



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:36 AM UTC

PDB ID : 1RRP / pdb_00001rrp
Title : STRUCTURE OF THE RAN-GPPNHP-RANBD1 COMPLEX
Authors : Vetter, I.R.; Nowak, C.; Nishimoto, T.; Kuhlmann, J.; Wittinghofer, A.
Deposited on : 1999-01-15
Resolution : 2.96 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

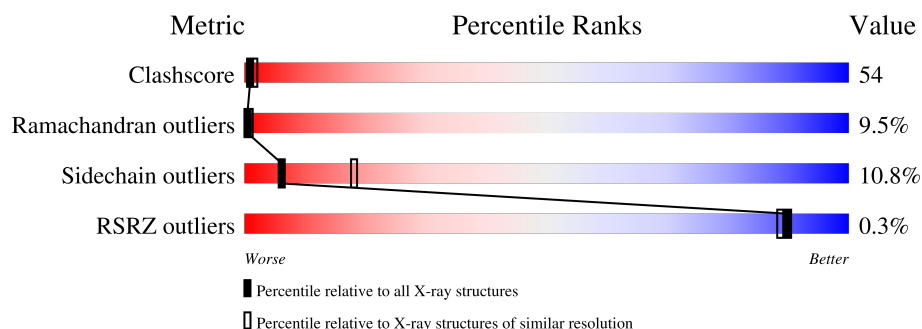
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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

Mol	Chain	Length	Quality of chain
1	A	204	24%59%13%.
1	C	204	25%52%8%.12%
2	B	134	28%52%19%.
2	D	134	31%52%16%.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5402 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 RAN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	204	Total	C	N	O	S	0	0	0
			1636	1058	282	290	6			
1	C	180	Total	C	N	O	S	0	0	0
			1454	945	254	250	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	ARG	SER	SEE REMARK 999	UNP P62826
C	129	ARG	SER	SEE REMARK 999	UNP P62826

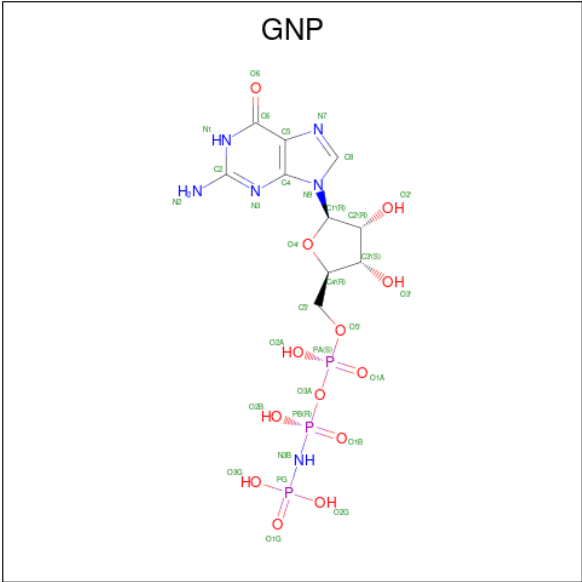
- Molecule 2 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP358.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	134	Total	C	N	O	S	0	0	0
			1105	706	192	202	5			
2	D	134	Total	C	N	O	S	0	0	0
			1105	706	192	202	5			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	C	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

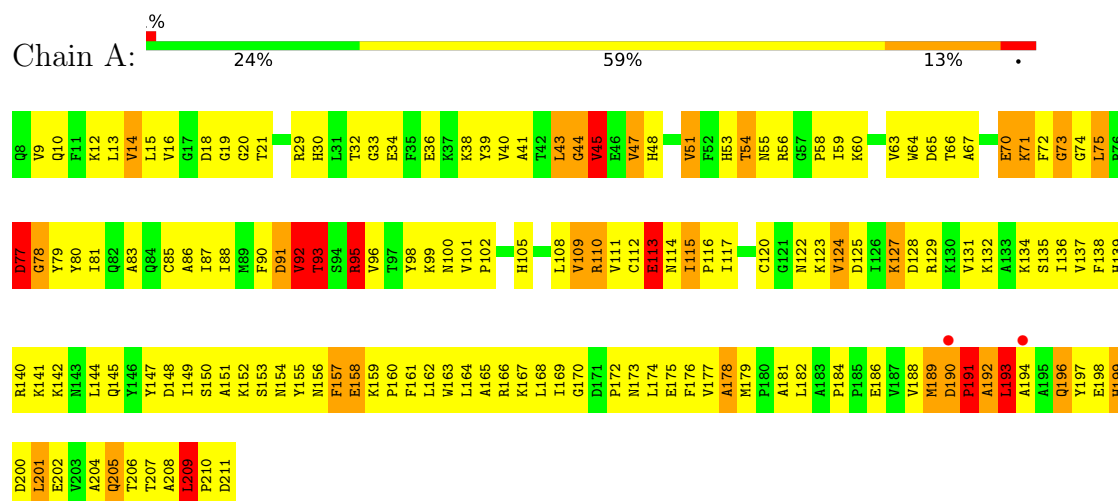
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	10	Total	O	0	0
			10	10		
5	B	7	Total	O	0	0
			7	7		
5	C	9	Total	O	0	0
			9	9		
5	D	10	Total	O	0	0
			10	10		

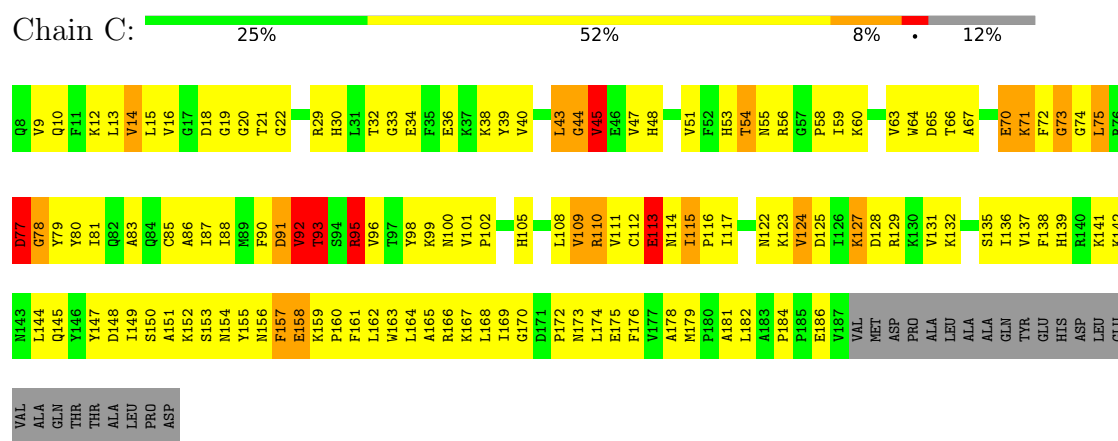
3 Residue-property plots

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.

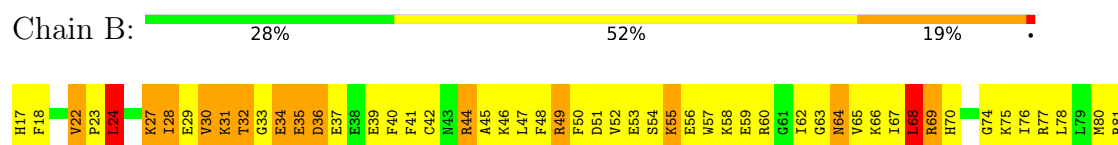
• Molecule 1: RAN



• Molecule 1: RAN

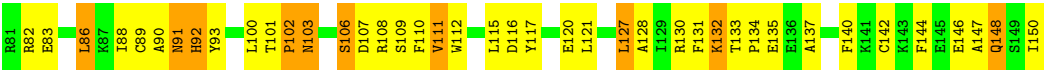
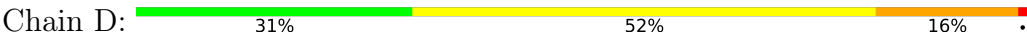


• Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP358





● Molecule 2: NUCLEAR PORE COMPLEX PROTEIN NUP358



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	121.34Å 139.46Å 91.65Å 90.00° 135.78° 90.00°	Depositor
Resolution (Å)	12.50 – 2.96 12.50 – 2.96	Depositor EDS
% Data completeness (in resolution range)	86.0 (12.50-2.96) 86.0 (12.50-2.96)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.90Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.252 , 0.304 0.269 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	71.6	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5402	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: GNP, MG

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	0.50	0/1677	1.08	14/2273 (0.6%)
1	C	0.52	0/1491	1.04	9/2017 (0.4%)
2	B	0.48	0/1131	0.99	7/1519 (0.5%)
2	D	0.44	0/1131	0.96	5/1519 (0.3%)
All	All	0.49	0/5430	1.03	35/7328 (0.5%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	ASP	N-CA-C	-10.37	102.80	114.62
1	C	77	ASP	N-CA-C	-10.06	103.15	114.62
1	C	91	ASP	N-CA-C	8.94	122.19	111.82
1	A	91	ASP	N-CA-C	8.78	122.00	111.82
2	B	148	GLN	N-CA-C	-6.90	104.99	113.41
2	D	148	GLN	N-CA-C	-6.81	105.10	113.41
1	A	209	LEU	CA-C-N	6.66	127.02	119.83
1	A	209	LEU	C-N-CA	6.66	127.02	119.83
2	D	92	HIS	N-CA-C	6.47	118.91	110.43
2	B	64	ASN	N-CA-C	6.41	119.17	108.73
2	B	92	HIS	N-CA-C	6.35	118.75	110.43
2	D	64	ASN	N-CA-C	6.29	118.97	108.73
1	A	192	ALA	N-CA-C	-6.18	104.62	111.36
2	D	127	LEU	N-CA-C	5.98	118.96	109.81
1	A	127	LYS	N-CA-C	5.71	117.20	110.97
1	A	33	GLY	N-CA-C	-5.71	107.37	115.30
1	C	51	VAL	N-CA-C	5.61	116.02	108.17
2	B	126	GLN	N-CA-C	-5.47	100.33	109.24
1	C	127	LYS	N-CA-C	5.43	116.89	110.97
2	B	127	LEU	N-CA-C	5.42	118.10	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	VAL	N-CA-C	5.39	115.72	108.17
1	A	78	GLY	N-CA-C	-5.36	105.82	113.86
1	A	51	VAL	N-CA-C	5.34	115.64	108.17
1	A	93	THR	N-CA-C	-5.27	106.53	113.17
1	C	93	THR	N-CA-C	-5.26	106.54	113.17
1	C	33	GLY	N-CA-C	-5.26	107.99	115.30
1	C	78	GLY	N-CA-C	-5.25	105.99	113.86
1	C	79	TYR	N-CA-C	-5.23	105.58	111.28
1	A	79	TYR	N-CA-C	-5.21	105.61	111.28
1	C	45	VAL	N-CA-C	5.15	120.05	109.34
1	A	41	ALA	N-CA-C	5.12	117.52	110.35
2	B	68	LEU	N-CA-C	5.09	117.54	109.24
2	B	24	LEU	N-CA-C	5.09	116.94	109.71
2	D	68	LEU	N-CA-C	5.07	117.50	109.24
1	A	45	VAL	N-CA-C	5.03	119.81	109.34

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1636	0	1650	217	0
1	C	1454	0	1481	175	0
2	B	1105	0	1102	119	0
2	D	1105	0	1102	113	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	32	0	13	6	0
4	C	32	0	13	8	0
5	A	10	0	0	2	0
5	B	7	0	0	1	0
5	C	9	0	0	2	0
5	D	10	0	0	0	0
All	All	5402	0	5361	578	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 54.

All (578) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:LEU:H	1:A:75:LEU:HD23	1.07	1.15
1:C:75:LEU:H	1:C:75:LEU:HD23	1.04	1.12
1:A:54:THR:HB	1:A:174:LEU:HD21	1.43	1.00
1:A:32:THR:HB	1:A:34:GLU:HG2	1.44	0.99
1:C:32:THR:HB	1:C:34:GLU:HG2	1.43	0.98
1:C:54:THR:HB	1:C:174:LEU:HD21	1.44	0.97
1:C:56:ARG:NE	2:D:24:LEU:HD11	1.81	0.95
1:C:56:ARG:HE	2:D:24:LEU:HD11	1.29	0.94
1:A:209:LEU:HD13	1:A:210:PRO:HD2	1.51	0.93
1:C:80:TYR:HB3	1:C:111:VAL:HG21	1.53	0.91
1:C:43:LEU:HD22	1:C:43:LEU:H	1.34	0.91
1:A:80:TYR:HB3	1:A:111:VAL:HG21	1.52	0.90
1:A:184:PRO:HG2	2:B:93:TYR:CE2	2.08	0.89
1:A:43:LEU:HD22	1:A:43:LEU:H	1.37	0.89
1:C:75:LEU:HD23	1:C:75:LEU:N	1.90	0.86
1:A:75:LEU:H	1:A:75:LEU:CD2	1.85	0.86
1:A:174:LEU:HD23	1:A:175:GLU:N	1.90	0.85
1:C:184:PRO:HG2	2:D:93:TYR:CE2	2.10	0.85
1:C:184:PRO:HG2	2:D:93:TYR:CD2	2.13	0.84
2:B:27:LYS:O	2:B:28:ILE:HD12	1.78	0.83
1:C:174:LEU:HD23	1:C:175:GLU:N	1.94	0.83
1:A:190:ASP:C	1:A:190:ASP:OD1	2.22	0.81
1:C:170:GLY:O	1:C:172:PRO:HD3	1.80	0.81
1:A:14:VAL:HG23	1:A:86:ALA:HB2	1.63	0.81
1:C:14:VAL:HG23	1:C:86:ALA:HB2	1.63	0.81
1:A:45:VAL:HA	1:A:66:THR:HA	1.62	0.81
1:A:75:LEU:HD23	1:A:75:LEU:N	1.93	0.81
1:A:95:ARG:N	1:A:95:ARG:HE	1.79	0.81
2:D:22:VAL:HG22	2:D:23:PRO:HD2	1.61	0.81
1:C:75:LEU:H	1:C:75:LEU:CD2	1.83	0.80
2:D:35:GLU:O	2:D:37:GLU:N	2.15	0.80
1:A:190:ASP:N	1:A:191:PRO:HD2	1.96	0.79
1:A:170:GLY:O	1:A:172:PRO:HD3	1.82	0.79
1:A:10:GLN:HE21	1:A:60:LYS:HD2	1.48	0.79
2:B:35:GLU:O	2:B:37:GLU:N	2.14	0.79
1:C:95:ARG:N	1:C:95:ARG:HE	1.80	0.79
2:D:70:HIS:HB3	2:D:74:GLY:H	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:VAL:HA	1:C:66:THR:HA	1.64	0.78
2:D:32:THR:HG23	2:D:34:GLU:H	1.48	0.78
1:A:43:LEU:HD22	1:A:43:LEU:N	1.98	0.78
1:C:43:LEU:HD22	1:C:43:LEU:N	1.99	0.77
1:C:54:THR:CB	1:C:174:LEU:HD21	2.15	0.76
1:C:162:LEU:HD11	1:C:166:ARG:HE	1.50	0.76
1:A:54:THR:CB	1:A:174:LEU:HD21	2.15	0.76
1:A:12:LYS:HE3	1:A:64:TRP:CE2	2.21	0.76
2:B:32:THR:HG23	2:B:34:GLU:H	1.51	0.76
1:C:12:LYS:HE3	1:C:64:TRP:CE2	2.20	0.76
2:B:70:HIS:HB3	2:B:74:GLY:H	1.50	0.75
1:A:162:LEU:HD11	1:A:166:ARG:HE	1.51	0.74
2:D:27:LYS:O	2:D:28:ILE:HD13	1.88	0.74
1:A:78:GLY:HA3	1:C:78:GLY:HA3	1.70	0.73
1:C:10:GLN:HE21	1:C:60:LYS:HD2	1.53	0.73
1:A:196:GLN:HE22	1:A:200:ASP:HB2	1.54	0.72
1:C:162:LEU:HD21	1:C:166:ARG:HH21	1.53	0.72
2:D:22:VAL:CG2	2:D:23:PRO:HD2	2.19	0.72
1:A:162:LEU:HD21	1:A:166:ARG:HH21	1.55	0.72
1:A:54:THR:HB	1:A:174:LEU:CD2	2.19	0.71
1:A:19:GLY:HA2	4:A:250:GNP:HNB3	1.55	0.71
1:C:54:THR:HB	1:C:174:LEU:CD2	2.19	0.70
2:D:69:ARG:HH22	2:D:150:ILE:HG21	1.57	0.70
1:A:201:LEU:HD22	2:B:126:GLN:OE1	1.92	0.70
1:A:209:LEU:HD13	1:A:210:PRO:CD	2.20	0.70
1:A:56:ARG:HE	2:B:24:LEU:CD1	2.05	0.69
1:C:12:LYS:HD3	1:C:83:ALA:HA	1.73	0.69
2:B:111:VAL:HG23	2:B:127:LEU:O	1.93	0.68
1:C:19:GLY:HA2	4:C:250:GNP:HNB3	1.58	0.68
1:A:95:ARG:N	1:A:95:ARG:NE	2.40	0.68
1:C:149:ILE:HG22	1:C:150:SER:H	1.57	0.68
2:D:111:VAL:HG23	2:D:127:LEU:O	1.93	0.68
1:A:105:HIS:O	1:A:109:VAL:HG22	1.93	0.68
1:A:29:ARG:NH2	2:B:59:GLU:OE2	2.27	0.68
1:A:179:MET:SD	2:B:88:ILE:HG13	2.34	0.68
1:A:178:ALA:HA	2:B:86:LEU:HB3	1.75	0.68
1:A:12:LYS:HD3	1:A:83:ALA:HA	1.75	0.68
1:C:34:GLU:OE1	2:D:58:LYS:HD3	1.94	0.67
1:C:105:HIS:O	1:C:109:VAL:HG22	1.94	0.67
1:C:149:ILE:HG22	1:C:150:SER:N	2.09	0.67
1:A:149:ILE:HG22	1:A:150:SER:H	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:34:GLU:O	2:D:35:GLU:O	2.13	0.67
1:C:138:PHE:HA	1:C:141:LYS:HG2	1.77	0.67
1:C:95:ARG:N	1:C:95:ARG:NE	2.42	0.66
1:A:138:PHE:HA	1:A:141:LYS:HG2	1.76	0.66
2:B:100:LEU:HD23	2:B:112:TRP:HB3	1.76	0.66
1:A:149:ILE:HG22	1:A:150:SER:N	2.11	0.66
2:B:69:ARG:HH22	2:B:150:ILE:HG21	1.59	0.66
1:A:78:GLY:O	1:A:81:ILE:HG12	1.96	0.65
2:D:100:LEU:HD23	2:D:112:TRP:HB3	1.79	0.65
1:A:43:LEU:H	1:A:43:LEU:CD2	2.10	0.65
2:B:46:LYS:HE3	2:B:48:PHE:CZ	2.32	0.65
2:B:22:VAL:HG23	2:B:23:PRO:HD2	1.79	0.65
2:D:46:LYS:HE3	2:D:48:PHE:CZ	2.31	0.65
1:A:205:GLN:HB3	2:B:111:VAL:HG11	1.78	0.65
2:D:41:PHE:CE2	2:D:140:PHE:HA	2.32	0.65
2:B:41:PHE:CE2	2:B:140:PHE:HA	2.32	0.65
2:B:34:GLU:O	2:B:35:GLU:O	2.15	0.65
1:A:124:VAL:HG22	1:A:149:ILE:O	1.97	0.64
1:C:70:GLU:H	1:C:70:GLU:CD	2.04	0.64
1:A:174:LEU:HD23	1:A:175:GLU:H	1.60	0.64
1:A:101:VAL:HB	1:A:102:PRO:HD3	1.79	0.64
1:A:191:PRO:HB2	1:A:193:LEU:HD22	1.79	0.64
1:A:197:TYR:O	1:A:201:LEU:HD23	1.98	0.64
1:C:101:VAL:HB	1:C:102:PRO:HD3	1.79	0.64
2:D:44:ARG:HA	2:D:64:ASN:HA	1.79	0.64
1:C:43:LEU:H	1:C:43:LEU:CD2	2.07	0.64
2:B:49:ARG:HH11	2:B:49:ARG:HB3	1.63	0.64
2:B:132:LYS:HB2	2:B:132:LYS:NZ	2.12	0.64
2:B:32:THR:C	2:B:34:GLU:H	2.05	0.63
2:B:44:ARG:HA	2:B:64:ASN:HA	1.79	0.63
2:D:48:PHE:HB2	2:D:128:ALA:HB3	1.79	0.63
1:A:80:TYR:CB	1:A:111:VAL:HG21	2.27	0.63
1:A:30:HIS:HE1	1:A:157:PHE:HB2	1.63	0.63
1:C:56:ARG:HE	2:D:24:LEU:CD1	2.08	0.63
1:C:12:LYS:HE3	1:C:64:TRP:NE1	2.13	0.63
2:D:27:LYS:C	2:D:28:ILE:HD13	2.24	0.63
1:C:39:TYR:HD1	1:C:40:VAL:N	1.96	0.62
1:A:179:MET:H	2:B:81:ARG:HH12	1.46	0.62
2:D:132:LYS:HB2	2:D:132:LYS:NZ	2.12	0.62
2:B:35:GLU:C	2:B:37:GLU:H	2.06	0.62
2:D:28:ILE:HG22	2:D:29:GLU:N	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:HD21	2:B:113:HIS:HB2	1.80	0.62
1:C:78:GLY:O	1:C:81:ILE:HG12	1.99	0.62
1:A:162:LEU:CD1	1:A:166:ARG:HE	2.12	0.62
2:D:32:THR:C	2:D:34:GLU:H	2.08	0.62
1:A:12:LYS:HE3	1:A:64:TRP:NE1	2.15	0.62
1:C:162:LEU:CD1	1:C:166:ARG:HE	2.12	0.62
2:B:35:GLU:C	2:B:37:GLU:N	2.58	0.61
1:A:116:PRO:HB2	1:A:164:LEU:HD23	1.81	0.61
1:A:70:GLU:CD	1:A:70:GLU:H	2.08	0.61
2:B:48:PHE:HB2	2:B:128:ALA:HB3	1.83	0.61
1:A:51:VAL:HG23	2:B:87:LYS:NZ	2.16	0.61
1:C:20:GLY:H	4:C:250:GNP:HNB3	1.49	0.61
1:C:80:TYR:CB	1:C:111:VAL:HG21	2.27	0.61
2:D:35:GLU:C	2:D:37:GLU:H	2.07	0.61
2:D:46:LYS:HE3	2:D:48:PHE:HZ	1.64	0.61
1:A:190:ASP:N	1:A:191:PRO:CD	2.64	0.61
1:C:116:PRO:HB2	1:C:164:LEU:HD23	1.83	0.61
1:C:157:PHE:CD1	1:C:158:GLU:HG3	2.36	0.60
2:D:28:ILE:HG22	2:D:29:GLU:H	1.66	0.60
1:A:164:LEU:O	1:A:168:LEU:HD23	2.00	0.60
1:A:157:PHE:CD1	1:A:158:GLU:HG3	2.37	0.60
1:A:153:SER:C	1:A:155:TYR:H	2.10	0.60
1:C:111:VAL:HG23	1:C:112:CYS:SG	2.42	0.60
1:C:30:HIS:HE1	1:C:157:PHE:HB2	1.66	0.60
1:C:114:ASN:OD1	1:C:115:ILE:N	2.35	0.60
1:A:179:MET:H	2:B:81:ARG:NH1	2.00	0.60
2:B:44:ARG:HA	2:B:63:GLY:O	2.02	0.60
1:C:123:LYS:C	1:C:125:ASP:H	2.10	0.60
1:A:36:GLU:OE1	1:A:38:LYS:HG2	2.02	0.59
2:B:70:HIS:HB3	2:B:74:GLY:N	2.17	0.59
2:D:100:LEU:HG	2:D:144:PHE:CE2	2.37	0.59
1:C:124:VAL:HG22	1:C:149:ILE:O	2.02	0.59
2:B:76:ILE:HG21	2:B:147:ALA:HB1	1.83	0.59
2:B:109:SER:HB3	2:B:130:ARG:HA	1.85	0.59
2:D:70:HIS:HB3	2:D:74:GLY:N	2.16	0.59
1:C:70:GLU:C	1:C:72:PHE:H	2.10	0.59
1:A:20:GLY:H	4:A:250:GNP:HNB3	1.50	0.59
1:A:114:ASN:OD1	1:A:115:ILE:N	2.36	0.59
1:A:10:GLN:HG2	1:A:60:LYS:HB3	1.84	0.59
2:B:32:THR:O	2:B:34:GLU:N	2.36	0.59
2:B:82:ARG:O	2:B:86:LEU:HA	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:PRO:O	1:A:211:ASP:HB2	2.03	0.59
1:A:39:TYR:HD1	1:A:40:VAL:N	2.01	0.58
2:D:76:ILE:HG21	2:D:147:ALA:HB1	1.85	0.58
2:B:80:MET:HG2	2:B:89:CYS:SG	2.42	0.58
1:A:70:GLU:C	1:A:72:PHE:H	2.10	0.58
1:A:162:LEU:HA	1:A:176:PHE:CZ	2.39	0.58
1:C:10:GLN:HG2	1:C:60:LYS:HB3	1.85	0.58
2:D:44:ARG:HA	2:D:63:GLY:O	2.04	0.58
1:C:153:SER:C	1:C:155:TYR:H	2.11	0.58
1:C:36:GLU:OE1	1:C:38:LYS:HG2	2.04	0.57
1:A:178:ALA:HA	2:B:86:LEU:CB	2.34	0.57
2:D:47:LEU:HD12	2:D:128:ALA:O	2.04	0.57
1:A:56:ARG:NE	2:B:24:LEU:CD1	2.68	0.57
1:A:190:ASP:H	1:A:191:PRO:HD2	1.69	0.57
2:B:46:LYS:HE3	2:B:48:PHE:HZ	1.68	0.57
2:B:100:LEU:HG	2:B:144:PHE:CE2	2.39	0.57
1:C:162:LEU:HA	1:C:176:PHE:CZ	2.40	0.57
2:D:22:VAL:HG22	2:D:23:PRO:CD	2.34	0.57
2:D:80:MET:HG2	2:D:89:CYS:SG	2.45	0.57
2:D:109:SER:HB3	2:D:130:ARG:HG3	1.87	0.57
1:A:91:ASP:C	1:A:93:THR:H	2.12	0.57
1:C:70:GLU:C	1:C:72:PHE:N	2.62	0.57
1:C:91:ASP:C	1:C:93:THR:H	2.13	0.57
2:D:82:ARG:O	2:D:86:LEU:HA	2.04	0.57
1:C:110:ARG:HG3	1:C:110:ARG:HH11	1.70	0.57
2:D:133:THR:HB	2:D:134:PRO:HD2	1.86	0.57
1:A:99:LYS:O	1:A:102:PRO:HD2	2.05	0.57
2:B:133:THR:HB	2:B:134:PRO:HD2	1.86	0.56
1:C:179:MET:SD	2:D:88:ILE:HG13	2.45	0.56
1:A:19:GLY:HA2	4:A:250:GNP:N3B	2.20	0.56
1:A:70:GLU:C	1:A:72:PHE:N	2.63	0.56
1:A:123:LYS:C	1:A:125:ASP:H	2.12	0.56
1:C:47:VAL:HG22	1:C:64:TRP:HA	1.88	0.56
1:A:181:ALA:HA	2:B:88:ILE:HD11	1.86	0.56
2:D:66:LYS:HB3	2:D:68:LEU:HD21	1.88	0.56
1:C:112:CYS:HB2	1:C:115:ILE:HD12	1.88	0.56
1:C:168:LEU:O	2:D:20:PRO:HA	2.05	0.56
1:C:174:LEU:HD23	1:C:175:GLU:H	1.66	0.56
2:D:35:GLU:C	2:D:37:GLU:N	2.60	0.56
1:A:110:ARG:HG3	1:A:110:ARG:HH11	1.70	0.56
2:B:109:SER:HB3	2:B:130:ARG:HG3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:51:ASP:C	2:B:53:GLU:H	2.14	0.55
1:C:99:LYS:O	1:C:102:PRO:HD2	2.06	0.55
2:D:109:SER:HB3	2:D:130:ARG:HA	1.87	0.55
1:A:138:PHE:CZ	1:A:142:LYS:HG2	2.41	0.55
2:D:51:ASP:C	2:D:53:GLU:H	2.14	0.55
2:B:78:LEU:C	2:B:78:LEU:HD23	2.31	0.55
1:C:164:LEU:O	1:C:168:LEU:HD23	2.05	0.55
2:D:32:THR:O	2:D:34:GLU:N	2.39	0.55
2:D:49:ARG:HH11	2:D:49:ARG:HB3	1.71	0.55
1:A:194:ALA:O	1:A:198:GLU:HG3	2.07	0.55
1:C:44:GLY:H	1:C:67:ALA:HB2	1.72	0.55
1:A:9:VAL:HG11	1:A:59:ILE:HG22	1.88	0.55
2:B:32:THR:C	2:B:34:GLU:N	2.65	0.55
2:D:31:LYS:O	2:D:32:THR:HB	2.07	0.55
2:B:47:LEU:HD12	2:B:128:ALA:O	2.06	0.54
1:C:122:ASN:CG	1:C:123:LYS:N	2.65	0.54
2:B:31:LYS:O	2:B:32:THR:HB	2.07	0.54
2:B:80:MET:HB3	2:B:90:ALA:HB3	1.90	0.54
2:B:131:PHE:CD2	2:B:137:ALA:HA	2.42	0.54
1:C:90:PHE:HE1	1:C:92:VAL:HG23	1.72	0.54
2:D:78:LEU:C	2:D:78:LEU:HD23	2.33	0.54
1:C:150:SER:HB3	1:C:155:TYR:HB3	1.89	0.54
1:C:56:ARG:HH21	2:D:24:LEU:HD21	1.73	0.54
1:A:111:VAL:HG23	1:A:112:CYS:SG	2.47	0.54
2:B:66:LYS:HB3	2:B:68:LEU:HD21	1.90	0.54
1:C:32:THR:CB	1:C:34:GLU:HG2	2.30	0.53
1:C:85:CYS:HB3	1:C:116:PRO:HG2	1.90	0.53
1:A:90:PHE:HE1	1:A:92:VAL:HG23	1.72	0.53
1:C:145:GLN:HG3	1:C:147:TYR:CE2	2.43	0.53
1:A:47:VAL:HG22	1:A:64:TRP:HA	1.91	0.53
1:A:122:ASN:CG	1:A:123:LYS:N	2.66	0.53
2:B:134:PRO:HG2	2:B:135:GLU:OE2	2.09	0.53
2:D:131:PHE:CD2	2:D:137:ALA:HA	2.44	0.53
1:A:34:GLU:OE1	2:B:58:LYS:HD3	2.07	0.53
1:C:45:VAL:CA	1:C:66:THR:HA	2.37	0.53
1:C:71:LYS:NZ	1:C:71:LYS:HB3	2.24	0.53
1:A:112:CYS:HB2	1:A:115:ILE:HD12	1.90	0.53
1:C:132:LYS:O	1:C:135:SER:HB2	2.09	0.53
1:C:181:ALA:HA	2:D:88:ILE:HD11	1.91	0.53
2:D:68:LEU:O	2:D:76:ILE:HA	2.08	0.53
1:C:138:PHE:CZ	1:C:142:LYS:HG2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:CYS:HB3	1:A:116:PRO:HG2	1.89	0.52
2:B:51:ASP:O	2:B:53:GLU:N	2.38	0.52
1:A:71:LYS:NZ	1:A:71:LYS:HB3	2.24	0.52
1:C:116:PRO:HB2	1:C:164:LEU:CD2	2.40	0.52
2:D:31:LYS:O	2:D:32:THR:CB	2.58	0.52
2:D:21:VAL:O	2:D:22:VAL:HB	2.10	0.52
1:A:44:GLY:H	1:A:67:ALA:HB2	1.75	0.52
1:A:116:PRO:HB2	1:A:164:LEU:CD2	2.39	0.52
1:A:132:LYS:O	1:A:135:SER:HB2	2.09	0.52
2:D:67:ILE:C	2:D:68:LEU:HD23	2.35	0.52
1:A:159:LYS:N	1:A:160:PRO:CD	2.73	0.52
1:C:148:ASP:O	1:C:149:ILE:HD13	2.09	0.52
1:A:45:VAL:CA	1:A:66:THR:HA	2.37	0.52
1:A:179:MET:N	2:B:81:ARG:NH1	2.58	0.52
1:A:190:ASP:O	1:A:191:PRO:C	2.53	0.52
1:C:169:ILE:O	2:D:20:PRO:HB3	2.09	0.52
2:D:41:PHE:CD1	2:D:42:CYS:N	2.78	0.52
1:A:145:GLN:HG3	1:A:147:TYR:CE2	2.44	0.51
1:A:150:SER:HB3	1:A:155:TYR:HB3	1.92	0.51
2:D:32:THR:C	2:D:34:GLU:N	2.66	0.51
1:A:150:SER:O	1:A:152:LYS:N	2.43	0.51
1:C:123:LYS:O	1:C:125:ASP:N	2.44	0.51
2:D:80:MET:HB3	2:D:90:ALA:HB3	1.92	0.51
1:A:108:LEU:C	1:A:110:ARG:H	2.19	0.51
2:B:31:LYS:O	2:B:32:THR:CB	2.57	0.51
1:A:53:HIS:CE1	1:A:179:MET:HG3	2.45	0.51
1:A:184:PRO:HG2	2:B:93:TYR:CD2	2.45	0.51
2:B:68:LEU:O	2:B:76:ILE:HA	2.11	0.51
1:C:53:HIS:CE1	1:C:179:MET:HG3	2.45	0.51
1:A:14:VAL:HG23	1:A:86:ALA:CB	2.38	0.51
2:B:44:ARG:HB3	2:B:64:ASN:OD1	2.11	0.51
1:C:159:LYS:N	1:C:160:PRO:CD	2.74	0.51
1:A:162:LEU:O	1:A:166:ARG:HG3	2.11	0.51
1:A:196:GLN:C	1:A:198:GLU:N	2.65	0.51
1:A:210:PRO:O	1:A:211:ASP:CB	2.58	0.51
1:C:19:GLY:HA2	4:C:250:GNP:N3B	2.22	0.51
1:A:32:THR:CB	1:A:34:GLU:HG2	2.31	0.51
2:B:111:VAL:HA	2:B:127:LEU:O	2.11	0.51
2:D:37:GLU:HB3	2:D:68:LEU:HB3	1.93	0.51
1:A:148:ASP:O	1:A:149:ILE:HD13	2.11	0.51
2:B:28:ILE:O	2:B:30:VAL:N	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:PHE:CD1	2:B:42:CYS:N	2.79	0.51
1:C:39:TYR:CD1	1:C:39:TYR:C	2.89	0.51
2:D:68:LEU:HD23	2:D:68:LEU:N	2.26	0.51
2:D:134:PRO:HG2	2:D:135:GLU:OE2	2.11	0.51
2:D:111:VAL:HA	2:D:127:LEU:O	2.11	0.50
1:A:138:PHE:CE1	1:A:142:LYS:HD3	2.47	0.50
1:A:95:ARG:NH2	1:A:96:VAL:HG23	2.27	0.50
2:B:37:GLU:HB3	2:B:68:LEU:HB3	1.93	0.50
1:C:13:LEU:CD1	1:C:85:CYS:SG	3.00	0.50
1:C:150:SER:O	1:C:152:LYS:N	2.44	0.50
1:C:157:PHE:CE1	1:C:158:GLU:HG3	2.47	0.50
1:C:85:CYS:HA	1:C:115:ILE:CG2	2.42	0.50
2:B:92:HIS:CE1	2:B:112:TRP:HE1	2.30	0.50
1:C:139:HIS:HB2	1:C:144:LEU:O	2.11	0.50
1:C:162:LEU:O	1:C:166:ARG:HG3	2.12	0.50
1:C:164:LEU:O	1:C:165:ALA:C	2.53	0.50
2:B:51:ASP:OD2	2:B:53:GLU:HB3	2.12	0.50
2:B:110:PHE:O	2:B:128:ALA:HA	2.12	0.50
1:C:9:VAL:HG11	1:C:59:ILE:HG22	1.93	0.50
1:C:98:TYR:HA	1:C:101:VAL:HG23	1.94	0.50
2:D:62:ILE:HG23	2:D:62:ILE:O	2.10	0.50
1:A:100:ASN:O	1:A:101:VAL:C	2.54	0.49
2:D:44:ARG:HB3	2:D:64:ASN:OD1	2.12	0.49
1:A:113:GLU:HG2	1:A:114:ASN:ND2	2.28	0.49
1:C:100:ASN:O	1:C:101:VAL:C	2.55	0.49
1:A:30:HIS:CD2	1:A:161:PHE:CE2	3.00	0.49
1:A:95:ARG:NE	1:A:95:ARG:H	2.08	0.49
1:A:164:LEU:O	1:A:165:ALA:C	2.56	0.49
1:A:179:MET:N	2:B:81:ARG:HH12	2.09	0.49
2:B:41:PHE:CD1	2:B:41:PHE:C	2.91	0.49
1:C:95:ARG:NH2	1:C:96:VAL:HG23	2.26	0.49
1:C:14:VAL:HG23	1:C:86:ALA:CB	2.39	0.49
1:A:150:SER:C	1:A:152:LYS:N	2.69	0.49
1:A:56:ARG:HE	2:B:24:LEU:HD13	1.78	0.49
1:C:186:GLU:HG2	2:D:75:LYS:NZ	2.28	0.49
1:A:139:HIS:HB2	1:A:144:LEU:O	2.13	0.49
1:C:30:HIS:CD2	1:C:161:PHE:CE2	3.01	0.49
2:D:29:GLU:O	2:D:31:LYS:N	2.46	0.49
2:D:54:SER:OG	2:D:56:GLU:HG2	2.13	0.49
1:A:85:CYS:HA	1:A:115:ILE:CG2	2.43	0.48
1:A:157:PHE:CE1	1:A:158:GLU:HG3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:ARG:HH21	1:C:96:VAL:HG23	1.78	0.48
1:C:123:LYS:C	1:C:125:ASP:N	2.71	0.48
2:D:41:PHE:CD1	2:D:41:PHE:C	2.91	0.48
1:C:108:LEU:C	1:C:110:ARG:H	2.19	0.48
1:C:156:ASN:O	1:C:160:PRO:HD3	2.14	0.48
2:D:92:HIS:CE1	2:D:112:TRP:HE1	2.32	0.48
1:A:88:ILE:HD11	1:A:108:LEU:HD12	1.95	0.48
1:A:192:ALA:O	1:A:193:LEU:C	2.56	0.48
1:C:184:PRO:HG3	2:D:91:ASN:O	2.13	0.48
1:A:90:PHE:CD1	1:A:90:PHE:C	2.91	0.48
1:A:204:ALA:C	1:A:206:THR:H	2.22	0.48
2:B:62:ILE:HG23	2:B:62:ILE:O	2.13	0.48
1:A:95:ARG:HH21	1:A:96:VAL:HG23	1.78	0.48
1:A:150:SER:C	1:A:152:LYS:H	2.21	0.48
1:C:70:GLU:O	1:C:72:PHE:N	2.47	0.48
1:C:138:PHE:CE1	1:C:142:LYS:HD3	2.48	0.48
1:A:140:ARG:NH2	5:A:471:HOH:O	2.46	0.48
2:B:102:PRO:O	2:B:103:ASN:CB	2.62	0.48
1:A:19:GLY:CA	4:A:250:GNP:HNB3	2.24	0.48
2:B:120:GLU:O	2:B:121:LEU:HD23	2.14	0.48
1:C:90:PHE:CD1	1:C:90:PHE:C	2.92	0.48
1:A:123:LYS:O	1:A:125:ASP:N	2.47	0.48
2:B:68:LEU:N	2:B:68:LEU:HD23	2.28	0.47
1:A:123:LYS:C	1:A:125:ASP:N	2.73	0.47
1:A:18:ASP:O	1:A:21:THR:HG23	2.14	0.47
1:A:98:TYR:HA	1:A:101:VAL:HG23	1.95	0.47
2:D:102:PRO:O	2:D:103:ASN:CB	2.63	0.47
1:A:70:GLU:O	1:A:72:PHE:N	2.48	0.47
1:A:115:ILE:O	1:A:117:ILE:HG13	2.14	0.47
1:A:157:PHE:CD1	1:A:157:PHE:C	2.91	0.47
1:C:45:VAL:HA	1:C:65:ASP:O	2.14	0.47
1:C:88:ILE:HD11	1:C:108:LEU:HD12	1.96	0.47
2:D:120:GLU:O	2:D:121:LEU:HD23	2.14	0.47
1:A:196:GLN:O	1:A:198:GLU:N	2.47	0.47
2:B:54:SER:OG	2:B:56:GLU:HG2	2.15	0.47
1:A:81:ILE:HG13	1:A:81:ILE:O	2.14	0.47
2:B:67:ILE:C	2:B:68:LEU:HD23	2.39	0.47
1:C:98:TYR:CD1	1:C:98:TYR:C	2.92	0.47
1:C:113:GLU:HG2	1:C:114:ASN:ND2	2.29	0.47
1:C:114:ASN:O	1:C:115:ILE:HB	2.14	0.47
1:A:45:VAL:HA	1:A:65:ASP:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:LYS:HA	5:A:471:HOH:O	2.15	0.47
2:B:77:ARG:NH1	2:B:91:ASN:HD21	2.13	0.47
2:B:88:ILE:HG22	2:B:90:ALA:H	1.80	0.47
1:C:56:ARG:CD	2:D:24:LEU:HD11	2.44	0.47
2:B:106:SER:C	2:B:108:ARG:H	2.23	0.47
1:C:123:LYS:HA	4:C:250:GNP:O6	2.15	0.47
1:C:150:SER:C	1:C:152:LYS:H	2.23	0.47
1:A:114:ASN:O	1:A:115:ILE:HB	2.15	0.46
2:B:17:HIS:ND1	2:B:17:HIS:C	2.71	0.46
2:D:77:ARG:NH1	2:D:91:ASN:HD21	2.13	0.46
1:A:98:TYR:CD1	1:A:98:TYR:C	2.93	0.46
2:D:37:GLU:HG2	2:D:70:HIS:HA	1.98	0.46
2:B:51:ASP:C	2:B:53:GLU:N	2.73	0.46
1:C:115:ILE:O	1:C:117:ILE:HG13	2.16	0.46
1:C:157:PHE:CD1	1:C:157:PHE:C	2.92	0.46
1:C:136:ILE:HG22	1:C:139:HIS:ND1	2.31	0.46
1:A:190:ASP:OD1	1:A:190:ASP:O	2.33	0.46
2:B:54:SER:OG	2:B:55:LYS:N	2.48	0.46
2:B:69:ARG:HG3	2:B:69:ARG:O	2.14	0.46
1:C:56:ARG:O	2:D:25:PRO:HB2	2.15	0.46
2:B:69:ARG:NH2	2:B:150:ILE:HG21	2.30	0.46
1:C:18:ASP:O	1:C:21:THR:HG23	2.16	0.46
1:C:150:SER:C	1:C:152:LYS:N	2.72	0.46
2:D:51:ASP:OD2	2:D:53:GLU:HB3	2.15	0.46
1:A:135:SER:O	1:A:137:VAL:HG23	2.15	0.46
1:A:202:GLU:O	1:A:206:THR:HG23	2.16	0.46
1:C:81:ILE:O	1:C:81:ILE:HG13	2.15	0.46
1:A:9:VAL:CG1	1:A:59:ILE:HG22	2.46	0.46
2:D:106:SER:C	2:D:108:ARG:H	2.23	0.46
2:D:117:TYR:CE1	2:D:120:GLU:C	2.94	0.46
1:A:91:ASP:OD1	1:A:93:THR:HB	2.16	0.46
1:A:136:ILE:HG22	1:A:139:HIS:ND1	2.30	0.46
1:A:153:SER:C	1:A:155:TYR:N	2.73	0.46
1:A:204:ALA:O	1:A:207:THR:N	2.45	0.46
2:B:49:ARG:HB3	2:B:49:ARG:NH1	2.28	0.46
1:C:95:ARG:NE	1:C:95:ARG:H	2.12	0.46
1:C:149:ILE:CG2	1:C:150:SER:N	2.79	0.46
2:D:110:PHE:O	2:D:128:ALA:HA	2.15	0.46
2:B:34:GLU:HB2	5:B:468:HOH:O	2.16	0.46
2:B:76:ILE:HD12	2:B:147:ALA:O	2.16	0.46
1:C:13:LEU:HD13	1:C:85:CYS:SG	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:49:ARG:HB3	2:D:49:ARG:NH1	2.31	0.46
2:D:88:ILE:HG22	2:D:90:ALA:H	1.81	0.46
1:A:188:VAL:O	1:A:189:MET:HB2	2.15	0.45
2:B:132:LYS:HB2	2:B:132:LYS:HZ3	1.81	0.45
2:B:50:PHE:HD2	2:B:52:VAL:HG23	1.80	0.45
1:C:158:GLU:C	1:C:160:PRO:HD2	2.41	0.45
1:C:173:ASN:O	1:C:174:LEU:C	2.58	0.45
2:D:50:PHE:HD2	2:D:52:VAL:HG23	1.80	0.45
1:A:39:TYR:CD1	1:A:39:TYR:C	2.94	0.45
1:A:72:PHE:O	1:A:74:GLY:N	2.49	0.45
1:A:158:GLU:C	1:A:160:PRO:HD2	2.41	0.45
1:C:30:HIS:NE2	1:C:157:PHE:O	2.48	0.45
1:C:55:ASN:O	2:D:28:ILE:HG12	2.16	0.45
1:C:72:PHE:O	1:C:74:GLY:N	2.49	0.45
2:D:76:ILE:HD12	2:D:147:ALA:O	2.15	0.45
1:A:156:ASN:O	1:A:160:PRO:HD3	2.16	0.45
2:B:37:GLU:HG2	2:B:70:HIS:HA	1.98	0.45
1:C:43:LEU:HD21	5:C:479:HOH:O	2.16	0.45
2:D:45:ALA:HB2	2:D:131:PHE:CE1	2.51	0.45
1:A:55:ASN:O	2:B:28:ILE:HB	2.15	0.45
1:C:19:GLY:CA	4:C:250:GNP:HNB3	2.28	0.45
1:C:153:SER:C	1:C:155:TYR:N	2.74	0.45
2:B:30:VAL:HG23	2:B:30:VAL:O	2.17	0.45
2:B:35:GLU:O	2:B:36:ASP:C	2.60	0.45
2:D:52:VAL:C	2:D:54:SER:N	2.74	0.45
2:D:69:ARG:O	2:D:69:ARG:HG3	2.16	0.45
1:A:158:GLU:C	1:A:160:PRO:CD	2.90	0.45
1:A:204:ALA:C	1:A:206:THR:N	2.75	0.45
1:C:163:TRP:CZ2	1:C:167:LYS:HE3	2.52	0.45
2:D:132:LYS:HB2	2:D:132:LYS:HZ3	1.79	0.45
2:B:45:ALA:HB2	2:B:131:PHE:CE1	2.51	0.45
1:C:15:LEU:HD12	1:C:87:ILE:O	2.17	0.45
2:D:51:ASP:C	2:D:53:GLU:N	2.74	0.44
1:C:95:ARG:HA	1:C:131:VAL:HG22	1.99	0.44
1:A:30:HIS:NE2	1:A:157:PHE:O	2.47	0.44
1:C:20:GLY:N	4:C:250:GNP:HNB3	2.14	0.44
1:C:22:GLY:N	4:C:250:GNP:O1B	2.51	0.44
1:C:39:TYR:CD1	1:C:40:VAL:N	2.81	0.44
2:D:51:ASP:O	2:D:53:GLU:N	2.41	0.44
1:A:196:GLN:O	1:A:197:TYR:C	2.60	0.44
1:A:209:LEU:HA	1:A:210:PRO:HD3	1.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:13:LEU:HD12	1:C:85:CYS:SG	2.58	0.44
1:C:75:LEU:O	1:C:77:ASP:N	2.46	0.44
1:A:190:ASP:O	1:A:191:PRO:O	2.35	0.44
2:B:60:ARG:HD2	2:B:60:ARG:HA	1.74	0.44
2:D:34:GLU:O	2:D:35:GLU:C	2.60	0.44
2:B:117:TYR:CE1	2:B:120:GLU:C	2.96	0.44
1:C:91:ASP:O	1:C:92:VAL:HG12	2.16	0.44
1:C:158:GLU:C	1:C:160:PRO:CD	2.90	0.44
1:A:93:THR:O	1:A:93:THR:HG23	2.18	0.44
2:B:77:ARG:HA	2:B:93:TYR:HA	1.99	0.44
2:B:101:THR:O	2:B:102:PRO:O	2.36	0.44
1:A:15:LEU:HD12	1:A:87:ILE:O	2.18	0.43
1:A:111:VAL:HG23	1:A:112:CYS:N	2.33	0.43
1:A:199:HIS:CG	1:A:200:ASP:N	2.84	0.43
2:B:148:GLN:C	2:B:150:ILE:H	2.24	0.43
1:C:29:ARG:NH2	2:D:59:GLU:OE2	2.51	0.43
1:C:30:HIS:CD2	1:C:161:PHE:HE2	2.36	0.43
1:A:13:LEU:CD1	1:A:85:CYS:SG	3.06	0.43
1:A:145:GLN:HG2	1:A:163:TRP:CG	2.53	0.43
2:D:69:ARG:NH2	2:D:150:ILE:HG21	2.29	0.43
1:A:30:HIS:CD2	1:A:161:PHE:HE2	2.37	0.43
1:A:177:VAL:O	1:A:178:ALA:C	2.61	0.43
1:C:111:VAL:HG23	1:C:112:CYS:N	2.33	0.43
2:D:31:LYS:HB3	2:D:32:THR:H	1.51	0.43
1:A:12:LYS:CD	1:A:83:ALA:HA	2.46	0.43
1:A:125:ASP:HB3	1:A:150:SER:OG	2.19	0.43
1:C:91:ASP:OD1	1:C:93:THR:HB	2.17	0.43
1:C:125:ASP:HB3	1:C:150:SER:OG	2.19	0.43
2:D:35:GLU:O	2:D:36:ASP:C	2.61	0.43
1:C:70:GLU:HG2	5:C:463:HOH:O	2.18	0.43
1:A:10:GLN:HE21	1:A:60:LYS:CD	2.26	0.43
1:A:93:THR:O	1:A:93:THR:CG2	2.64	0.43
2:B:34:GLU:O	2:B:35:GLU:C	2.62	0.43
2:B:52:VAL:C	2:B:54:SER:N	2.73	0.43
1:A:75:LEU:O	1:A:77:ASP:N	2.47	0.43
2:B:40:PHE:CZ	2:B:146:GLU:HG2	2.54	0.43
1:C:135:SER:O	1:C:137:VAL:HG23	2.18	0.43
2:D:54:SER:OG	2:D:55:LYS:N	2.51	0.43
1:A:39:TYR:CD1	1:A:40:VAL:N	2.83	0.43
1:A:95:ARG:HA	1:A:131:VAL:HG22	2.01	0.43
2:B:31:LYS:HB3	2:B:32:THR:H	1.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:PHE:HZ	2:B:146:GLU:HG2	1.84	0.42
1:C:127:LYS:O	1:C:129:ARG:N	2.48	0.42
1:A:91:ASP:O	1:A:92:VAL:HG12	2.19	0.42
1:A:123:LYS:HA	4:A:250:GNP:O6	2.18	0.42
1:C:145:GLN:HG2	1:C:163:TRP:CG	2.53	0.42
2:D:101:THR:O	2:D:102:PRO:O	2.37	0.42
1:A:12:LYS:HD3	1:A:83:ALA:CA	2.46	0.42
1:A:91:ASP:O	1:A:93:THR:N	2.51	0.42
2:D:40:PHE:CZ	2:D:146:GLU:HG2	2.54	0.42
1:C:93:THR:O	1:C:93:THR:CG2	2.66	0.42
1:C:181:ALA:O	2:D:77:ARG:NH1	2.44	0.42
1:A:20:GLY:N	4:A:250:GNP:HNB3	2.14	0.42
2:B:31:LYS:O	2:B:32:THR:HG22	2.20	0.42
1:C:47:VAL:HA	1:C:63:VAL:O	2.20	0.42
2:D:28:ILE:CG2	2:D:29:GLU:N	2.82	0.42
2:D:30:VAL:HG23	2:D:30:VAL:O	2.19	0.42
2:D:77:ARG:HA	2:D:93:TYR:HA	2.01	0.42
1:A:162:LEU:O	1:A:162:LEU:HD12	2.20	0.42
1:A:173:ASN:O	1:A:174:LEU:C	2.61	0.42
1:A:204:ALA:O	1:A:206:THR:N	2.51	0.42
1:C:12:LYS:HD3	1:C:83:ALA:CA	2.45	0.42
1:C:91:ASP:O	1:C:93:THR:N	2.51	0.42
2:D:148:GLN:C	2:D:150:ILE:H	2.26	0.42
1:A:113:GLU:O	1:A:114:ASN:C	2.62	0.42
1:A:157:PHE:HD1	1:A:158:GLU:HG3	1.83	0.42
2:D:65:VAL:CG1	2:D:80:MET:SD	3.08	0.42
1:A:91:ASP:C	1:A:93:THR:N	2.77	0.42
1:A:127:LYS:O	1:A:129:ARG:N	2.47	0.42
2:B:50:PHE:N	2:B:57:TRP:CZ3	2.88	0.42
1:C:12:LYS:CD	1:C:83:ALA:HA	2.45	0.42
1:A:136:ILE:HG22	1:A:139:HIS:CE1	2.55	0.42
1:A:196:GLN:C	1:A:198:GLU:H	2.28	0.42
1:A:196:GLN:C	1:A:196:GLN:CD	2.88	0.42
2:B:40:PHE:O	2:B:40:PHE:HD1	2.03	0.42
1:A:154:ASN:HA	1:A:157:PHE:CD2	2.55	0.41
2:B:51:ASP:CG	2:B:53:GLU:HB3	2.45	0.41
1:C:122:ASN:O	1:C:123:LYS:HB2	2.20	0.41
1:A:116:PRO:HA	2:B:18:PHE:CE2	2.56	0.41
2:D:40:PHE:HZ	2:D:146:GLU:HG2	1.84	0.41
1:A:53:HIS:CE1	1:A:179:MET:HE3	2.54	0.41
1:A:149:ILE:CG2	1:A:150:SER:N	2.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:TRP:CZ2	1:A:167:LYS:HE3	2.55	0.41
1:A:164:LEU:C	1:A:168:LEU:HD23	2.45	0.41
1:A:196:GLN:O	1:A:196:GLN:NE2	2.53	0.41
1:C:44:GLY:N	1:C:67:ALA:HB2	2.34	0.41
1:C:44:GLY:O	1:C:45:VAL:HG12	2.21	0.41
1:C:98:TYR:CE2	1:C:136:ILE:HA	2.55	0.41
1:A:108:LEU:C	1:A:110:ARG:N	2.79	0.41
1:A:190:ASP:H	1:A:191:PRO:CD	2.29	0.41
2:B:65:VAL:O	2:B:65:VAL:HG23	2.20	0.41
1:A:194:ALA:CB	2:B:97:ASP:HB3	2.49	0.41
1:A:155:TYR:CD1	1:A:155:TYR:C	2.99	0.41
1:C:176:PHE:CD1	1:C:176:PHE:N	2.88	0.41
1:A:13:LEU:HD12	1:A:85:CYS:O	2.21	0.41
2:B:28:ILE:C	2:B:30:VAL:N	2.78	0.41
2:B:132:LYS:HB2	2:B:132:LYS:HZ2	1.86	0.41
1:C:136:ILE:HG22	1:C:139:HIS:CE1	2.55	0.41
2:D:83:GLU:H	2:D:83:GLU:HG2	1.70	0.41
1:A:85:CYS:HB2	1:A:164:LEU:HD22	2.02	0.41
1:A:120:CYS:HB3	1:A:149:ILE:HG13	2.02	0.41
1:A:13:LEU:HD13	1:A:85:CYS:SG	2.60	0.41
1:A:44:GLY:O	1:A:45:VAL:HG12	2.20	0.41
1:A:72:PHE:O	1:A:73:GLY:C	2.64	0.41
2:B:28:ILE:HG22	2:B:30:VAL:N	2.35	0.41
2:D:60:ARG:HD2	2:D:60:ARG:HA	1.77	0.41
1:A:122:ASN:O	1:A:123:LYS:HB2	2.20	0.41
1:A:186:GLU:CD	2:B:75:LYS:NZ	2.79	0.41
1:C:108:LEU:C	1:C:110:ARG:N	2.79	0.41
1:C:155:TYR:CD1	1:C:155:TYR:C	2.99	0.41
1:C:186:GLU:HG2	2:D:75:LYS:HZ3	1.83	0.41
1:A:176:PHE:N	1:A:176:PHE:CD1	2.87	0.40
2:B:119:ASP:O	2:B:120:GLU:HB2	2.20	0.40
1:C:70:GLU:N	1:C:70:GLU:OE1	2.53	0.40
1:C:113:GLU:O	1:C:114:ASN:C	2.63	0.40
1:C:162:LEU:O	1:C:162:LEU:HD12	2.21	0.40
1:C:165:ALA:O	1:C:166:ARG:C	2.64	0.40
2:D:31:LYS:O	2:D:32:THR:HG22	2.20	0.40
2:D:51:ASP:CG	2:D:53:GLU:HB3	2.46	0.40
2:D:62:ILE:O	2:D:83:GLU:HG2	2.22	0.40
2:B:24:LEU:HD22	2:B:24:LEU:HA	1.87	0.40
1:C:123:LYS:HG2	4:C:250:GNP:C6	2.51	0.40
1:C:164:LEU:C	1:C:168:LEU:HD23	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:90:ALA:HA	2:D:116:ASP:OD1	2.22	0.40
1:A:44:GLY:N	1:A:67:ALA:HB2	2.36	0.40
1:A:47:VAL:HA	1:A:63:VAL:O	2.22	0.40
1:A:169:ILE:HD13	2:B:22:VAL:HG13	2.03	0.40
1:A:186:GLU:OE2	2:B:75:LYS:NZ	2.51	0.40
1:C:72:PHE:O	1:C:73:GLY:C	2.64	0.40
1:A:169:ILE:HG22	2:B:24:LEU:CD2	2.52	0.40
1:C:154:ASN:HA	1:C:157:PHE:CD2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	202/204 (99%)	141 (70%)	43 (21%)	18 (9%)	0	1
1	C	178/204 (87%)	130 (73%)	35 (20%)	13 (7%)	1	1
2	B	132/134 (98%)	102 (77%)	14 (11%)	16 (12%)	0	0
2	D	132/134 (98%)	100 (76%)	18 (14%)	14 (11%)	0	0
All	All	644/676 (95%)	473 (73%)	110 (17%)	61 (10%)	0	1

All (61) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	VAL
1	A	191	PRO
1	A	193	LEU
2	B	30	VAL
2	B	31	LYS
2	B	32	THR
2	B	34	GLU

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Mol	Chain	Res	Type
2	B	35	GLU
2	B	36	ASP
2	B	55	LYS
2	B	102	PRO
2	B	103	ASN
1	C	45	VAL
2	D	31	LYS
2	D	32	THR
2	D	35	GLU
2	D	36	ASP
2	D	55	LYS
2	D	102	PRO
2	D	103	ASN
1	A	44	GLY
1	A	73	GLY
1	A	92	VAL
1	A	95	ARG
1	A	113	GLU
1	A	124	VAL
1	A	182	LEU
1	A	205	GLN
2	B	27	LYS
2	B	33	GLY
2	B	106	SER
1	C	44	GLY
1	C	73	GLY
1	C	92	VAL
1	C	95	ARG
1	C	113	GLU
1	C	124	VAL
2	D	30	VAL
2	D	34	GLU
2	D	106	SER
1	A	128	ASP
1	A	151	ALA
1	A	178	ALA
2	B	142	CYS
1	C	151	ALA
1	C	182	LEU
2	D	142	CYS
1	A	115	ILE
1	C	115	ILE

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Mol	Chain	Res	Type
1	C	128	ASP
2	D	33	GLY
1	A	189	MET
1	A	208	ALA
2	B	39	GLU
2	B	107	ASP
1	C	178	ALA
2	D	86	LEU
2	D	107	ASP
2	B	86	LEU
1	C	109	VAL
1	A	109	VAL

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	176/176 (100%)	151 (86%)	25 (14%)	3	9
1	C	157/176 (89%)	140 (89%)	17 (11%)	6	18
2	B	120/120 (100%)	108 (90%)	12 (10%)	7	20
2	D	120/120 (100%)	112 (93%)	8 (7%)	15	36
All	All	573/592 (97%)	511 (89%)	62 (11%)	6	18

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	VAL
1	A	16	VAL
1	A	43	LEU
1	A	45	VAL
1	A	48	HIS
1	A	54	THR
1	A	58	PRO
1	A	70	GLU
1	A	71	LYS

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Mol	Chain	Res	Type
1	A	75	LEU
1	A	77	ASP
1	A	92	VAL
1	A	93	THR
1	A	95	ARG
1	A	110	ARG
1	A	113	GLU
1	A	157	PHE
1	A	158	GLU
1	A	190	ASP
1	A	191	PRO
1	A	193	LEU
1	A	196	GLN
1	A	199	HIS
1	A	201	LEU
1	A	209	LEU
2	B	22	VAL
2	B	24	LEU
2	B	28	ILE
2	B	29	GLU
2	B	44	ARG
2	B	49	ARG
2	B	68	LEU
2	B	69	ARG
2	B	91	ASN
2	B	111	VAL
2	B	115	LEU
2	B	132	LYS
1	C	14	VAL
1	C	16	VAL
1	C	43	LEU
1	C	48	HIS
1	C	54	THR
1	C	58	PRO
1	C	70	GLU
1	C	71	LYS
1	C	75	LEU
1	C	77	ASP
1	C	92	VAL
1	C	93	THR
1	C	95	ARG
1	C	110	ARG

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Mol	Chain	Res	Type
1	C	113	GLU
1	C	157	PHE
1	C	158	GLU
2	D	44	ARG
2	D	49	ARG
2	D	68	LEU
2	D	69	ARG
2	D	91	ASN
2	D	111	VAL
2	D	115	LEU
2	D	132	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	48	HIS
1	A	53	HIS
1	A	69	GLN
1	A	103	ASN
1	A	156	ASN
1	A	196	GLN
1	A	199	HIS
2	B	84	GLN
2	B	91	ASN
2	B	92	HIS
1	C	10	GLN
1	C	53	HIS
1	C	69	GLN
1	C	103	ASN
2	D	84	GLN
2	D	91	ASN
2	D	92	HIS

5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	GNP	C	250	3	34,34,34	1.25	3 (8%)	47,54,54	0.94	1 (2%)
4	GNP	A	250	3	34,34,34	1.25	3 (8%)	47,54,54	0.93	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GNP	C	250	3	-	6/18/38/38	0/3/3/3
4	GNP	A	250	3	-	6/18/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	250	GNP	PB-O2B	-4.06	1.46	1.56
4	C	250	GNP	PG-O2G	-3.68	1.47	1.56
4	A	250	GNP	PB-O2B	-3.55	1.47	1.56
4	A	250	GNP	PG-O2G	-3.34	1.47	1.56
4	A	250	GNP	PA-O3A	2.86	1.62	1.59
4	C	250	GNP	PA-O3A	2.07	1.61	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	250	GNP	O3G-PG-O1G	-3.62	104.37	113.45
4	C	250	GNP	O3G-PG-O1G	-3.40	104.93	113.45

There are no chirality outliers.

All (12) torsion outliers are listed below:

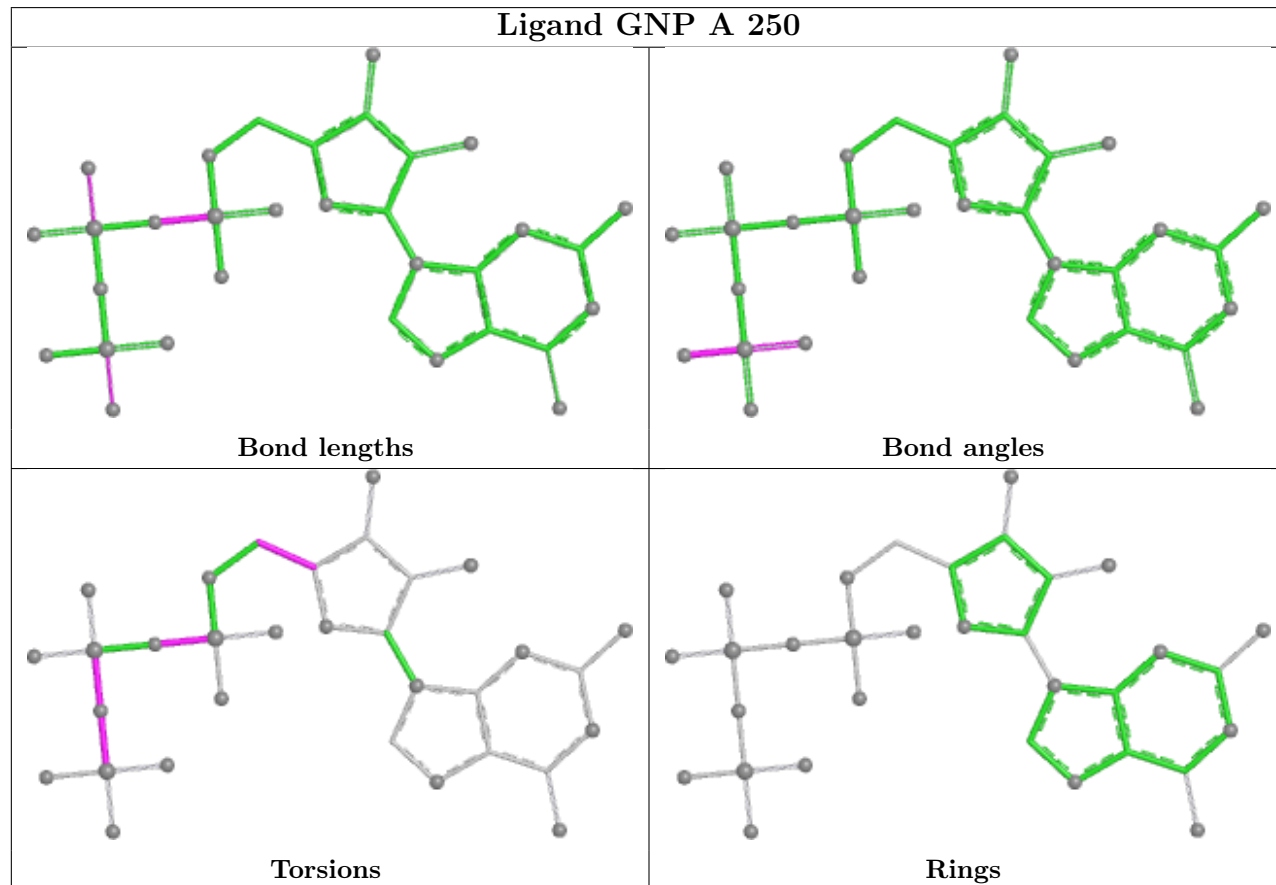
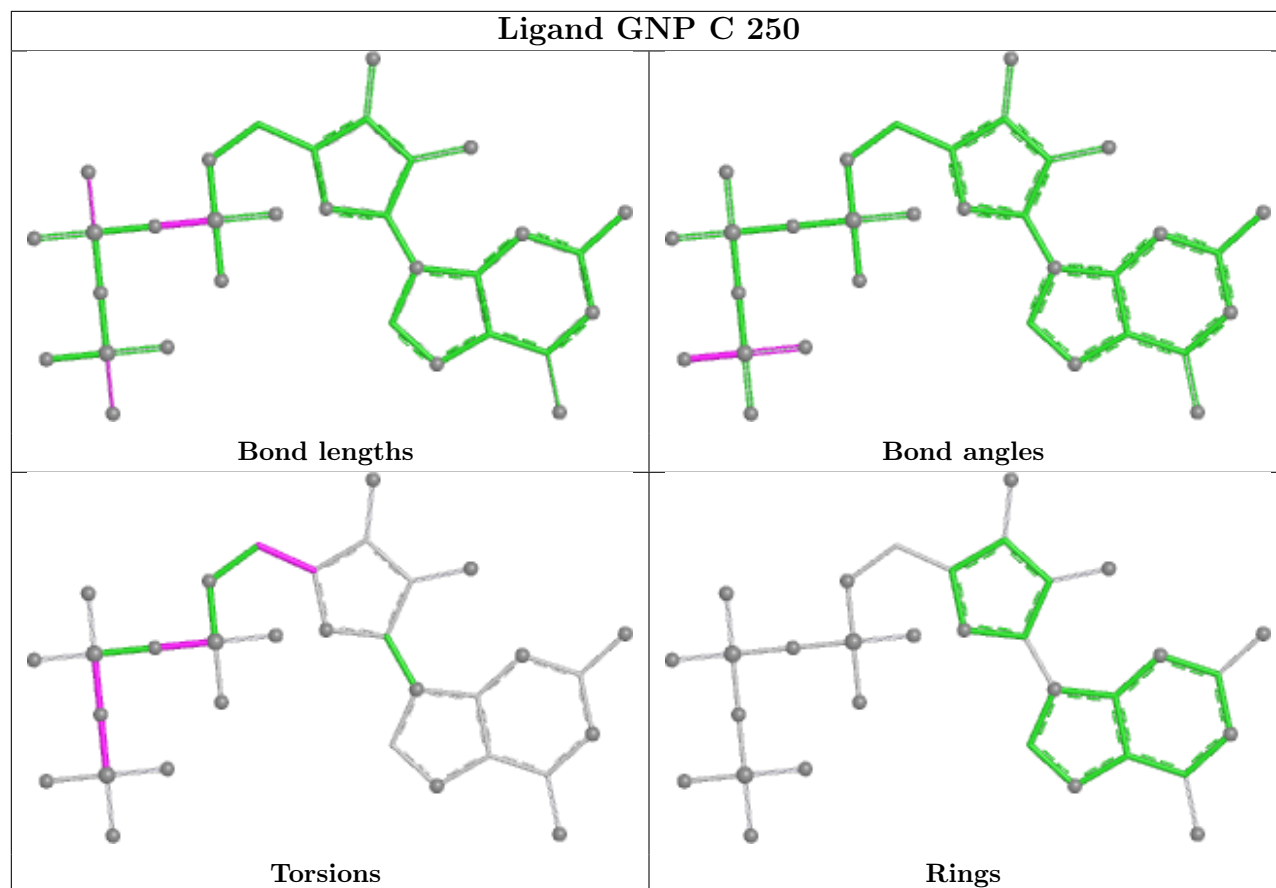
Mol	Chain	Res	Type	Atoms
4	A	250	GNP	PB-N3B-PG-O1G
4	A	250	GNP	PG-N3B-PB-O1B
4	C	250	GNP	PB-N3B-PG-O1G
4	C	250	GNP	PG-N3B-PB-O1B
4	A	250	GNP	O4'-C4'-C5'-O5'
4	C	250	GNP	O4'-C4'-C5'-O5'
4	C	250	GNP	C3'-C4'-C5'-O5'
4	A	250	GNP	C3'-C4'-C5'-O5'
4	C	250	GNP	PB-O3A-PA-O1A
4	A	250	GNP	PB-O3A-PA-O1A
4	A	250	GNP	PB-O3A-PA-O2A
4	C	250	GNP	PB-O3A-PA-O2A

There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	250	GNP	8	0
4	A	250	GNP	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	204/204 (100%)	-0.20	2 (0%) 79 74	17, 51, 93, 105	0
1	C	180/204 (88%)	-0.22	0 100 100	17, 49, 90, 101	0
2	B	134/134 (100%)	-0.23	0 100 100	19, 55, 89, 103	0
2	D	134/134 (100%)	-0.23	0 100 100	31, 59, 93, 105	0
All	All	652/676 (96%)	-0.22	2 (0%) 90 88	17, 53, 93, 105	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	190	ASP	2.6
1	A	194	ALA	2.2

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](#)

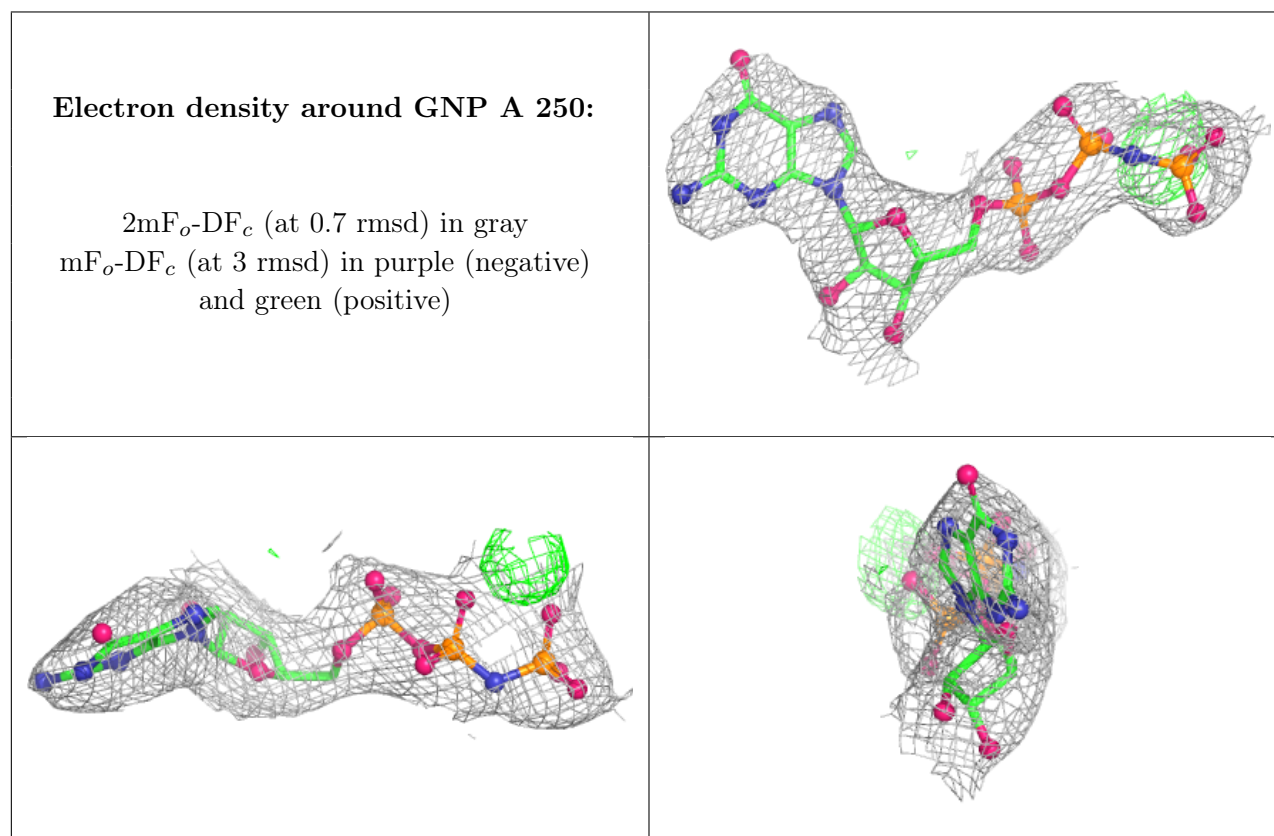
There are no oligosaccharides in this entry.

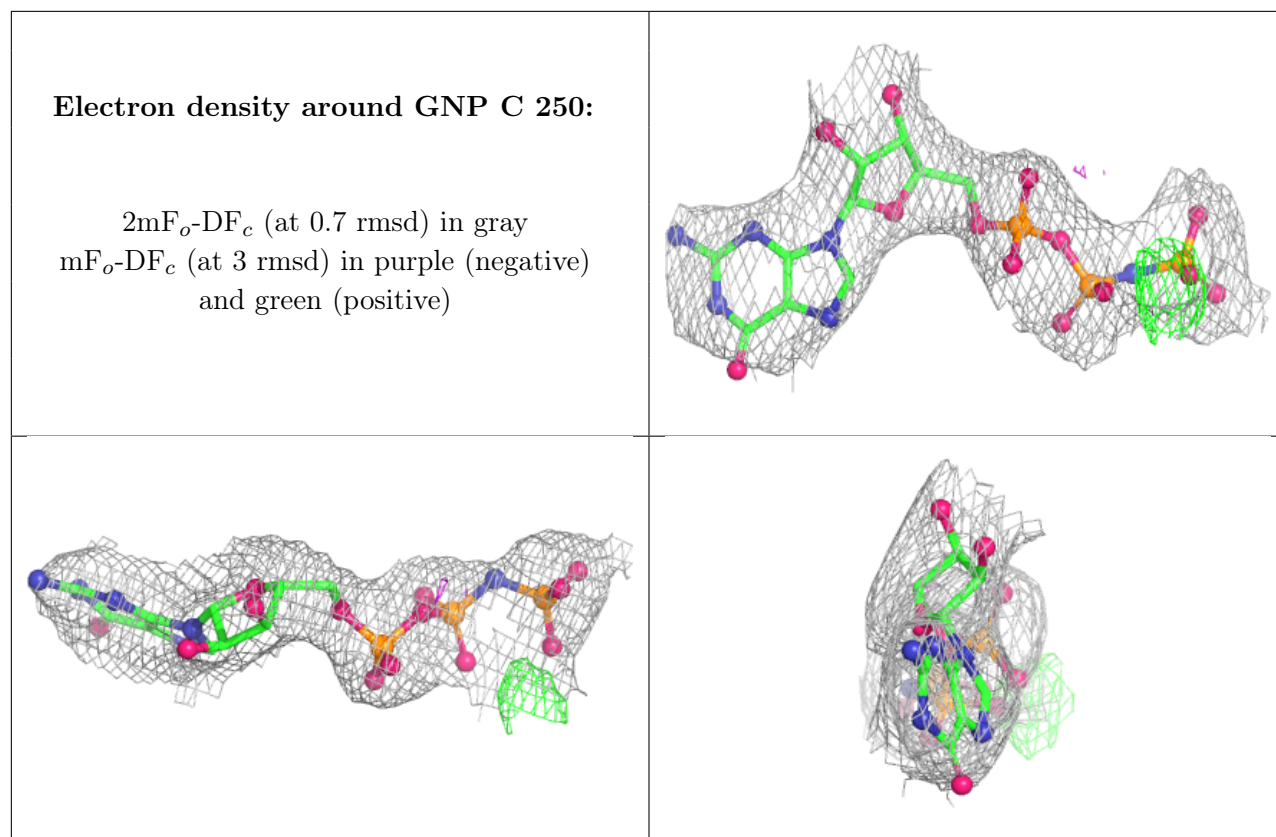
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	251	1/1	0.93	0.22	39,39,39,39	0
3	MG	C	251	1/1	0.96	0.17	44,44,44,44	0
4	GNP	A	250	32/32	0.96	0.07	14,43,65,67	0
4	GNP	C	250	32/32	0.96	0.07	9,46,61,66	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.