



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:27 PM UTC

PDB ID : 6M4X / pdb_00006m4x
Title : Co-crystal structure of Ac-AChBPP in complex with [N9A]LvIA
Authors : Wang, X.Q.; Pan, S.; Luo, S.L.; Zhu, X.P.
Deposited on : 2020-03-09
Resolution : 3.00 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

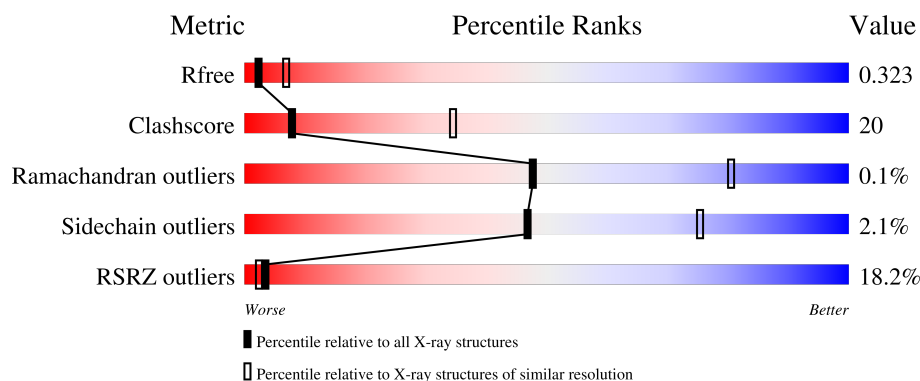
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



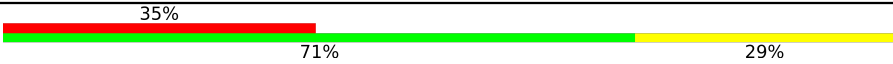
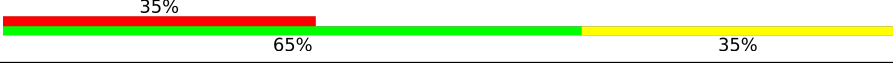
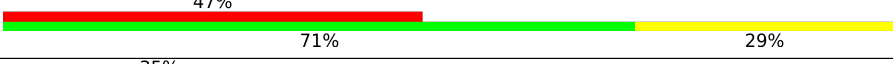
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	207	15% 68% 31% .
1	B	207	12% 61% 36% .
1	D	207	20% 60% 39% .
1	G	207	15% 60% 38% .
1	I	207	20% 57% 39% .

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Mol	Chain	Length	Quality of chain
2	C	17	
2	E	17	
2	F	17	
2	H	17	
2	J	17	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8820 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 Soluble acetylcholine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1653	1045	271	328	9			
1	B	207	Total	C	N	O	S	0	0	0
			1653	1045	271	328	9			
1	D	207	Total	C	N	O	S	0	0	0
			1653	1045	271	328	9			
1	G	207	Total	C	N	O	S	0	0	0
			1653	1045	271	328	9			
1	I	207	Total	C	N	O	S	0	0	0
			1653	1045	271	328	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	VAL	ALA	conflict	UNP Q8WSF8
A	136	VAL	ALA	conflict	UNP Q8WSF8
B	41	VAL	ALA	conflict	UNP Q8WSF8
B	136	VAL	ALA	conflict	UNP Q8WSF8
D	41	VAL	ALA	conflict	UNP Q8WSF8
D	136	VAL	ALA	conflict	UNP Q8WSF8
G	41	VAL	ALA	conflict	UNP Q8WSF8
G	136	VAL	ALA	conflict	UNP Q8WSF8
I	41	VAL	ALA	conflict	UNP Q8WSF8
I	136	VAL	ALA	conflict	UNP Q8WSF8

- Molecule 2 is a protein called Alpha-conotoxin LvIA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	17	Total	C	N	O	S	1	0	1
			111	65	21	21	4			
2	C	17	Total	C	N	O	S	1	0	1
			111	65	21	21	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	17	Total 111	C 65	N 21	O 21	S 4	1	0	1
2	H	17	Total 111	C 65	N 21	O 21	S 4	1	0	1
2	J	17	Total 111	C 65	N 21	O 21	S 4	1	0	1

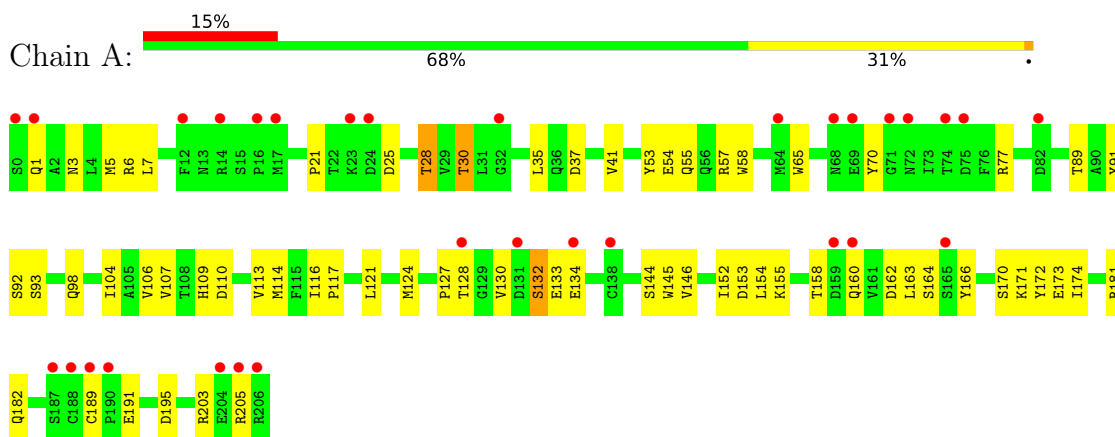
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	409	ALA	ASN	engineered mutation	UNP L8BU87
F	417	NH2	-	amidation	UNP L8BU87
C	409	ALA	ASN	engineered mutation	UNP L8BU87
C	417	NH2	-	amidation	UNP L8BU87
E	409	ALA	ASN	engineered mutation	UNP L8BU87
E	417	NH2	-	amidation	UNP L8BU87
H	409	ALA	ASN	engineered mutation	UNP L8BU87
H	417	NH2	-	amidation	UNP L8BU87
J	409	ALA	ASN	engineered mutation	UNP L8BU87
J	417	NH2	-	amidation	UNP L8BU87

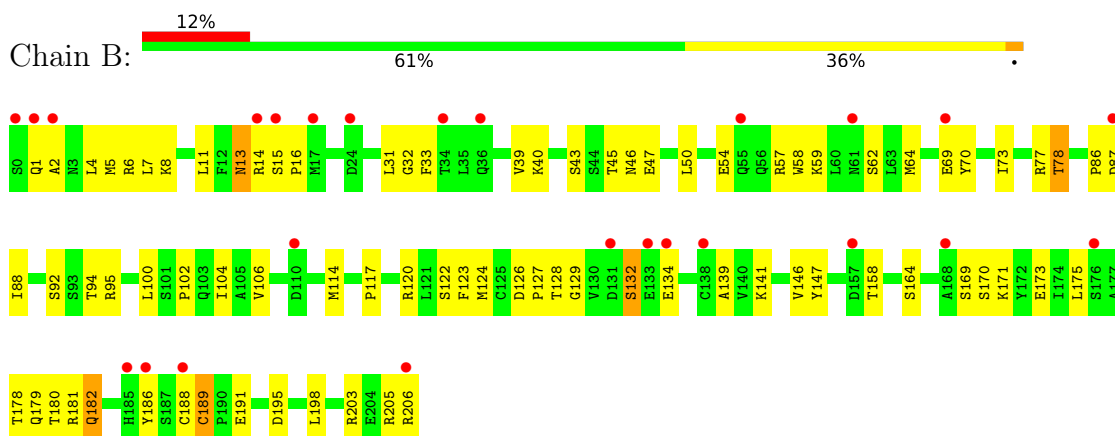
3 Residue-property plots [i](#)

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.

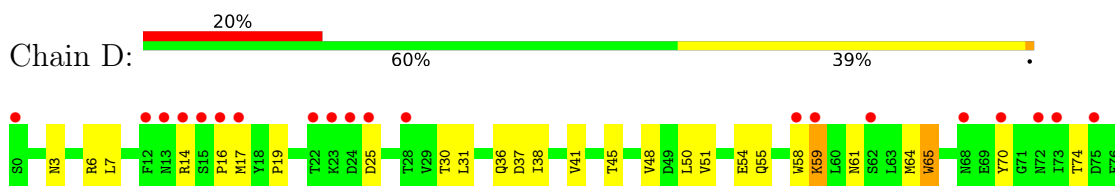
• Molecule 1: Soluble acetylcholine receptor

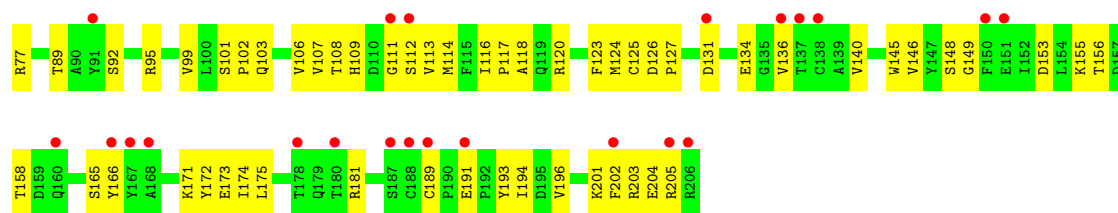


• Molecule 1: Soluble acetylcholine receptor

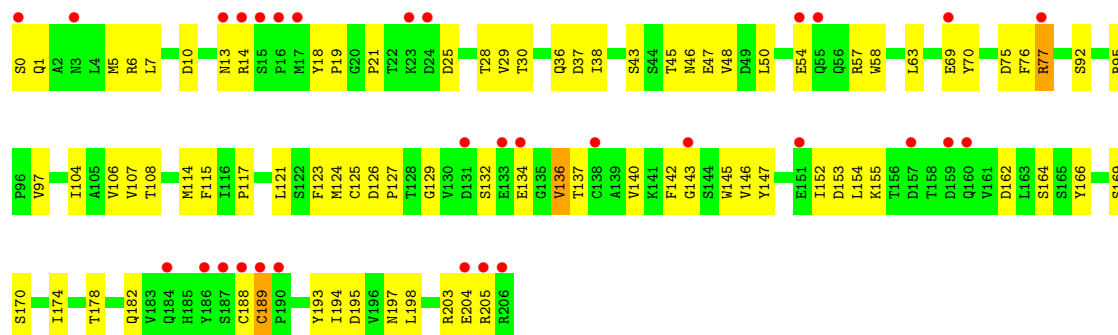


• Molecule 1: Soluble acetylcholine receptor

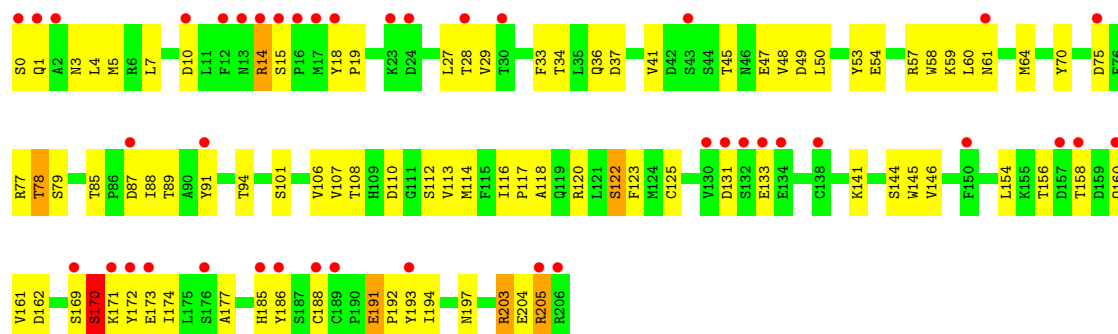




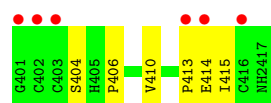
● Molecule 1: Soluble acetylcholine receptor



● Molecule 1: Soluble acetylcholine receptor

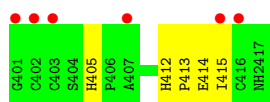


● Molecule 2: Alpha-conotoxin LvIA

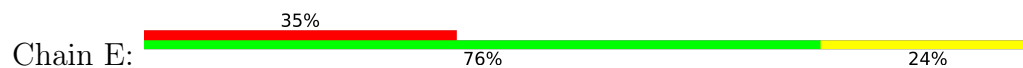


● Molecule 2: Alpha-conotoxin LvIA

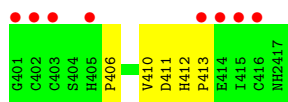
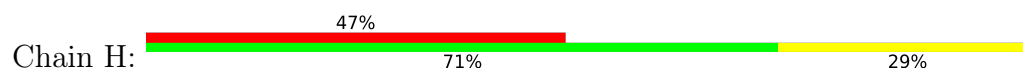




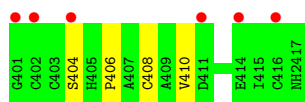
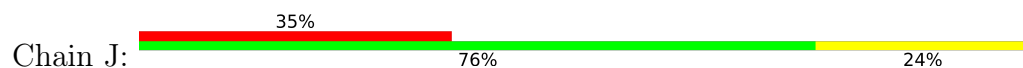
- Molecule 2: Alpha-conotoxin LvIA



- Molecule 2: Alpha-conotoxin LvIA



- Molecule 2: Alpha-conotoxin LvIA



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	207.44Å 207.44Å 114.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.58 – 3.00 48.58 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.7 (48.58-3.00) 95.5 (48.58-3.00)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.263 , 0.316 0.270 , 0.323	Depositor DCC
R_{free} test set	2462 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	55.4	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.40$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	8820	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NH2

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	0.53	0/1693	0.83	0/2309
1	B	0.57	2/1693 (0.1%)	0.85	0/2309
1	D	0.65	3/1693 (0.2%)	0.87	2/2309 (0.1%)
1	G	0.63	4/1693 (0.2%)	0.87	1/2309 (0.0%)
1	I	0.61	2/1693 (0.1%)	0.93	8/2309 (0.3%)
2	C	0.43	0/113	0.72	0/154
2	E	0.49	0/113	0.92	0/154
2	F	0.42	0/113	0.74	0/154
2	H	0.56	0/113	0.83	0/154
2	J	0.42	0/113	0.92	0/154
All	All	0.59	11/9030 (0.1%)	0.87	11/12315 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
1	G	0	1
All	All	0	2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	203	ARG	NE-CZ	-9.07	1.23	1.33
1	I	203	ARG	CZ-NH2	-8.92	1.21	1.33
1	G	77	ARG	NE-CZ	-8.67	1.23	1.33
1	G	77	ARG	CZ-NH2	-7.91	1.23	1.33
1	B	181	ARG	NE-CZ	-7.71	1.24	1.33
1	G	77	ARG	CZ-NH1	-7.58	1.22	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	77	ARG	CD-NE	-7.03	1.36	1.46
1	D	65	TRP	C-N	6.66	1.47	1.33
1	D	134	GLU	CD-OE1	-6.66	1.12	1.25
1	B	181	ARG	CZ-NH1	-6.14	1.24	1.32
1	D	134	GLU	CD-OE2	-6.12	1.13	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	14	ARG	CA-C-N	-7.11	109.49	123.56
1	I	14	ARG	C-N-CA	-7.11	109.49	123.56
1	G	189	CYS	N-CA-C	6.21	120.35	109.48
1	I	205	ARG	CD-NE-CZ	-5.89	116.15	124.40
1	D	59	LYS	N-CA-C	5.71	118.51	108.75
1	I	170	SER	CA-C-N	-5.45	113.54	122.54
1	I	170	SER	C-N-CA	-5.45	113.54	122.54
1	I	188	CYS	CB-CA-C	-5.41	99.66	110.42
1	I	133	GLU	N-CA-C	-5.17	107.63	114.04
1	D	59	LYS	CB-CG-CD	-5.08	99.61	111.30
1	I	205	ARG	NE-CZ-NH2	-5.01	114.69	119.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	14	ARG	Peptide
1	G	188	CYS	Peptide

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	1653	0	1590	55	0
1	B	1653	0	1590	67	0
1	D	1653	0	1590	79	0
1	G	1653	0	1590	68	0
1	I	1653	0	1590	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	111	0	91	6	0
2	E	111	0	91	5	0
2	F	111	0	91	9	0
2	H	111	0	91	11	0
2	J	111	0	91	6	0
All	All	8820	0	8405	341	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 20.

All (341) 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:114:MET:HE2	2:E:410:VAL:HA	1.21	1.14
1:B:114:MET:CE	2:E:410:VAL:HA	1.82	1.09
1:D:58:TRP:O	1:D:59:LYS:NZ	1.87	1.07
1:I:141:LYS:HG2	1:I:197:ASN:HD22	1.26	0.99
1:B:33:PHE:H	1:B:179:GLN:NE2	1.67	0.93
1:D:59:LYS:HZ2	1:D:113:VAL:H	1.14	0.93
1:B:33:PHE:H	1:B:179:GLN:HE22	1.15	0.92
1:B:6:ARG:NH2	1:B:69:GLU:O	2.06	0.89
1:B:102:PRO:HD3	1:D:89:THR:HG21	1.54	0.88
1:D:77:ARG:NH1	1:I:146:VAL:O	2.06	0.88
1:D:114:MET:HE3	2:J:410:VAL:HA	1.56	0.88
1:D:107:VAL:HA	1:D:112:SER:O	1.76	0.85
1:G:97:VAL:HG12	1:G:121:LEU:HD23	1.59	0.83
1:G:21:PRO:HG3	1:G:152:ILE:HD11	1.61	0.81
1:G:19:PRO:HB2	1:I:4:LEU:HD22	1.61	0.81
1:I:158:THR:HG22	1:I:160:GLN:H	1.46	0.80
2:E:414:GLU:HG3	2:E:415:ILE:HD12	1.63	0.80
1:G:146:VAL:O	1:I:77:ARG:NH1	2.15	0.80
1:D:58:TRP:CE2	1:D:113:VAL:HG21	2.18	0.78
1:G:170:SER:O	1:G:205:ARG:NH2	2.16	0.78
1:D:108:THR:HB	1:D:112:SER:HB2	1.65	0.77
1:A:114:MET:HE1	2:C:413:PRO:HB3	1.67	0.77
1:I:10:ASP:O	1:I:14:ARG:HG2	1.85	0.76
1:D:55:GLN:HB2	1:D:116:ILE:HG12	1.70	0.73
1:A:28:THR:HB	1:A:153:ASP:HB3	1.71	0.73
1:B:33:PHE:N	1:B:179:GLN:HE22	1.87	0.73
1:D:59:LYS:NZ	1:D:113:VAL:H	1.87	0.73
1:B:126:ASP:OD1	1:B:128:THR:HG23	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:GLU:HG3	1:B:205:ARG:HG2	1.71	0.72
2:F:404:SER:OG	1:G:164:SER:OG	2.08	0.72
1:D:102:PRO:HD3	1:I:89:THR:HG21	1.71	0.71
1:D:166:TYR:CE1	1:D:174:ILE:HD11	2.25	0.71
1:G:10:ASP:HA	1:G:14:ARG:HD3	1.74	0.70
1:G:182:GLN:NE2	1:G:195:ASP:OD2	2.23	0.70
2:F:414:GLU:HG3	2:F:415:ILE:HG13	1.73	0.70
1:G:25:ASP:OD2	1:I:1:GLN:NE2	2.26	0.69
1:I:14:ARG:NE	1:I:15:SER:HB2	2.08	0.69
1:G:75:ASP:HB3	1:G:108:THR:HG22	1.75	0.68
1:B:4:LEU:HD23	1:D:19:PRO:HB2	1.75	0.68
1:D:59:LYS:CE	1:D:112:SER:HA	2.23	0.68
1:D:54:GLU:O	1:D:117:PRO:HD2	1.93	0.68
1:D:166:TYR:CZ	1:D:174:ILE:HD11	2.30	0.66
1:D:153:ASP:OD1	1:D:181:ARG:NH2	2.28	0.65
1:A:77:ARG:HG3	1:A:106:VAL:HG22	1.78	0.65
1:G:38:ILE:HD13	1:G:50:LEU:HD11	1.78	0.65
1:A:127:PRO:O	1:A:130:VAL:HG23	1.97	0.65
1:B:1:GLN:O	1:B:5:MET:HG2	1.97	0.64
2:H:410:VAL:HB	1:I:106:VAL:HG11	1.79	0.64
1:A:182:GLN:NE2	1:A:195:ASP:OD1	2.31	0.64
1:I:191:GLU:HG3	1:I:193:TYR:HE1	1.62	0.64
1:D:59:LYS:HE3	1:D:112:SER:HA	1.79	0.64
1:I:41:VAL:HG12	1:I:48:VAL:HG22	1.80	0.63
1:D:175:LEU:HD12	1:D:201:LYS:HG2	1.79	0.63
1:B:100:LEU:HD11	1:B:120:ARG:HB2	1.82	0.62
1:I:145:TRP:CH2	2:J:406:PRO:HG2	2.34	0.62
1:D:58:TRP:CZ2	1:D:113:VAL:HG21	2.34	0.62
1:G:0:SER:HB3	1:G:1:GLN:NE2	2.15	0.62
1:I:1:GLN:CD	1:I:1:GLN:H	2.07	0.62
1:D:30:THR:HG22	1:D:155:LYS:HB2	1.81	0.61
1:D:102:PRO:CD	1:I:89:THR:HG21	2.30	0.61
1:G:6:ARG:NH2	1:G:69:GLU:O	2.33	0.61
1:I:50:LEU:HD13	1:I:123:PHE:HE2	1.65	0.60
1:A:109:HIS:HD2	1:A:110:ASP:H	1.46	0.60
1:I:191:GLU:HG3	1:I:193:TYR:CE1	2.36	0.60
1:D:101:SER:HB3	1:D:118:ALA:HB3	1.83	0.60
1:D:77:ARG:HG2	1:D:106:VAL:HG23	1.84	0.60
2:C:414:GLU:HG3	2:C:415:ILE:HG13	1.83	0.59
1:I:141:LYS:HG2	1:I:197:ASN:ND2	2.08	0.59
1:I:156:THR:OG1	1:I:158:THR:O	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:ARG:HD3	1:B:147:TYR:CE1	2.37	0.59
1:G:145:TRP:CZ2	2:H:406:PRO:HG2	2.37	0.58
1:I:14:ARG:HG3	1:I:15:SER:N	2.18	0.58
1:I:18:TYR:HD2	1:I:19:PRO:HD2	1.67	0.58
1:A:57:ARG:C	1:A:57:ARG:HD3	2.28	0.58
1:D:165:SER:OG	2:J:404:SER:HB2	2.03	0.58
1:A:109:HIS:HD2	1:A:110:ASP:N	2.00	0.58
1:I:172:TYR:C	1:I:205:ARG:HH22	2.12	0.58
1:D:77:ARG:HH11	1:I:146:VAL:HB	1.68	0.58
1:I:154:LEU:H	1:I:194:ILE:HD13	1.68	0.58
1:I:205:ARG:HD2	1:I:205:ARG:N	2.19	0.57
1:I:0:SER:O	1:I:3:ASN:HB2	2.05	0.57
1:D:59:LYS:HD2	1:D:111:GLY:O	2.04	0.57
1:B:77:ARG:HG3	1:B:106:VAL:HG22	1.87	0.56
1:B:104:ILE:HB	1:D:146:VAL:HG11	1.87	0.56
1:I:94:THR:HG23	1:I:122:SER:HB3	1.86	0.56
1:A:7:LEU:HD12	1:A:70:TYR:CD2	2.40	0.56
1:G:0:SER:HB3	1:G:1:GLN:HE22	1.70	0.56
1:I:50:LEU:HD13	1:I:123:PHE:CE2	2.40	0.56
1:A:91:TYR:OH	1:A:144:SER:O	2.22	0.56
1:I:27:LEU:HD11	1:I:58:TRP:HB2	1.87	0.56
1:D:166:TYR:CD1	1:D:174:ILE:HD11	2.41	0.56
1:I:49:ASP:OD1	1:I:122:SER:OG	2.23	0.56
1:A:3:ASN:OD1	1:A:6:ARG:NH2	2.37	0.56
1:A:114:MET:CE	2:C:413:PRO:HB3	2.36	0.56
1:I:158:THR:CG2	1:I:160:GLN:H	2.18	0.56
1:I:172:TYR:CA	1:I:205:ARG:HH22	2.19	0.56
1:B:32:GLY:HA2	1:B:179:GLN:HE22	1.72	0.55
1:B:169:SER:HB3	1:D:126:ASP:HB2	1.88	0.55
1:I:78:THR:HG23	1:I:79:SER:O	2.07	0.55
1:G:142:PHE:HE2	1:G:198:LEU:HD22	1.72	0.55
1:A:162:ASP:OD1	1:A:164:SER:OG	2.24	0.55
1:B:1:GLN:OE1	1:B:1:GLN:N	2.25	0.55
1:B:175:LEU:HD21	1:B:203:ARG:HH11	1.71	0.55
1:B:31:LEU:HD21	1:B:88:ILE:HG21	1.89	0.55
1:B:141:LYS:NZ	1:B:182:GLN:OE1	2.37	0.55
1:G:178:THR:O	1:G:198:LEU:HA	2.06	0.55
1:A:109:HIS:CD2	1:A:110:ASP:N	2.75	0.55
1:D:3:ASN:ND2	1:D:6:ARG:HH22	2.05	0.55
1:G:143:GLY:HA2	1:G:154:LEU:HD21	1.88	0.55
1:D:41:VAL:HG12	1:D:172:TYR:OH	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:PHE:N	1:B:179:GLN:NE2	2.48	0.54
1:A:93:SER:HB3	1:A:121:LEU:HD11	1.90	0.54
1:D:171:LYS:HB3	1:D:172:TYR:CE1	2.42	0.54
1:B:132:SER:OG	1:B:134:GLU:N	2.41	0.54
1:I:41:VAL:HG12	1:I:48:VAL:HG13	1.90	0.54
1:D:59:LYS:HD2	1:D:112:SER:HA	1.90	0.53
1:G:77:ARG:HH11	1:G:106:VAL:HG22	1.72	0.53
1:I:158:THR:HG22	1:I:160:GLN:N	2.19	0.53
1:G:189:CYS:SG	2:H:412:HIS:CE1	3.02	0.53
2:H:411:ASP:C	2:H:412:HIS:CD2	2.86	0.53
1:D:36:GLN:HB3	1:D:51:VAL:HG12	1.90	0.53
1:G:121:LEU:HD11	1:G:123:PHE:HB3	1.89	0.53
1:I:131:ASP:HB2	1:I:204:GLU:OE1	2.07	0.53
1:G:57:ARG:HG3	1:G:114:MET:HE2	1.90	0.53
1:D:156:THR:OG1	1:D:158:THR:O	2.25	0.53
1:G:76:PHE:CE1	1:G:107:VAL:HG13	2.43	0.53
1:B:50:LEU:HD13	1:B:123:PHE:CE2	2.44	0.53
1:B:50:LEU:HD13	1:B:123:PHE:HE2	1.73	0.53
1:A:124:MET:HE1	1:G:36:GLN:HG2	1.91	0.52
1:I:59:LYS:HA	1:I:112:SER:HA	1.91	0.52
1:I:87:ASP:OD1	1:I:146:VAL:HG22	2.09	0.52
1:D:48:VAL:HG23	1:D:125:CYS:HB3	1.90	0.52
1:I:193:TYR:HE2	2:J:408:CYS:CA	2.22	0.52
1:A:158:THR:HG22	1:A:160:GLN:H	1.75	0.52
1:I:57:ARG:HD3	1:I:57:ARG:C	2.35	0.52
1:I:192:PRO:C	1:I:193:TYR:HD1	2.18	0.52
1:D:102:PRO:HG2	1:I:87:ASP:OD2	2.10	0.52
2:H:411:ASP:C	2:H:412:HIS:HD2	2.18	0.51
1:A:145:TRP:CZ2	2:F:406:PRO:HG2	2.45	0.51
1:B:129:GLY:O	1:B:132:SER:HB3	2.10	0.51
1:G:1:GLN:H	1:G:1:GLN:CD	2.18	0.51
1:G:129:GLY:O	1:G:132:SER:OG	2.24	0.51
1:B:54:GLU:O	1:B:117:PRO:HD2	2.11	0.51
1:B:189:CYS:HB2	1:B:191:GLU:OE1	2.10	0.51
1:D:131:ASP:OD1	1:D:131:ASP:N	2.44	0.51
1:D:31:LEU:HD12	1:D:196:VAL:HG11	1.93	0.51
1:G:182:GLN:NE2	1:G:197:ASN:HB2	2.26	0.51
1:A:170:SER:OG	1:A:171:LYS:N	2.43	0.51
1:D:109:HIS:C	1:D:111:GLY:H	2.17	0.51
1:I:45:THR:OG1	1:I:47:GLU:HG3	2.10	0.51
1:A:55:GLN:HA	1:A:116:ILE:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:406:PRO:O	2:F:410:VAL:HG22	2.10	0.50
1:D:174:ILE:N	1:D:174:ILE:HD12	2.27	0.50
1:B:45:THR:OG1	1:B:47:GLU:HG2	2.10	0.50
1:D:59:LYS:CD	1:D:112:SER:HA	2.41	0.50
2:F:410:VAL:HB	1:G:106:VAL:HG21	1.93	0.50
1:B:139:ALA:HA	1:B:198:LEU:O	2.12	0.50
1:A:133:GLU:O	1:A:203:ARG:NH2	2.45	0.50
1:G:92:SER:O	1:G:124:MET:HG3	2.11	0.50
1:G:134:GLU:OE2	1:G:134:GLU:N	2.44	0.50
1:I:54:GLU:OE2	1:I:88:ILE:HD11	2.12	0.49
1:D:108:THR:N	1:D:112:SER:O	2.45	0.49
1:I:7:LEU:HB2	1:I:70:TYR:CD1	2.45	0.49
1:A:25:ASP:OD2	1:G:1:GLN:NE2	2.45	0.49
1:A:146:VAL:HG11	1:G:104:ILE:HB	1.95	0.49
1:B:7:LEU:HB2	1:B:70:TYR:CD2	2.47	0.49
1:I:41:VAL:HG22	1:I:172:TYR:OH	2.11	0.49
1:B:13:ASN:OD1	1:B:13:ASN:N	2.40	0.49
1:D:173:GLU:HG3	1:D:205:ARG:HD2	1.93	0.49
1:G:45:THR:OG1	1:G:47:GLU:HG2	2.12	0.48
1:B:5:MET:HE2	1:D:16:PRO:HG2	1.94	0.48
1:I:58:TRP:HD1	1:I:60:LEU:HD13	1.78	0.48
1:B:57:ARG:HD3	1:B:57:ARG:C	2.38	0.48
1:G:28:THR:HG23	1:G:153:ASP:HB3	1.95	0.48
1:G:29:VAL:HG12	1:G:58:TRP:HB3	1.96	0.48
1:G:95:ARG:HH11	1:I:120:ARG:CZ	2.25	0.48
1:G:182:GLN:HB2	1:G:195:ASP:OD1	2.13	0.48
1:B:59:LYS:NZ	1:B:64:MET:HE3	2.29	0.48
1:D:59:LYS:HD2	1:D:111:GLY:C	2.39	0.48
1:G:193:TYR:C	1:G:194:ILE:HD13	2.38	0.48
1:G:46:ASN:ND2	1:I:169:SER:O	2.47	0.48
1:G:169:SER:C	1:G:205:ARG:HH22	2.21	0.48
2:F:413:PRO:HB3	1:G:114:MET:CE	2.44	0.48
1:D:92:SER:O	1:D:124:MET:HG3	2.13	0.48
1:G:203:ARG:HG2	1:G:204:GLU:N	2.28	0.48
1:I:172:TYR:C	1:I:205:ARG:HH12	2.21	0.48
1:D:127:PRO:O	1:D:136:VAL:HG11	2.14	0.48
1:I:91:TYR:OH	1:I:144:SER:O	2.29	0.48
1:I:101:SER:HB3	1:I:118:ALA:HB3	1.96	0.48
1:B:94:THR:HG22	1:B:122:SER:C	2.39	0.47
1:B:189:CYS:HB3	2:C:412:HIS:CE1	2.49	0.47
1:D:189:CYS:HB3	1:D:191:GLU:OE1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:107:VAL:HG22	1:I:113:VAL:HB	1.95	0.47
1:A:145:TRP:CH2	2:F:406:PRO:HG2	2.49	0.47
1:B:7:LEU:CD2	1:B:73:ILE:HD11	2.44	0.47
1:B:15:SER:OG	1:B:16:PRO:HD2	2.15	0.47
1:I:193:TYR:HE2	2:J:408:CYS:HA	1.80	0.47
1:B:8:LYS:NZ	1:B:78:THR:HG23	2.30	0.47
1:B:102:PRO:HB2	1:B:104:ILE:HD12	1.97	0.47
1:G:7:LEU:HB2	1:G:70:TYR:CD1	2.49	0.47
1:A:107:VAL:HG22	1:A:113:VAL:HG12	1.95	0.47
1:D:77:ARG:NH1	1:I:146:VAL:C	2.72	0.47
1:D:166:TYR:CE2	1:D:174:ILE:HD11	2.50	0.47
1:I:18:TYR:CD2	1:I:19:PRO:HD2	2.48	0.47
1:B:46:ASN:ND2	1:B:127:PRO:HD2	2.30	0.47
1:D:148:SER:HB2	1:D:193:TYR:CE1	2.50	0.47
1:D:59:LYS:HA	1:D:59:LYS:HD3	1.52	0.47
1:G:48:VAL:HG12	1:G:125:CYS:HB3	1.96	0.47
1:G:115:PHE:CE2	1:G:117:PRO:HG3	2.50	0.47
1:I:64:MET:HG2	1:I:110:ASP:O	2.15	0.47
1:I:54:GLU:O	1:I:54:GLU:HG3	2.14	0.46
1:I:94:THR:CG2	1:I:122:SER:HB3	2.45	0.46
1:I:64:MET:HG2	1:I:110:ASP:C	2.39	0.46
1:I:94:THR:HG22	1:I:122:SER:O	2.16	0.46
1:G:43:SER:O	1:I:171:LYS:NZ	2.41	0.46
1:A:54:GLU:O	1:A:117:PRO:HD2	2.14	0.46
1:D:61:ASN:O	1:D:64:MET:HG3	2.15	0.46
1:B:170:SER:OG	1:B:171:LYS:N	2.49	0.46
1:G:121:LEU:CD1	1:G:123:PHE:HB3	2.44	0.46
1:I:94:THR:HG22	1:I:122:SER:C	2.41	0.46
1:G:37:ASP:HA	1:G:166:TYR:CE1	2.50	0.46
1:G:54:GLU:O	1:G:117:PRO:HD2	2.15	0.46
1:I:88:ILE:C	1:I:88:ILE:HD12	2.41	0.46
1:A:37:ASP:HA	1:A:166:TYR:CE1	2.51	0.46
1:B:6:ARG:NH2	1:B:70:TYR:HA	2.31	0.46
2:F:404:SER:OG	1:G:162:ASP:OD2	2.34	0.46
1:I:18:TYR:CD1	1:I:60:LEU:HD21	2.51	0.46
1:A:104:ILE:HB	1:B:146:VAL:HG11	1.97	0.46
1:G:174:ILE:HD12	1:G:174:ILE:N	2.31	0.46
1:G:95:ARG:NH1	1:I:120:ARG:CZ	2.79	0.45
1:G:97:VAL:CG1	1:G:121:LEU:HD23	2.40	0.45
1:G:134:GLU:CD	1:G:134:GLU:H	2.24	0.45
1:G:92:SER:OG	1:G:140:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:410:VAL:HG13	1:I:116:ILE:HD13	1.98	0.45
1:I:1:GLN:CD	1:I:1:GLN:N	2.74	0.45
1:B:87:ASP:OD2	1:B:146:VAL:HG22	2.16	0.45
1:B:206:ARG:CZ	1:B:206:ARG:HB3	2.45	0.45
1:A:163:LEU:HD22	1:A:174:ILE:HG21	1.99	0.45
1:D:59:LYS:HE3	1:D:112:SER:OG	2.17	0.45
1:B:141:LYS:HD3	1:B:195:ASP:OD2	2.17	0.45
1:D:108:THR:CB	1:D:112:SER:HB2	2.39	0.45
1:I:75:ASP:HA	1:I:107:VAL:O	2.16	0.45
1:B:120:ARG:NH2	1:D:95:ARG:HH21	2.15	0.45
1:I:191:GLU:H	1:I:191:GLU:HG2	1.35	0.45
1:A:171:LYS:HG2	1:B:46:ASN:OD1	2.17	0.45
1:A:189:CYS:HB3	1:A:191:GLU:OE1	2.17	0.45
1:A:174:ILE:HD13	1:A:174:ILE:HA	1.79	0.44
1:I:33:PHE:HB2	1:I:161:VAL:HG13	1.98	0.44
1:I:54:GLU:O	1:I:117:PRO:HD2	2.17	0.44
1:D:7:LEU:HB2	1:D:70:TYR:CD1	2.53	0.44
1:G:1:GLN:O	1:G:5:MET:HG3	2.17	0.44
1:G:166:TYR:CE1	1:G:174:ILE:HD11	2.53	0.44
1:I:161:VAL:HG23	1:I:177:ALA:C	2.42	0.44
1:D:7:LEU:HD21	1:D:65:TRP:CE2	2.53	0.44
1:D:203:ARG:HG3	1:D:204:GLU:O	2.18	0.44
1:I:191:GLU:CG	1:I:193:TYR:HE1	2.30	0.44
1:I:193:TYR:CE2	2:J:408:CYS:HA	2.53	0.44
1:A:154:LEU:O	1:A:181:ARG:HD2	2.18	0.44
1:I:173:GLU:CD	1:I:174:ILE:H	2.25	0.44
1:B:92:SER:HB2	1:B:124:MET:HE2	1.99	0.44
1:B:114:MET:HE2	2:E:410:VAL:CA	2.15	0.44
1:D:31:LEU:HD12	1:D:196:VAL:CG1	2.47	0.44
1:G:13:ASN:OD1	1:G:13:ASN:N	2.44	0.44
1:A:21:PRO:HG2	1:A:152:ILE:HD11	1.99	0.44
1:B:186:TYR:OH	2:C:405:HIS:ND1	2.49	0.44
1:D:145:TRP:CZ2	2:E:406:PRO:HG2	2.52	0.44
1:G:126:ASP:O	1:G:136:VAL:HG11	2.18	0.44
1:I:34:THR:HG23	1:I:162:ASP:HB3	2.00	0.44
1:A:173:GLU:HG3	1:A:205:ARG:CZ	2.48	0.43
1:D:3:ASN:ND2	1:D:6:ARG:NH2	2.66	0.43
1:D:123:PHE:CD2	1:D:140:VAL:HB	2.53	0.43
1:A:7:LEU:HD11	1:A:65:TRP:CD1	2.53	0.43
1:D:191:GLU:H	1:D:191:GLU:CD	2.25	0.43
1:A:171:LYS:HE3	1:B:43:SER:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:VAL:HG21	1:B:120:ARG:NH2	2.33	0.43
1:A:41:VAL:HG22	1:A:172:TYR:OH	2.19	0.43
1:D:50:LEU:HD23	1:D:50:LEU:HA	1.78	0.43
2:H:406:PRO:O	2:H:410:VAL:HG22	2.18	0.43
1:I:1:GLN:O	1:I:5:MET:HG3	2.19	0.43
1:I:61:ASN:HD22	1:I:64:MET:HE2	1.82	0.43
1:B:50:LEU:O	1:B:120:ARG:HA	2.18	0.43
2:H:411:ASP:HB3	2:H:412:HIS:CD2	2.54	0.43
1:I:58:TRP:CE2	1:I:113:VAL:HG11	2.53	0.43
1:A:127:PRO:O	1:A:128:THR:C	2.61	0.43
1:B:11:LEU:HA	1:B:11:LEU:HD23	1.71	0.43
1:B:40:LYS:HB2	1:D:45:THR:HG22	1.99	0.43
1:I:27:LEU:HD12	1:I:28:THR:H	1.83	0.43
1:A:106:VAL:O	1:A:113:VAL:HA	2.18	0.43
1:B:1:GLN:NE2	1:D:25:ASP:HB2	2.34	0.43
1:B:14:ARG:HG3	1:B:15:SER:N	2.34	0.43
1:D:37:ASP:HA	1:D:166:TYR:CE1	2.53	0.43
1:A:1:GLN:O	1:A:5:MET:HG3	2.18	0.43
1:A:1:GLN:CD	1:A:1:GLN:H	2.28	0.42
1:A:132:SER:OG	1:A:134:GLU:HG2	2.19	0.42
1:A:57:ARG:HG3	1:A:114:MET:HE2	2.01	0.42
1:B:1:GLN:H	1:B:1:GLN:CD	2.19	0.42
1:D:149:GLY:CA	1:D:194:ILE:HD12	2.49	0.42
1:G:1:GLN:CD	1:G:1:GLN:N	2.77	0.42
1:I:48:VAL:HG23	1:I:125:CYS:HB3	2.01	0.42
1:I:50:LEU:O	1:I:120:ARG:HA	2.19	0.42
2:F:413:PRO:HB3	1:G:114:MET:HE1	2.01	0.42
1:D:38:ILE:HD13	1:D:50:LEU:HD21	2.01	0.42
1:G:18:TYR:CD2	1:G:19:PRO:HD2	2.54	0.42
1:B:5:MET:HE1	1:D:17:MET:O	2.19	0.42
1:A:58:TRP:CE2	1:A:113:VAL:HG21	2.54	0.42
1:A:89:THR:CG2	1:A:145:TRP:HB2	2.49	0.42
1:G:125:CYS:O	1:G:127:PRO:HD3	2.20	0.42
1:D:30:THR:HA	1:D:155:LYS:O	2.20	0.41
1:B:58:TRP:CH2	1:B:86:PRO:HD3	2.55	0.41
1:B:191:GLU:OE2	2:C:412:HIS:NE2	2.50	0.41
1:A:98:GLN:NE2	1:B:95:ARG:HH21	2.17	0.41
1:D:173:GLU:O	1:D:202:PHE:HB2	2.20	0.41
1:G:63:LEU:HA	1:G:63:LEU:HD23	1.82	0.41
1:A:114:MET:HB2	1:A:114:MET:HE3	1.66	0.41
2:H:411:ASP:O	2:H:412:HIS:HD2	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:THR:HA	1:A:155:LYS:O	2.21	0.41
1:D:74:THR:O	1:D:108:THR:HA	2.21	0.41
1:I:37:ASP:OD1	1:I:170:SER:HB2	2.20	0.41
1:A:53:TYR:N	1:A:53:TYR:CD1	2.87	0.41
1:B:2:ALA:HA	1:B:5:MET:HG2	2.03	0.41
1:D:50:LEU:O	1:D:120:ARG:HA	2.21	0.41
1:G:30:THR:HG22	1:G:155:LYS:HB3	2.02	0.41
1:I:4:LEU:C	1:I:4:LEU:HD23	2.46	0.41
1:A:89:THR:HG21	1:A:145:TRP:HB2	2.03	0.41
1:G:147:TYR:CE1	1:I:77:ARG:HG3	2.56	0.41
1:I:87:ASP:OD2	1:I:87:ASP:O	2.38	0.41
1:A:174:ILE:HD12	1:A:174:ILE:HG23	1.78	0.41
1:D:99:VAL:HG21	1:D:103:GLN:HE21	1.86	0.41
1:I:75:ASP:HB3	1:I:108:THR:HG22	2.02	0.41
1:B:33:PHE:HD1	1:B:179:GLN:HE21	1.69	0.41
1:G:29:VAL:O	1:G:154:LEU:HA	2.21	0.41
2:H:413:PRO:HB3	1:I:114:MET:HE2	2.02	0.41
1:G:114:MET:HE3	1:G:114:MET:HB2	1.97	0.40
1:I:203:ARG:HG2	1:I:204:GLU:O	2.22	0.40
2:H:410:VAL:HB	1:I:106:VAL:CG1	2.49	0.40
1:D:109:HIS:C	1:D:111:GLY:N	2.80	0.40
1:I:36:GLN:OE1	1:I:53:TYR:CZ	2.74	0.40
1:I:172:TYR:HA	1:I:205:ARG:HH22	1.86	0.40
1:A:35:LEU:HD23	1:A:166:TYR:CD1	2.56	0.40
1:A:92:SER:O	1:A:124:MET:HG3	2.21	0.40
1:I:185:HIS:O	1:I:186:TYR:CD2	2.74	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	205/207 (99%)	198 (97%)	6 (3%)	1 (0%)	24	60
1	B	205/207 (99%)	200 (98%)	5 (2%)	0	100	100
1	D	205/207 (99%)	196 (96%)	9 (4%)	0	100	100
1	G	205/207 (99%)	200 (98%)	5 (2%)	0	100	100
1	I	205/207 (99%)	197 (96%)	8 (4%)	0	100	100
2	C	15/17 (88%)	14 (93%)	1 (7%)	0	100	100
2	E	15/17 (88%)	15 (100%)	0	0	100	100
2	F	15/17 (88%)	15 (100%)	0	0	100	100
2	H	15/17 (88%)	15 (100%)	0	0	100	100
2	J	15/17 (88%)	15 (100%)	0	0	100	100
All	All	1100/1120 (98%)	1065 (97%)	34 (3%)	1 (0%)	48	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	SER

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	190/190 (100%)	188 (99%)	2 (1%)	65	83
1	B	190/190 (100%)	179 (94%)	11 (6%)	18	51
1	D	190/190 (100%)	190 (100%)	0	100	100
1	G	190/190 (100%)	188 (99%)	2 (1%)	65	83
1	I	190/190 (100%)	184 (97%)	6 (3%)	34	67
2	C	13/13 (100%)	13 (100%)	0	100	100
2	E	13/13 (100%)	13 (100%)	0	100	100
2	F	13/13 (100%)	13 (100%)	0	100	100
2	H	13/13 (100%)	13 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	13/13 (100%)	13 (100%)	0	100	100
All	All	1015/1015 (100%)	994 (98%)	21 (2%)	47	75

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	THR
1	A	30	THR
1	B	13	ASN
1	B	62	SER
1	B	78	THR
1	B	132	SER
1	B	158	THR
1	B	164	SER
1	B	178	THR
1	B	180	THR
1	B	182	GLN
1	B	188	CYS
1	B	189	CYS
1	G	136	VAL
1	G	137	THR
1	I	29	VAL
1	I	78	THR
1	I	85	THR
1	I	122	SER
1	I	170	SER
1	I	191	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	98	GLN
1	A	182	GLN
1	A	184	GLN
2	F	405	HIS
1	B	36	GLN
1	B	46	ASN
1	B	61	ASN
1	B	68	ASN
1	B	98	GLN

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Mol	Chain	Res	Type
1	B	179	GLN
1	B	185	HIS
1	D	3	ASN
1	D	36	GLN
1	D	61	ASN
1	D	103	GLN
1	D	182	GLN
1	D	185	HIS
1	G	1	GLN
1	G	109	HIS
2	H	412	HIS
1	I	13	ASN
1	I	61	ASN
1	I	109	HIS
1	I	182	GLN
1	I	197	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 ⓘ

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	207/207 (100%)	1.01	31 (14%) 5 3	31, 49, 80, 109	0
1	B	207/207 (100%)	1.06	25 (12%) 8 5	29, 52, 86, 112	0
1	D	207/207 (100%)	1.38	42 (20%) 3 2	39, 60, 94, 120	0
1	G	207/207 (100%)	1.02	31 (14%) 5 3	33, 52, 90, 121	0
1	I	207/207 (100%)	1.31	42 (20%) 3 2	36, 60, 100, 121	0
2	C	16/17 (94%)	2.01	6 (37%) 1 1	61, 77, 92, 102	0
2	E	16/17 (94%)	1.81	6 (37%) 1 1	52, 76, 86, 90	0
2	F	16/17 (94%)	1.72	6 (37%) 1 1	58, 72, 84, 86	0
2	H	16/17 (94%)	2.29	8 (50%) 0 0	59, 86, 105, 109	0
2	J	16/17 (94%)	2.05	6 (37%) 1 1	65, 83, 105, 108	0
All	All	1115/1120 (99%)	1.21	203 (18%) 3 2	29, 56, 93, 121	0

All (203) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	206	ARG	6.0
1	G	206	ARG	5.9
1	B	17	MET	5.7
2	H	401	GLY	5.4
1	I	17	MET	5.3
2	C	416	CYS	5.2
1	D	17	MET	5.2
1	A	206	ARG	5.1
1	D	205	ARG	5.1
1	D	72	ASN	4.8
1	D	206	ARG	4.8
1	A	17	MET	4.5
1	D	0	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	G	16	PRO	4.5
1	B	14	ARG	4.4
2	J	402	CYS	4.4
1	D	15	SER	4.3
1	D	16	PRO	4.3
1	A	187	SER	4.1
2	J	401	GLY	4.1
1	G	17	MET	4.1
2	E	402	CYS	4.0
1	B	188	CYS	3.9
1	I	131	ASP	3.9
1	I	1	GLN	3.9
1	D	187	SER	3.9
1	D	178	THR	3.8
1	I	14	ARG	3.8
1	I	188	CYS	3.8
1	G	54	GLU	3.7
1	B	206	ARG	3.7
1	D	112	SER	3.7
2	C	402	CYS	3.7
1	I	0	SER	3.7
1	I	132	SER	3.6
1	I	91	TYR	3.6
1	I	186	TYR	3.6
1	D	138	CYS	3.5
2	H	416	CYS	3.5
1	D	59	LYS	3.5
2	E	416	CYS	3.5
1	A	14	ARG	3.5
2	H	402	CYS	3.5
1	D	24	ASP	3.5
2	H	405	HIS	3.5
1	B	36	GLN	3.4
1	G	188	CYS	3.4
2	C	403	CYS	3.4
2	J	416	CYS	3.4
1	D	25	ASP	3.4
1	I	138	CYS	3.4
1	A	0	SER	3.4
1	I	15	SER	3.4
1	G	14	ARG	3.3
1	A	72	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	G	133	GLU	3.3
1	I	134	GLU	3.3
1	D	189	CYS	3.3
1	A	160	GLN	3.3
1	A	24	ASP	3.3
1	B	138	CYS	3.2
1	A	23	LYS	3.2
1	D	68	ASN	3.2
1	A	1	GLN	3.2
1	I	158	THR	3.2
1	A	188	CYS	3.2
1	A	131	ASP	3.2
1	A	69	GLU	3.2
1	I	176	SER	3.1
1	D	191	GLU	3.1
1	I	133	GLU	3.1
1	I	173	GLU	3.1
1	D	14	ARG	3.1
1	B	24	ASP	3.1
1	I	169	SER	3.1
1	I	160	GLN	3.1
1	B	87	ASP	3.1
1	D	188	CYS	3.0
1	A	205	ARG	3.0
1	D	13	ASN	3.0
1	G	24	ASP	3.0
1	A	75	ASP	2.9
1	B	0	SER	2.9
1	B	133	GLU	2.9
2	F	402	CYS	2.9
2	H	415	ILE	2.9
2	H	414	GLU	2.9
2	F	416	CYS	2.9
1	B	69	GLU	2.9
1	B	2	ALA	2.9
1	B	110	ASP	2.9
1	G	157	ASP	2.9
1	D	180	THR	2.9
1	I	28	THR	2.9
1	G	189	CYS	2.9
2	J	411	ASP	2.8
1	D	131	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	137	THR	2.8
1	A	32	GLY	2.8
2	F	403	CYS	2.8
1	B	15	SER	2.8
1	B	186	TYR	2.7
1	D	111	GLY	2.7
1	G	138	CYS	2.7
1	B	157	ASP	2.7
1	G	160	GLN	2.7
2	E	414	GLU	2.7
1	G	13	ASN	2.7
1	I	10	ASP	2.7
1	I	87	ASP	2.7
1	I	130	VAL	2.6
2	H	403	CYS	2.6
2	C	415	ILE	2.6
1	I	43	SER	2.6
1	I	171	LYS	2.6
1	D	150	PHE	2.6
1	G	190	PRO	2.5
1	A	204	GLU	2.5
1	I	205	ARG	2.5
1	I	185	HIS	2.5
1	I	75	ASP	2.5
1	I	16	PRO	2.5
1	B	1	GLN	2.5
1	I	172	TYR	2.4
1	B	34	THR	2.4
1	B	185	HIS	2.4
1	D	73	ILE	2.4
1	I	157	ASP	2.4
1	A	71	GLY	2.4
1	D	167	TYR	2.4
1	A	16	PRO	2.4
1	A	189	CYS	2.3
1	D	58	TRP	2.3
1	I	193	TYR	2.3
1	G	131	ASP	2.3
1	B	176	SER	2.3
2	F	401	GLY	2.3
1	A	134	GLU	2.3
2	E	411	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	160	GLN	2.3
1	I	189	CYS	2.3
2	E	405	HIS	2.3
1	G	77	ARG	2.3
1	A	68	ASN	2.3
1	A	74	THR	2.3
2	J	404	SER	2.3
1	G	23	LYS	2.2
1	D	28	THR	2.2
1	D	62	SER	2.2
1	D	12	PHE	2.2
1	B	168	ALA	2.2
1	I	2	ALA	2.2
1	A	82	ASP	2.2
1	A	159	ASP	2.2
1	D	22	THR	2.2
2	E	403	CYS	2.2
1	G	0	SER	2.2
1	G	187	SER	2.2
1	I	18	TYR	2.2
1	G	134	GLU	2.2
2	C	407	ALA	2.2
2	J	414	GLU	2.2
1	I	24	ASP	2.2
1	A	165	SER	2.2
1	D	168	ALA	2.2
1	G	159	ASP	2.2
1	D	136	VAL	2.1
2	C	401	GLY	2.1
1	I	12	PHE	2.1
1	G	69	GLU	2.1
1	G	204	GLU	2.1
1	D	75	ASP	2.1
1	G	143	GLY	2.1
1	I	30	THR	2.1
1	D	70	TYR	2.1
1	G	205	ARG	2.1
1	A	138	CYS	2.1
1	G	151	GLU	2.1
1	G	55	GLN	2.1
1	A	128	THR	2.1
1	B	131	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	202	PHE	2.1
1	D	151	GLU	2.1
1	G	15	SER	2.1
1	B	55	GLN	2.1
2	F	413	PRO	2.1
1	B	61	ASN	2.1
1	G	3	ASN	2.1
1	I	61	ASN	2.1
2	F	414	GLU	2.1
1	D	91	TYR	2.1
1	G	184	GLN	2.0
1	I	13	ASN	2.0
1	I	150	PHE	2.0
1	D	23	LYS	2.0
1	G	186	TYR	2.0
1	A	64	MET	2.0
1	A	190	PRO	2.0
2	H	413	PRO	2.0
1	A	12	PHE	2.0
1	B	134	GLU	2.0
1	I	23	LYS	2.0
1	D	166	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.