.98	0.45
1:D:155:GLU:O	1:D:161:TRP:NE1	2.49	0.45
1:G:302:LEU:C	1:G:305:PRO:HD2	2.41	0.45
1:J:302:LEU:C	1:J:305:PRO:HD2	2.41	0.45
1:A:262:ILE:O	1:A:266:ILE:HG12	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:ARG:HG3	1:C:142:PHE:CD2	2.51	0.45
1:F:278:LEU:O	1:F:282:PHE:N	2.37	0.45
1:F:302:LEU:C	1:F:305:PRO:HD2	2.41	0.45
1:E:170:ILE:HG12	1:E:191:ILE:HG12	1.98	0.45
1:F:155:GLU:C	1:F:161:TRP:HE1	2.24	0.45
1:I:204:TYR:O	1:I:208:PHE:HB2	2.16	0.45
1:E:279:LEU:HD22	1:E:304:PHE:CE1	2.51	0.45
1:G:243:VAL:HA	1:G:270:TYR:OH	2.17	0.45
1:A:214:LEU:HD23	1:B:270:TYR:HB3	1.99	0.45
1:D:185:GLN:H	1:D:185:GLN:HG3	1.53	0.45
1:F:177:HIS:NE2	1:J:148:TYR:HE2	2.15	0.45
1:G:175:TYR:O	1:G:186:ASN:HB2	2.17	0.45
1:H:163:ARG:HD3	1:H:163:ARG:HA	1.79	0.45
1:H:205:LEU:HA	1:H:209:ILE:HB	1.98	0.45
1:A:258:TYR:HA	1:E:203:TYR:HB2	1.97	0.45
1:H:36:ASP:HB2	1:H:107:LEU:HD13	1.99	0.45
1:J:50:THR:OG1	1:J:53:ASP:HA	2.17	0.45
1:F:163:ARG:HD3	1:F:163:ARG:HA	1.71	0.45
1:F:178:LEU:HD12	1:F:178:LEU:HA	1.74	0.45
1:A:181:VAL:HG21	1:E:99:ARG:NH2	2.32	0.45
1:H:166:ALA:HB2	1:H:195:ILE:HG12	1.98	0.45
1:I:33:TYR:CE1	1:I:110:PHE:HB2	2.52	0.45
1:J:178:LEU:HD12	1:J:178:LEU:HA	1.79	0.45
1:A:33:TYR:CE1	1:A:110:PHE:HB2	2.52	0.45
1:B:220:TRP:NE1	1:B:272:SER:OG	2.43	0.45
1:C:145:ILE:HG13	1:C:166:ALA:HB3	1.98	0.45
1:D:123:ARG:HE	1:D:198:VAL:HG22	1.82	0.45
1:G:150:GLU:HG3	1:G:153:ASP:HB3	1.99	0.45
1:A:133:PHE:HE2	1:E:91:ARG:HB3	1.82	0.44
1:B:136:ASN:HB2	1:B:187:GLU:O	2.16	0.44
1:G:212:LEU:HD23	1:G:245:TYR:CD2	2.52	0.44
1:G:215:ILE:HG12	1:H:239:MET:HE3	1.99	0.44
1:H:20:ILE:HD12	1:H:195:ILE:HD11	1.98	0.44
1:E:156:GLU:H	1:E:156:GLU:CD	2.25	0.44
1:F:35:VAL:HG21	1:F:128:LEU:HD11	2.00	0.44
1:J:145:ILE:HG13	1:J:166:ALA:HB3	1.98	0.44
1:C:231:ARG:HB3	1:C:280:ILE:HD13	2.00	0.44
1:A:162:ILE:HD13	1:A:197:ALA:HB2	2.00	0.44
1:C:253:LEU:HD21	1:C:262:ILE:HD12	1.99	0.44
1:F:262:ILE:O	1:F:266:ILE:HG12	2.17	0.44
1:G:145:ILE:HG13	1:G:166:ALA:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:302:LEU:C	1:I:305:PRO:HD2	2.43	0.44
1:A:185:GLN:H	1:A:185:GLN:HG3	1.44	0.44
1:A:302:LEU:C	1:A:305:PRO:HD2	2.42	0.44
1:B:38:TYR:CZ	1:B:105:ARG:HD3	2.53	0.44
1:B:214:LEU:HD23	1:C:270:TYR:HB3	1.99	0.44
1:C:155:GLU:O	1:C:161:TRP:NE1	2.48	0.44
1:J:117:ARG:O	1:J:260:THR:HA	2.17	0.44
1:C:205:LEU:HA	1:C:209:ILE:HB	1.99	0.44
1:F:22:LYS:HE3	1:F:24:TYR:CD1	2.53	0.44
1:G:185:GLN:H	1:G:185:GLN:HG3	1.51	0.44
1:E:302:LEU:C	1:E:305:PRO:HD2	2.43	0.44
1:H:217:ALA:HA	1:H:220:TRP:CE3	2.53	0.44
1:J:21:ASN:HD21	1:J:38:TYR:HE1	1.65	0.44
1:C:263:ASP:O	1:C:267:ILE:HG12	2.18	0.44
1:F:300:CYS:O	1:F:304:PHE:HB2	2.17	0.44
1:G:118:LEU:HA	1:G:261:VAL:HG23	1.99	0.44
1:I:20:ILE:HD12	1:I:195:ILE:HD11	2.00	0.44
1:A:112:ASN:O	1:A:114:MET:HG3	2.18	0.43
1:C:20:ILE:HD12	1:C:195:ILE:HD11	1.99	0.43
1:C:150:GLU:HG3	1:C:153:ASP:HB3	1.99	0.43
1:B:217:ALA:HA	1:B:220:TRP:CE3	2.54	0.43
1:C:117:ARG:O	1:C:260:THR:HA	2.19	0.43
1:B:57:ILE:HD13	1:C:134:SER:HB3	2.00	0.43
1:B:95:PHE:HB2	1:B:99:ARG:HB2	2.00	0.43
1:B:118:LEU:HA	1:B:261:VAL:HG23	2.00	0.43
1:D:156:GLU:CD	1:D:156:GLU:H	2.26	0.43
1:H:212:LEU:HD23	1:H:245:TYR:CD2	2.54	0.43
1:H:279:LEU:HD22	1:H:304:PHE:CE1	2.53	0.43
1:H:291:VAL:HG12	1:H:293:ASP:H	1.82	0.43
1:I:42:GLN:HA	1:I:100:VAL:O	2.19	0.43
1:E:221:SER:HA	1:E:224:TRP:HD1	1.83	0.43
1:F:203:TYR:HB2	1:G:258:TYR:HA	2.00	0.43
1:G:140:LEU:HD13	1:G:191:ILE:HG13	1.99	0.43
1:J:38:TYR:CZ	1:J:105:ARG:HD3	2.53	0.43
1:B:263:ASP:O	1:B:267:ILE:HG12	2.19	0.43
1:E:140:LEU:HD13	1:E:191:ILE:HG13	2.00	0.43
1:G:21:ASN:HD21	1:G:38:TYR:HE1	1.67	0.43
1:I:156:GLU:CD	1:I:156:GLU:H	2.27	0.43
1:G:99:ARG:NH2	1:H:181:VAL:HG21	2.34	0.43
1:G:217:ALA:HA	1:G:220:TRP:CE3	2.54	0.43
1:F:78:PHE:HB2	1:F:81:VAL:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:263:ASP:O	1:F:267:ILE:HG12	2.18	0.43
1:A:278:LEU:O	1:A:282:PHE:N	2.43	0.43
1:C:63:ILE:HD12	1:C:90:LYS:HG3	2.01	0.43
1:F:247:PHE:HE2	1:J:247:PHE:CD2	2.37	0.43
1:H:214:LEU:HD23	1:I:270:TYR:HB3	1.99	0.43
1:I:185:GLN:H	1:I:185:GLN:HG3	1.53	0.43
1:I:210:LEU:HB3	1:I:211:PRO:HD3	2.01	0.43
1:D:253:LEU:HD21	1:D:262:ILE:HD12	2.01	0.42
1:E:11:PRO:HA	1:E:137:ASN:O	2.19	0.42
1:I:169:HIS:NE2	1:I:171:SER:HB3	2.33	0.42
1:F:20:ILE:HD12	1:F:195:ILE:HD11	2.00	0.42
1:C:206:TRP:O	1:C:211:PRO:HD3	2.19	0.42
1:G:37:GLY:O	1:G:105:ARG:HD2	2.19	0.42
1:D:166:ALA:CB	1:D:195:ILE:HG12	2.49	0.42
1:E:93:MET:HB3	1:E:101:ILE:HB	2.01	0.42
1:G:44:THR:HA	1:G:99:ARG:HA	2.00	0.42
1:I:166:ALA:HB2	1:I:195:ILE:HG12	2.01	0.42
1:B:212:LEU:HD23	1:B:245:TYR:CD2	2.55	0.42
1:D:212:LEU:CD1	1:D:265:MET:HB3	2.50	0.42
1:F:210:LEU:HB3	1:F:211:PRO:HD3	2.02	0.42
1:H:215:ILE:HG12	1:I:239:MET:HE3	2.01	0.42
1:I:92:LEU:HD23	1:I:92:LEU:HA	1.88	0.42
1:B:206:TRP:O	1:B:211:PRO:HD3	2.20	0.42
1:D:78:PHE:CE1	1:D:130:LEU:HG	2.55	0.42
1:F:118:LEU:HA	1:F:261:VAL:HG23	2.02	0.42
1:G:163:ARG:HA	1:G:163:ARG:HD3	1.78	0.42
1:G:224:TRP:CE2	1:G:301:ARG:HG2	2.55	0.42
1:J:212:LEU:HD23	1:J:245:TYR:CD2	2.55	0.42
1:J:231:ARG:HB3	1:J:280:ILE:HD13	2.00	0.42
1:B:91:ARG:HB3	1:C:133:PHE:HE2	1.85	0.42
1:D:55:PRO:HB3	1:D:95:PHE:CD1	2.55	0.42
1:D:99:ARG:NH2	1:E:181:VAL:HG21	2.34	0.42
1:B:155:GLU:C	1:B:161:TRP:HE1	2.28	0.41
1:B:163:ARG:HD3	1:B:163:ARG:HA	1.73	0.41
1:D:129:GLU:HA	1:D:191:ILE:O	2.20	0.41
1:G:40:VAL:HG22	1:G:103:ASN:OD1	2.20	0.41
1:G:147:VAL:HG21	1:G:195:ILE:HD13	2.02	0.41
1:G:305:PRO:O	1:G:309:LEU:HG	2.19	0.41
1:J:185:GLN:H	1:J:185:GLN:HG3	1.48	0.41
1:J:224:TRP:CE2	1:J:301:ARG:HG2	2.55	0.41
1:D:204:TYR:O	1:D:208:PHE:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:134:SER:HB3	1:J:57:ILE:HD13	2.02	0.41
1:F:231:ARG:HB3	1:F:280:ILE:HD13	2.02	0.41
1:H:99:ARG:NH2	1:I:181:VAL:HG21	2.35	0.41
1:A:123:ARG:HE	1:A:198:VAL:HG22	1.85	0.41
1:A:305:PRO:O	1:A:309:LEU:HG	2.20	0.41
1:J:118:LEU:HA	1:J:261:VAL:HG23	2.01	0.41
1:A:42:GLN:HA	1:A:100:VAL:O	2.21	0.41
1:D:155:GLU:C	1:D:161:TRP:HE1	2.28	0.41
1:C:92:LEU:HD23	1:C:92:LEU:HA	1.87	0.41
1:C:249:THR:O	1:C:253:LEU:HB2	2.21	0.41
1:H:224:TRP:CE2	1:H:301:ARG:HG2	2.56	0.41
1:F:182:GLN:H	1:F:182:GLN:CD	2.28	0.41
1:I:155:GLU:C	1:I:161:TRP:HE1	2.28	0.41
1:J:13:ASP:HB3	1:J:141:ARG:HD2	2.01	0.41
1:B:287:GLN:HG3	1:B:293:ASP:HB2	2.02	0.41
1:C:163:ARG:HD3	1:C:163:ARG:HA	1.72	0.41
1:C:282:PHE:CZ	1:C:286:ARG:HG3	2.56	0.41
1:E:21:ASN:HD21	1:E:38:TYR:HE1	1.68	0.41
1:E:35:VAL:HB	1:E:110:PHE:CE1	2.56	0.41
1:H:97:ASP:OD2	1:H:99:ARG:NH1	2.54	0.41
1:H:79:ILE:HD13	1:H:79:ILE:HA	1.95	0.41
1:A:178:LEU:HD12	1:A:178:LEU:HA	1.80	0.41
1:B:130:LEU:HD23	1:B:130:LEU:HA	1.90	0.41
1:C:182:GLN:H	1:C:182:GLN:CD	2.29	0.41
1:C:210:LEU:HB3	1:C:211:PRO:HD3	2.03	0.41
1:D:13:ASP:HB3	1:D:141:ARG:HD2	2.02	0.41
1:D:178:LEU:HA	1:D:178:LEU:HD12	1.80	0.41
1:E:200:ASN:HA	1:E:201:PRO:HD3	1.95	0.41
1:F:79:ILE:HD13	1:F:79:ILE:HA	1.94	0.41
1:I:200:ASN:HA	1:I:201:PRO:HD3	1.91	0.41
1:J:35:VAL:HB	1:J:110:PHE:CE1	2.56	0.41
1:J:260:THR:O	1:J:264:GLN:HG3	2.19	0.41
1:J:263:ASP:O	1:J:267:ILE:HG12	2.21	0.41
1:J:279:LEU:HD22	1:J:304:PHE:CE1	2.56	0.41
1:B:243:VAL:HA	1:B:270:TYR:OH	2.20	0.41
1:D:125:GLN:OE1	1:D:194:ARG:HD3	2.21	0.41
1:D:167:SER:OG	1:D:194:ARG:HB2	2.20	0.41
1:E:80:ASN:HB2	1:E:111:SER:O	2.20	0.41
1:G:19:PHE:CE2	1:G:146:GLN:HG3	2.56	0.41
1:G:260:THR:O	1:G:264:GLN:HG3	2.21	0.41
1:C:22:LYS:HE3	1:C:24:TYR:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:267:ILE:H	1:H:267:ILE:HG12	1.77	0.40
1:H:278:LEU:O	1:H:282:PHE:N	2.43	0.40
1:I:118:LEU:HA	1:I:261:VAL:HG23	2.03	0.40
1:I:130:LEU:HD23	1:I:130:LEU:HA	1.89	0.40
1:I:297:ILE:O	1:I:301:ARG:HB2	2.22	0.40
1:A:84:SER:OG	1:E:88:GLY:HA2	2.21	0.40
1:A:210:LEU:HB3	1:A:211:PRO:HD3	2.03	0.40
1:C:147:VAL:HG21	1:C:195:ILE:HD13	2.02	0.40
1:C:200:ASN:HA	1:C:201:PRO:HD3	1.91	0.40
1:D:300:CYS:O	1:D:304:PHE:HB2	2.21	0.40
1:E:112:ASN:O	1:E:114:MET:HG3	2.21	0.40
1:E:300:CYS:O	1:E:304:PHE:HB2	2.21	0.40
1:H:260:THR:O	1:H:264:GLN:HG3	2.20	0.40
1:I:78:PHE:CE1	1:I:130:LEU:HG	2.57	0.40
1:J:130:LEU:HD23	1:J:130:LEU:HA	1.87	0.40
1:A:131:GLU:HG3	1:A:189:SER:O	2.21	0.40
1:D:11:PRO:HA	1:D:137:ASN:O	2.20	0.40
1:E:118:LEU:HA	1:E:261:VAL:HG23	2.02	0.40
1:H:185:GLN:H	1:H:185:GLN:HG3	1.47	0.40
1:C:291:VAL:HG12	1:C:293:ASP:H	1.85	0.40
1:I:163:ARG:HA	1:I:163:ARG:HD3	1.83	0.40
1:E:163:ARG:HA	1:E:163:ARG:HD3	1.82	0.40
1:G:22:LYS:HE3	1:G:24:TYR:CD1	2.56	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	122/322 (38%)	109 (89%)	13 (11%)	0	100	100
1	D	71/322 (22%)	70 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	305/322 (95%)	286 (94%)	19 (6%)	0	100	100
1	F	305/322 (95%)	285 (93%)	20 (7%)	0	100	100
1	G	305/322 (95%)	285 (93%)	20 (7%)	0	100	100
1	H	305/322 (95%)	285 (93%)	20 (7%)	0	100	100
1	I	305/322 (95%)	285 (93%)	20 (7%)	0	100	100
1	J	305/322 (95%)	284 (93%)	21 (7%)	0	100	100
All	All	2023/2576 (78%)	1889 (93%)	134 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	275/284 (97%)	263 (96%)	12 (4%)	25	47
1	B	275/284 (97%)	264 (96%)	11 (4%)	28	49
1	C	275/284 (97%)	263 (96%)	12 (4%)	25	47
1	D	275/284 (97%)	263 (96%)	12 (4%)	25	47
1	E	275/284 (97%)	264 (96%)	11 (4%)	28	49
1	F	264/284 (93%)	252 (96%)	12 (4%)	24	46
1	G	275/284 (97%)	263 (96%)	12 (4%)	25	47
1	H	275/284 (97%)	262 (95%)	13 (5%)	23	45
1	I	275/284 (97%)	263 (96%)	12 (4%)	25	47
1	J	275/284 (97%)	264 (96%)	11 (4%)	28	49
All	All	2739/2840 (96%)	2621 (96%)	118 (4%)	26	48

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	VAL

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Mol	Chain	Res	Type
1	A	118	LEU
1	A	127	VAL
1	A	130	LEU
1	A	145	ILE
1	A	151	ASN
1	A	156	GLU
1	A	185	GLN
1	A	212	LEU
1	A	289	ASN
1	A	296	LEU
1	A	316	VAL
1	B	16	VAL
1	B	118	LEU
1	B	127	VAL
1	B	130	LEU
1	B	145	ILE
1	B	151	ASN
1	B	156	GLU
1	B	185	GLN
1	B	212	LEU
1	B	296	LEU
1	B	316	VAL
1	C	16	VAL
1	C	118	LEU
1	C	127	VAL
1	C	130	LEU
1	C	145	ILE
1	C	151	ASN
1	C	156	GLU
1	C	185	GLN
1	C	212	LEU
1	C	289	ASN
1	C	296	LEU
1	C	316	VAL
1	D	16	VAL
1	D	118	LEU
1	D	127	VAL
1	D	130	LEU
1	D	145	ILE
1	D	151	ASN
1	D	156	GLU
1	D	185	GLN

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Mol	Chain	Res	Type
1	D	212	LEU
1	D	289	ASN
1	D	296	LEU
1	D	316	VAL
1	E	16	VAL
1	E	118	LEU
1	E	127	VAL
1	E	130	LEU
1	E	145	ILE
1	E	151	ASN
1	E	156	GLU
1	E	185	GLN
1	E	212	LEU
1	E	296	LEU
1	E	316	VAL
1	F	16	VAL
1	F	118	LEU
1	F	127	VAL
1	F	130	LEU
1	F	145	ILE
1	F	151	ASN
1	F	156	GLU
1	F	185	GLN
1	F	212	LEU
1	F	289	ASN
1	F	296	LEU
1	F	316	VAL
1	G	16	VAL
1	G	118	LEU
1	G	127	VAL
1	G	130	LEU
1	G	145	ILE
1	G	151	ASN
1	G	156	GLU
1	G	185	GLN
1	G	212	LEU
1	G	289	ASN
1	G	296	LEU
1	G	316	VAL
1	H	16	VAL
1	H	62	GLN
1	H	118	LEU

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Mol	Chain	Res	Type
1	H	127	VAL
1	H	130	LEU
1	H	145	ILE
1	H	151	ASN
1	H	156	GLU
1	H	185	GLN
1	H	212	LEU
1	H	289	ASN
1	H	296	LEU
1	H	316	VAL
1	I	16	VAL
1	I	118	LEU
1	I	127	VAL
1	I	130	LEU
1	I	145	ILE
1	I	151	ASN
1	I	156	GLU
1	I	185	GLN
1	I	212	LEU
1	I	289	ASN
1	I	296	LEU
1	I	316	VAL
1	J	16	VAL
1	J	118	LEU
1	J	127	VAL
1	J	145	ILE
1	J	151	ASN
1	J	156	GLU
1	J	185	GLN
1	J	212	LEU
1	J	289	ASN
1	J	296	LEU
1	J	316	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	GLN
1	A	186	ASN
1	A	251	ASN
1	B	138	GLN
1	B	185	GLN

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Mol	Chain	Res	Type
1	B	200	ASN
1	C	69	ASN
1	C	138	GLN
1	C	185	GLN
1	C	284	HIS
1	D	138	GLN
1	D	185	GLN
1	D	186	ASN
1	D	251	ASN
1	D	264	GLN
1	D	284	HIS
1	E	136	ASN
1	E	251	ASN
1	F	136	ASN
1	F	138	GLN
1	F	186	ASN
1	F	251	ASN
1	F	284	HIS
1	F	285	HIS
1	G	136	ASN
1	G	138	GLN
1	G	186	ASN
1	G	284	HIS
1	H	138	GLN
1	H	200	ASN
1	I	186	ASN
1	I	251	ASN
1	I	287	GLN
1	J	136	ASN
1	J	138	GLN
1	J	185	GLN
1	J	251	ASN
1	J	284	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	307/322 (95%)	0.19	20 (6%)	25 26	224, 287, 369, 400	0
1	B	307/322 (95%)	0.26	22 (7%)	21 24	216, 277, 363, 417	0
1	C	307/322 (95%)	0.21	16 (5%)	33 31	220, 286, 370, 408	0
1	D	307/322 (95%)	0.31	15 (4%)	35 32	219, 281, 368, 438	0
1	E	307/322 (95%)	0.09	15 (4%)	35 32	224, 286, 358, 406	0
1	F	307/322 (95%)	0.00	5 (1%)	70 55	221, 288, 368, 431	0
1	G	307/322 (95%)	0.13	15 (4%)	35 32	216, 275, 373, 416	0
1	H	307/322 (95%)	0.11	13 (4%)	40 35	217, 277, 364, 404	0
1	I	307/322 (95%)	0.34	20 (6%)	25 26	218, 277, 363, 407	0
1	J	307/322 (95%)	0.07	14 (4%)	37 34	218, 282, 373, 411	0
All	All	3070/3220 (95%)	0.17	155 (5%)	34 31	216, 282, 368, 438	0

All (155) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	102	TYR	6.7
1	G	277	ILE	5.9
1	I	230	GLU	5.9
1	C	215	ILE	5.7
1	H	290	GLY	5.6
1	H	66	TRP	5.6
1	I	12	VAL	5.5
1	I	138	GLN	5.5
1	E	289	ASN	5.3
1	C	214	LEU	4.9
1	J	233	GLN	4.8
1	B	119	PHE	4.8
1	D	61	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	E	64	GLU	4.4
1	J	39	ILE	4.4
1	G	113	ASP	4.2
1	D	179	SER	4.1
1	H	258	TYR	4.1
1	D	172	ASP	4.0
1	D	126	PHE	4.0
1	D	173	ILE	4.0
1	B	221	SER	4.0
1	D	39	ILE	3.9
1	B	126	PHE	3.9
1	A	92	LEU	3.9
1	B	116	PHE	3.9
1	J	214	LEU	3.8
1	B	18	ILE	3.7
1	B	41	ALA	3.7
1	A	256	LEU	3.7
1	G	157	ILE	3.6
1	G	235	SER	3.5
1	A	138	GLN	3.5
1	G	126	PHE	3.5
1	C	73	VAL	3.5
1	H	116	PHE	3.5
1	E	126	PHE	3.5
1	B	102	TYR	3.4
1	G	102	TYR	3.3
1	G	232	LEU	3.3
1	E	145	ILE	3.2
1	I	157	ILE	3.2
1	B	74	PRO	3.2
1	I	76	LEU	3.2
1	I	208	PHE	3.2
1	B	20	ILE	3.2
1	H	21	ASN	3.1
1	C	74	PRO	3.1
1	B	23	ILE	3.1
1	H	289	ASN	3.0
1	J	103	ASN	3.0
1	B	145	ILE	3.0
1	I	70	GLY	3.0
1	C	241	THR	3.0
1	H	149	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	196	ASP	3.0
1	D	121	PHE	3.0
1	A	221	SER	3.0
1	J	40	VAL	2.9
1	C	128	LEU	2.9
1	F	18	ILE	2.9
1	A	57	ILE	2.9
1	D	274	PHE	2.9
1	A	18	ILE	2.8
1	G	23	ILE	2.8
1	H	256	LEU	2.8
1	B	62	GLN	2.8
1	C	18	ILE	2.8
1	C	76	LEU	2.8
1	F	39	ILE	2.8
1	I	69	ASN	2.8
1	F	258	TYR	2.7
1	I	248	TYR	2.7
1	I	14	VAL	2.7
1	G	315	LEU	2.7
1	B	73	VAL	2.7
1	G	314	VAL	2.7
1	B	147	VAL	2.7
1	J	229	SER	2.7
1	J	104	ALA	2.7
1	I	193	VAL	2.7
1	A	262	ILE	2.6
1	H	257	PRO	2.6
1	I	253	LEU	2.6
1	A	78	PHE	2.6
1	C	195	ILE	2.6
1	I	22	LYS	2.6
1	A	258	TYR	2.6
1	I	32	THR	2.6
1	A	233	GLN	2.6
1	A	116	PHE	2.6
1	C	126	PHE	2.6
1	J	92	LEU	2.6
1	D	236	PHE	2.5
1	A	130	LEU	2.5
1	E	259	THR	2.5
1	E	233	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	282	PHE	2.5
1	C	121	PHE	2.5
1	B	66	TRP	2.5
1	E	232	LEU	2.4
1	E	18	ILE	2.4
1	D	180	SER	2.4
1	H	76	LEU	2.4
1	A	159	GLU	2.4
1	A	53	ASP	2.4
1	G	273	ILE	2.4
1	I	102	TYR	2.4
1	D	306	LEU	2.4
1	B	223	PHE	2.4
1	G	158	ASP	2.4
1	D	265	MET	2.4
1	E	195	ILE	2.4
1	A	76	LEU	2.4
1	G	251	ASN	2.4
1	D	215	ILE	2.3
1	I	249	THR	2.3
1	J	18	ILE	2.3
1	E	147	VAL	2.3
1	H	291	VAL	2.3
1	B	92	LEU	2.2
1	C	35	VAL	2.2
1	A	20	ILE	2.2
1	E	236	PHE	2.2
1	J	308	PHE	2.2
1	F	29	LEU	2.2
1	E	290	GLY	2.2
1	J	76	LEU	2.2
1	E	84	SER	2.2
1	B	193	VAL	2.2
1	D	237	THR	2.2
1	A	39	ILE	2.2
1	C	23	ILE	2.2
1	H	11	PRO	2.2
1	J	73	VAL	2.2
1	B	236	PHE	2.1
1	A	102	TYR	2.1
1	G	265	MET	2.1
1	C	218	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	41	ALA	2.1
1	H	92	LEU	2.1
1	I	247	PHE	2.1
1	I	243	VAL	2.1
1	C	21	ASN	2.1
1	E	102	TYR	2.1
1	J	264	GLN	2.1
1	D	212	LEU	2.1
1	F	300	CYS	2.1
1	A	119	PHE	2.1
1	C	11	PRO	2.0
1	I	262	ILE	2.0
1	I	128	LEU	2.0
1	B	21	ASN	2.0
1	B	22	LYS	2.0
1	B	76	LEU	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.