



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 05:54 pm BST

PDB ID : 1K5D  
Title : Crystal structure of Ran-GPPNHP-RanBP1-RanGAP complex  
Authors : Seewald, M.J.; Koerner, C.; Wittinghofer, A.; Vetter, I.R.  
Deposited on : 2001-10-10  
Resolution : 2.70 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

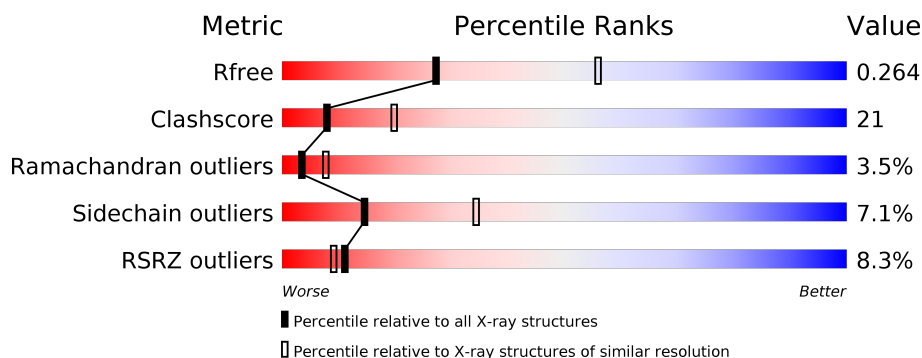
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	216	<div> <div>11%</div> <div> <div></div> <div>55%</div> <div>31%</div> <div>9%</div> <div>5%</div> </div> </div>
1	D	216	<div> <div>10%</div> <div> <div></div> <div>56%</div> <div>30%</div> <div>8%</div> <div>5%</div> </div> </div>
1	G	216	<div> <div>11%</div> <div> <div></div> <div>59%</div> <div>27%</div> <div>8%</div> <div>5%</div> </div> </div>
1	J	216	<div> <div>9%</div> <div> <div></div> <div>56%</div> <div>31%</div> <div>8%</div> <div>5%</div> </div> </div>
2	B	201	<div> <div>12%</div> <div> <div></div> <div>34%</div> <div>30%</div> <div>7%</div> <div>27%</div> </div> </div>
2	E	201	<div> <div>21%</div> <div> <div></div> <div>33%</div> <div>32%</div> <div>7%</div> <div>27%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	H	201	<div><div></div><div>12%</div><div>35%</div><div>30%</div><div>7%</div><div>27%</div></div>
2	K	201	<div><div></div><div>10%</div><div>35%</div><div>31%</div><div>6%</div><div>27%</div></div>
3	C	386	<div><div></div><div>%</div><div>60%</div><div>26%</div><div>•</div><div>11%</div></div>
3	F	386	<div><div></div><div>4%</div><div>64%</div><div>23%</div><div>•</div><div>11%</div></div>
3	I	386	<div><div></div><div>%</div><div>62%</div><div>25%</div><div>•</div><div>11%</div></div>
3	L	386	<div><div></div><div>3%</div><div>62%</div><div>24%</div><div>•</div><div>11%</div></div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22738 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 GTP-binding nuclear protein RAN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			
1	D	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			
1	G	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			
1	J	206	Total	C	N	O	S	0	0	0
			1652	1067	284	295	6			

- Molecule 2 is a protein called Ran-specific GTPase-activating protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			
2	E	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			
2	H	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			
2	K	146	Total	C	N	O	S	0	0	0
			1216	769	214	226	7			

- Molecule 3 is a protein called Ran GTPase activating protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			
3	F	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			
3	I	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			
3	L	344	Total	C	N	O	S	0	0	0
			2698	1699	469	522	8			

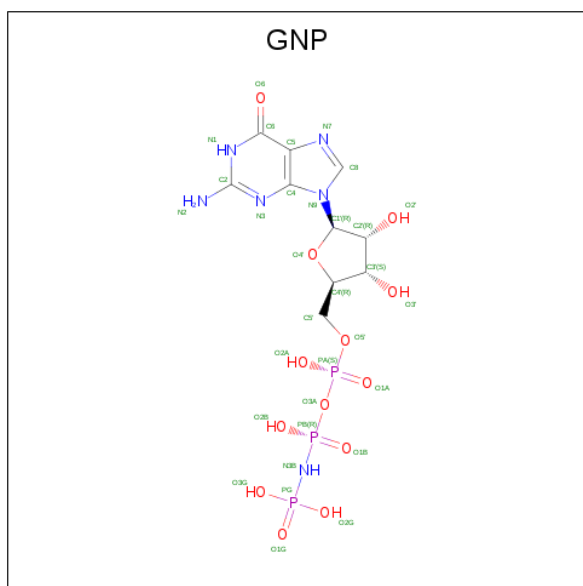
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2	ALA	SER	SEE REMARK 999	UNP P41391
F	2	ALA	SER	SEE REMARK 999	UNP P41391
I	2	ALA	SER	SEE REMARK 999	UNP P41391
L	2	ALA	SER	SEE REMARK 999	UNP P41391

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total Mg 1 1	0	0
4	J	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>13</sub>P<sub>3</sub>).



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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
5	J	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

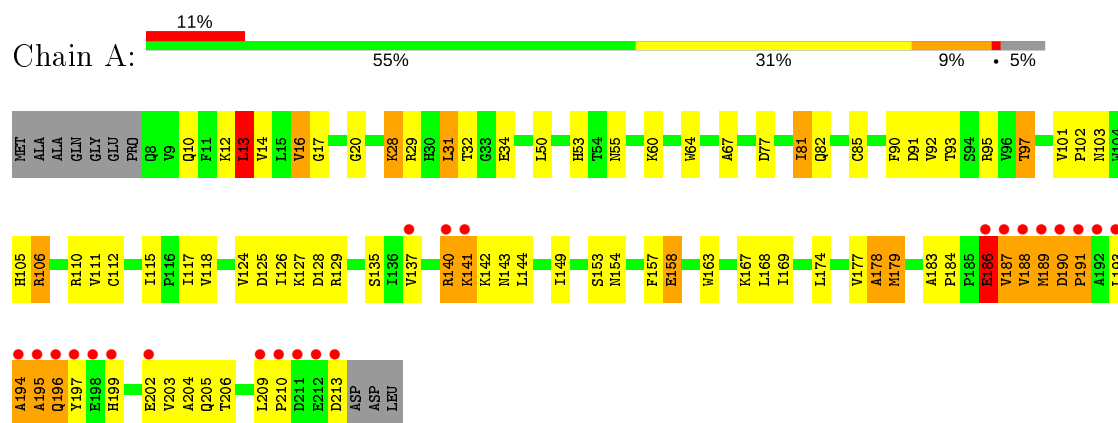
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	24	Total	O	0	0
			24	24		
6	B	3	Total	O	0	0
			3	3		
6	C	71	Total	O	0	0
			71	71		
6	D	29	Total	O	0	0
			29	29		
6	E	2	Total	O	0	0
			2	2		
6	F	47	Total	O	0	0
			47	47		
6	G	25	Total	O	0	0
			25	25		
6	H	5	Total	O	0	0
			5	5		
6	I	53	Total	O	0	0
			53	53		
6	J	31	Total	O	0	0
			31	31		
6	K	4	Total	O	0	0
			4	4		
6	L	48	Total	O	0	0
			48	48		

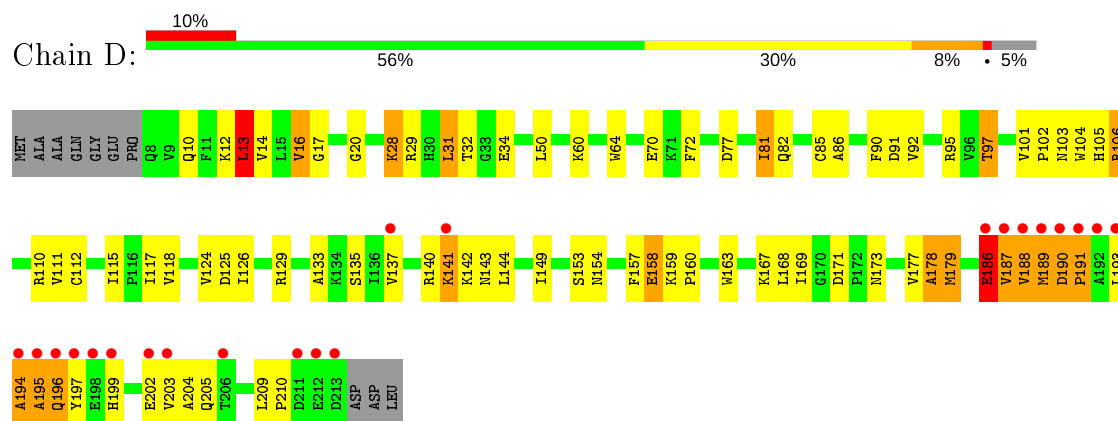
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

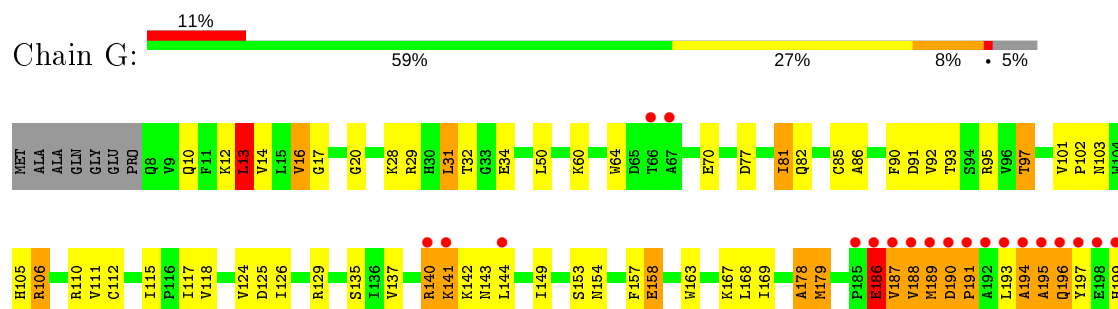
#### • Molecule 1: GTP-binding nuclear protein RAN

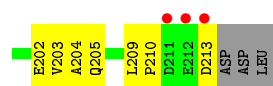


#### • Molecule 1: GTP-binding nuclear protein RAN

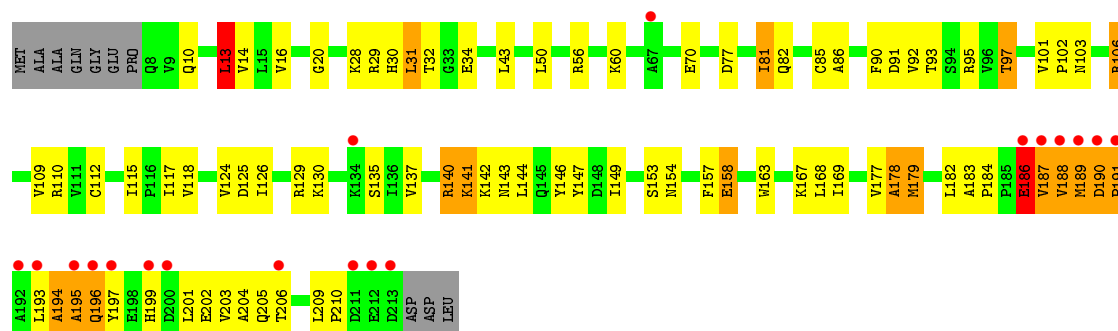


#### • Molecule 1: GTP-binding nuclear protein RAN

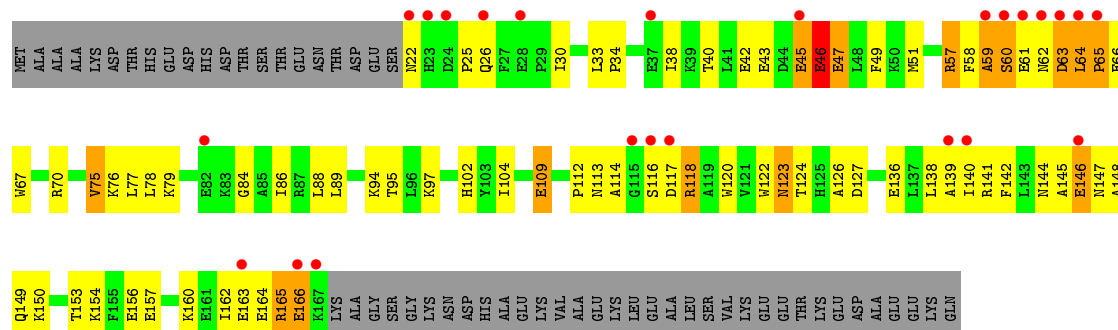




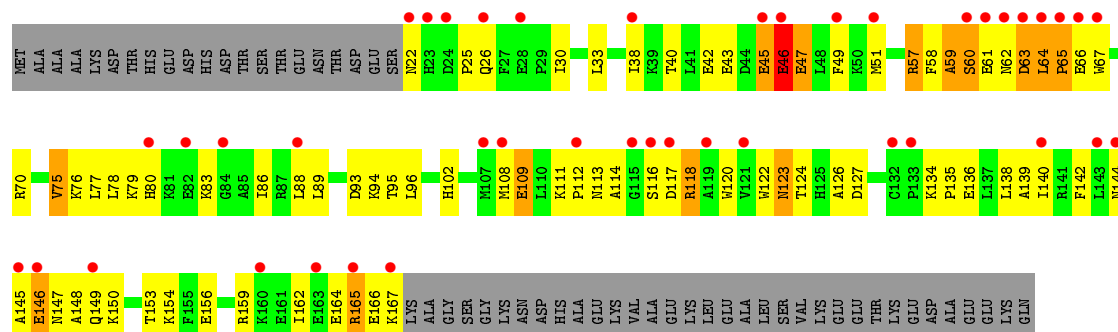
• Molecule 1: GTP-binding nuclear protein RAN



• Molecule 2: Ran-specific GTPase-activating protein

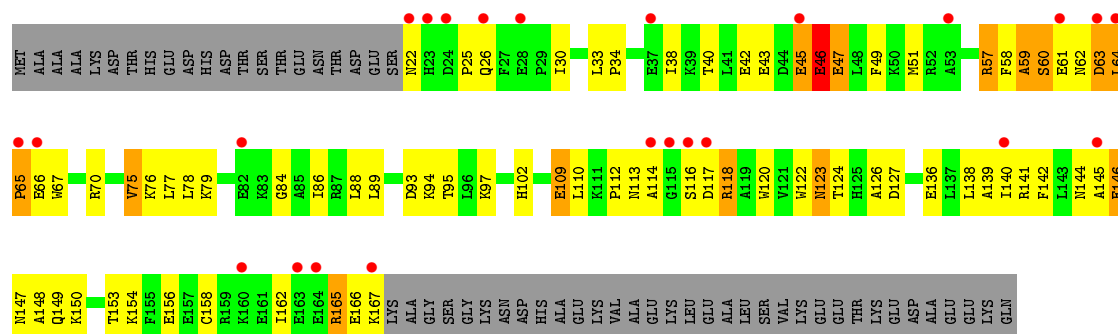


• Molecule 2: Ran-specific GTPase-activating protein

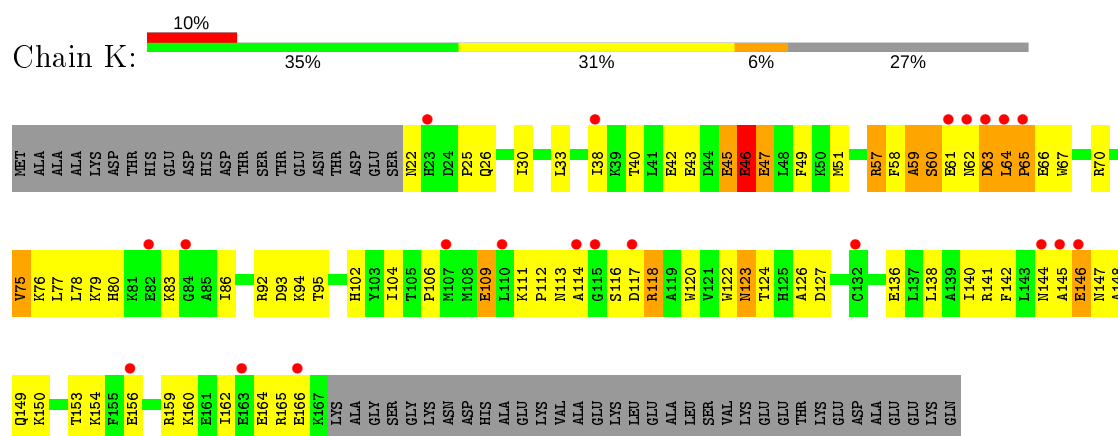


• Molecule 2: Ran-specific GTPase-activating protein

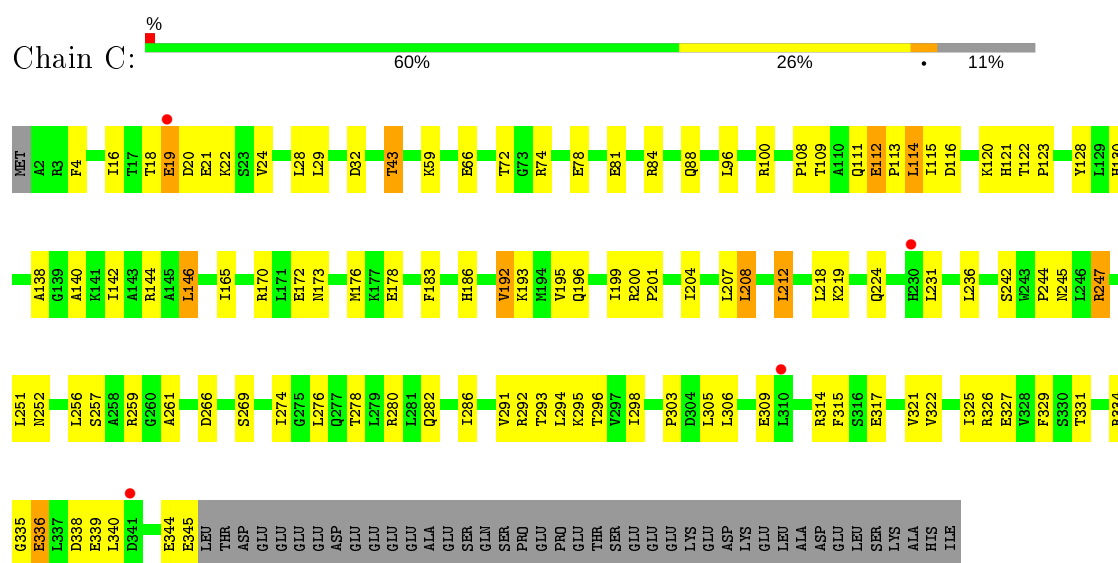




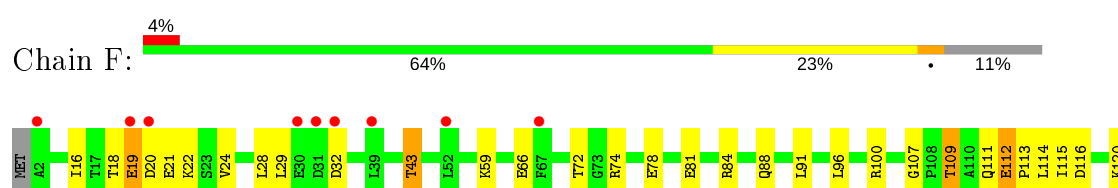
• Molecule 2: Ran-specific GTPase-activating protein

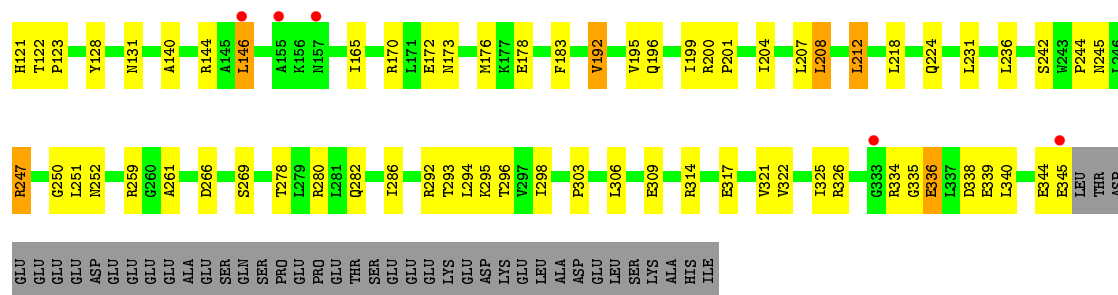


• Molecule 3: Ran GTPase activating protein 1

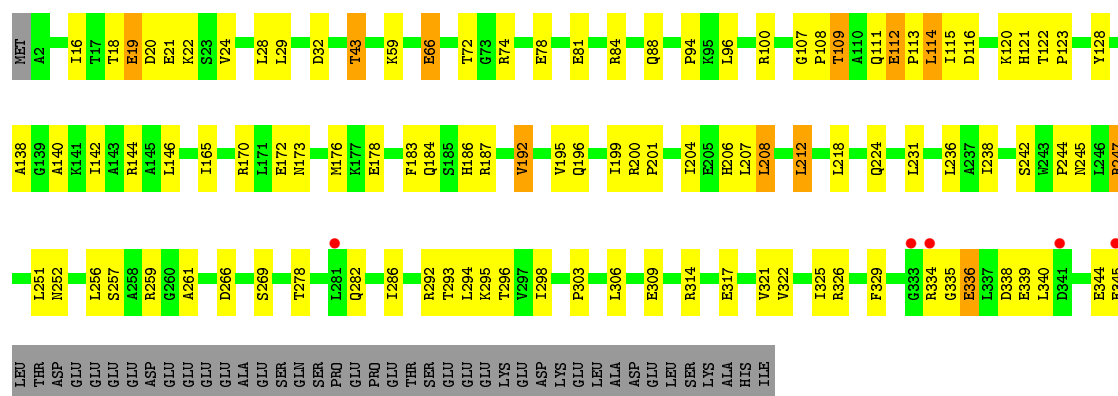


• Molecule 3: Ran GTPase activating protein 1

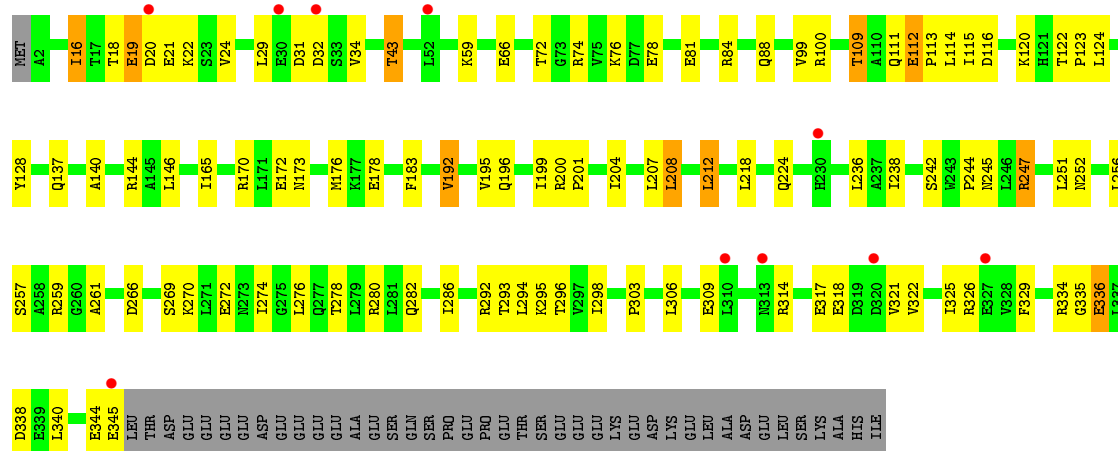




• Molecule 3: Ran GTPase activating protein 1



• Molecule 3: Ran GTPase activating protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.55Å 103.11Å 120.18Å 71.59° 80.55° 67.78°	Depositor
Resolution (Å)	20.00 – 2.70 20.07 – 2.41	Depositor EDS
% Data completeness (in resolution range)	98.0 (20.00-2.70) 96.3 (20.07-2.41)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.22 (at 2.41Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.237 , 0.267 0.237 , 0.264	Depositor DCC
$R_{free}$ test set	15265 reflections (9.59%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.9	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 55.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	22738	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.36% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.41	0/1693	0.65	1/2296 (0.0%)
1	D	0.41	0/1693	0.64	1/2296 (0.0%)
1	G	0.42	0/1693	0.64	1/2296 (0.0%)
1	J	0.43	0/1693	0.65	1/2296 (0.0%)
2	B	0.36	0/1242	0.62	0/1666
2	E	0.34	0/1242	0.61	0/1666
2	H	0.36	0/1242	0.63	0/1666
2	K	0.36	0/1242	0.62	0/1666
3	C	0.41	0/2737	0.66	0/3697
3	F	0.39	0/2737	0.65	0/3697
3	I	0.39	0/2737	0.66	0/3697
3	L	0.39	0/2737	0.66	0/3697
All	All	0.39	0/22688	0.64	4/30636 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	13	LEU	CA-CB-CG	5.55	128.07	115.30
1	J	13	LEU	CA-CB-CG	5.54	128.03	115.30
1	A	13	LEU	CA-CB-CG	5.28	127.43	115.30
1	D	13	LEU	CA-CB-CG	5.26	127.41	115.30

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	1652	0	1659	76	0
1	D	1652	0	1659	77	0
1	G	1652	0	1659	71	0
1	J	1652	0	1659	89	0
2	B	1216	0	1208	80	0
2	E	1216	0	1208	85	0
2	H	1216	0	1208	79	0
2	K	1216	0	1208	88	0
3	C	2698	0	2733	103	0
3	F	2698	0	2733	85	0
3	I	2698	0	2733	98	0
3	L	2698	0	2733	93	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	G	1	0	0	0	0
4	J	1	0	0	0	0
5	A	32	0	13	2	0
5	D	32	0	13	3	0
5	G	32	0	13	3	0
5	J	32	0	13	6	0
6	A	24	0	0	4	0
6	B	3	0	0	0	0
6	C	71	0	0	17	0
6	D	29	0	0	5	0
6	E	2	0	0	0	0
6	F	47	0	0	7	0
6	G	25	0	0	4	0
6	H	5	0	0	0	0
6	I	53	0	0	8	0
6	J	31	0	0	6	0
6	K	4	0	0	1	0
6	L	48	0	0	5	0
All	All	22738	0	22452	964	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 21.

All (964) 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)
3:C:165:ILE:HA	6:C:445:HOH:O	1.52	1.09
5:J:4250:GNP:PG	6:J:4252:HOH:O	2.14	1.03
1:A:91:ASP:H	1:A:97:THR:HG21	1.22	1.01
1:G:91:ASP:H	1:G:97:THR:HG21	1.21	1.00
1:J:91:ASP:H	1:J:97:THR:HG21	1.23	0.99
1:D:91:ASP:H	1:D:97:THR:HG21	1.24	0.98
2:H:86:ILE:HB	2:H:162:ILE:HD11	1.49	0.94
2:E:86:ILE:HB	2:E:162:ILE:HD11	1.46	0.93
2:E:42:GLU:O	2:E:45:GLU:HB3	1.69	0.93
2:B:42:GLU:O	2:B:45:GLU:HB3	1.70	0.91
2:H:42:GLU:O	2:H:45:GLU:HB3	1.68	0.91
2:K:42:GLU:O	2:K:45:GLU:HB3	1.71	0.91
1:J:158:GLU:HG2	2:K:94:LYS:HB3	1.52	0.90
1:D:158:GLU:HG2	2:E:94:LYS:HB3	1.55	0.88
1:J:206:THR:O	2:K:114:ALA:HB2	1.74	0.88
1:A:90:PHE:HB2	1:A:97:THR:HG23	1.57	0.86
2:B:86:ILE:HB	2:B:162:ILE:HD11	1.58	0.85
1:A:158:GLU:HG2	2:B:94:LYS:HB3	1.59	0.84
5:J:4250:GNP:O2G	6:J:4252:HOH:O	1.93	0.83
1:J:209:LEU:HD23	2:K:113:ASN:ND2	1.93	0.83
3:C:317:GLU:HG2	3:C:340:LEU:HB2	1.61	0.83
1:J:90:PHE:HB2	1:J:97:THR:HG23	1.62	0.81
1:G:90:PHE:HB2	1:G:97:THR:HG23	1.61	0.80
3:C:176:MET:HE3	3:C:207:LEU:HB2	1.63	0.80
1:G:91:ASP:H	1:G:97:THR:CG2	1.95	0.80
3:I:317:GLU:HG2	3:I:340:LEU:HB2	1.62	0.80
3:I:176:MET:HE3	3:I:207:LEU:HB2	1.63	0.80
1:D:90:PHE:HB2	1:D:97:THR:HG23	1.62	0.79
3:F:317:GLU:HG2	3:F:340:LEU:HB2	1.64	0.79
2:H:124:THR:HG22	2:H:126:ALA:H	1.47	0.79
3:L:176:MET:HE3	3:L:207:LEU:HB2	1.64	0.79
3:C:173:ASN:HD21	3:C:200:ARG:H	1.31	0.78
1:J:205:GLN:O	2:K:114:ALA:N	2.15	0.78
2:B:124:THR:HG22	2:B:126:ALA:H	1.49	0.78
1:D:143:ASN:ND2	2:E:25:PRO:HB3	1.99	0.78
1:G:158:GLU:HG2	2:H:94:LYS:HB3	1.64	0.77
1:J:205:GLN:HB2	2:K:112:PRO:O	1.84	0.77
2:K:124:THR:HG22	2:K:126:ALA:H	1.49	0.77
3:L:317:GLU:HG2	3:L:340:LEU:HB2	1.65	0.77
1:G:91:ASP:N	1:G:97:THR:HG21	1.98	0.77
1:J:91:ASP:N	1:J:97:THR:HG21	1.99	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:173:ASN:ND2	3:C:200:ARG:H	1.83	0.76
6:G:3266:HOH:O	3:I:72:THR:HG21	1.84	0.76
3:I:72:THR:HG23	6:I:431:HOH:O	1.84	0.76
1:J:91:ASP:H	1:J:97:THR:CG2	1.98	0.76
1:A:91:ASP:N	1:A:97:THR:HG21	2.00	0.76
3:F:173:ASN:HD21	3:F:200:ARG:H	1.33	0.76
1:J:143:ASN:HA	2:K:22:ASN:ND2	1.99	0.75
2:E:124:THR:HG22	2:E:126:ALA:H	1.51	0.75
3:F:173:ASN:ND2	3:F:200:ARG:H	1.84	0.75
3:F:176:MET:HE3	3:F:207:LEU:HB2	1.67	0.75
1:A:91:ASP:H	1:A:97:THR:CG2	2.00	0.75
1:D:91:ASP:H	1:D:97:THR:CG2	1.99	0.75
1:A:186:GLU:CD	1:A:187:VAL:H	1.90	0.74
3:L:259:ARG:NH1	3:L:259:ARG:HB3	2.02	0.74
1:J:186:GLU:CD	1:J:187:VAL:H	1.91	0.74
3:C:193:LYS:HB2	6:C:445:HOH:O	1.85	0.74
3:I:173:ASN:ND2	3:I:200:ARG:H	1.85	0.74
3:F:259:ARG:HB3	3:F:259:ARG:NH1	2.02	0.74
3:I:259:ARG:NH1	3:I:259:ARG:HB3	2.02	0.74
3:C:259:ARG:HB3	3:C:259:ARG:NH1	2.02	0.74
1:D:91:ASP:N	1:D:97:THR:HG21	2.00	0.74
1:G:20:GLY:H	5:G:3250:GNP:HNB3	1.34	0.73
1:G:186:GLU:CD	1:G:187:VAL:H	1.90	0.73
3:L:173:ASN:ND2	3:L:200:ARG:H	1.87	0.73
3:C:176:MET:CE	3:C:207:LEU:HB2	2.19	0.73
1:D:186:GLU:CD	1:D:187:VAL:H	1.92	0.73
3:I:173:ASN:HD21	3:I:200:ARG:H	1.36	0.72
1:A:20:GLY:H	5:A:1250:GNP:HNB3	1.38	0.71
2:E:46:GLU:HB2	2:E:79:LYS:O	1.91	0.71
3:L:43:THR:HG22	3:L:74:ARG:HE	1.56	0.71
1:D:70:GLU:HA	6:F:406:HOH:O	1.90	0.70
1:A:209:LEU:HD23	2:B:113:ASN:ND2	2.06	0.70
1:J:143:ASN:ND2	2:K:25:PRO:HB3	2.06	0.70
1:D:20:GLY:H	5:D:2250:GNP:HNB3	1.40	0.70
3:F:112:GLU:HB2	6:F:425:HOH:O	1.92	0.70
2:H:46:GLU:HB2	2:H:79:LYS:O	1.92	0.70
1:J:29:ARG:HD3	1:J:154:ASN:OD1	1.92	0.70
3:I:43:THR:HG22	3:I:74:ARG:HE	1.57	0.70
2:K:46:GLU:HB2	2:K:79:LYS:O	1.92	0.70
2:K:59:ALA:O	2:K:60:SER:HB2	1.93	0.69
2:H:146:GLU:O	2:H:150:LYS:HG3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:146:GLU:O	2:E:150:LYS:HG3	1.91	0.69
2:H:59:ALA:O	2:H:60:SER:HB2	1.92	0.69
1:J:20:GLY:H	5:J:4250:GNP:HNB3	1.41	0.69
2:B:146:GLU:O	2:B:150:LYS:HG3	1.93	0.69
3:L:32:ASP:HA	3:L:59:LYS:HE2	1.74	0.69
2:E:59:ALA:O	2:E:60:SER:HB2	1.92	0.68
3:F:20:ASP:O	3:F:22:LYS:N	2.26	0.68
1:J:189:MET:O	1:J:190:ASP:HB2	1.91	0.68
1:A:189:MET:O	1:A:190:ASP:HB2	1.91	0.68
2:B:46:GLU:HB2	2:B:79:LYS:O	1.94	0.68
1:D:189:MET:O	1:D:190:ASP:HB2	1.92	0.68
5:D:2250:GNP:PG	6:D:2252:HOH:O	2.51	0.68
2:E:75:VAL:HG21	2:E:140:ILE:HD11	1.76	0.68
3:F:170:ARG:NH1	6:F:426:HOH:O	2.22	0.68
1:G:143:ASN:ND2	2:H:25:PRO:HB3	2.08	0.68
1:G:189:MET:O	1:G:190:ASP:HB2	1.92	0.68
3:L:173:ASN:HD21	3:L:200:ARG:H	1.42	0.68
3:I:176:MET:CE	3:I:207:LEU:HB2	2.23	0.68
2:K:146:GLU:O	2:K:150:LYS:HG3	1.94	0.68
2:B:59:ALA:O	2:B:60:SER:HB2	1.93	0.67
1:D:29:ARG:HD3	1:D:154:ASN:OD1	1.94	0.67
2:B:75:VAL:HG21	2:B:140:ILE:HD11	1.77	0.67
3:F:43:THR:HG22	3:F:74:ARG:HE	1.59	0.67
2:K:75:VAL:HG21	2:K:140:ILE:HD11	1.75	0.67
1:G:29:ARG:HD3	1:G:154:ASN:OD1	1.94	0.67
3:F:204:ILE:HG23	3:F:208:LEU:CD2	2.25	0.67
3:F:32:ASP:HA	3:F:59:LYS:HE2	1.77	0.67
1:G:169:ILE:HD12	2:H:33:LEU:HD12	1.75	0.67
3:L:204:ILE:HG23	3:L:208:LEU:CD2	2.25	0.67
3:L:176:MET:CE	3:L:207:LEU:HB2	2.25	0.66
3:C:20:ASP:O	3:C:22:LYS:N	2.28	0.66
1:D:32:THR:HG22	1:D:34:GLU:H	1.59	0.66
3:L:20:ASP:O	3:L:22:LYS:N	2.28	0.66
2:B:117:ASP:OD2	2:B:145:ALA:HB2	1.95	0.66
1:G:32:THR:HG22	1:G:34:GLU:H	1.61	0.66
3:I:192:VAL:HG12	3:I:218:LEU:HD11	1.76	0.66
2:B:123:ASN:HD22	2:B:124:THR:H	1.44	0.66
2:E:62:ASN:O	2:E:64:LEU:HD22	1.96	0.66
3:C:327:GLU:HG3	1:J:109:VAL:HG21	1.76	0.66
2:E:59:ALA:HB2	2:E:65:PRO:HA	1.78	0.66
2:K:59:ALA:HB2	2:K:65:PRO:HA	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:123:ASN:HD22	2:E:124:THR:H	1.44	0.65
1:A:13:LEU:HB2	1:A:85:CYS:SG	2.36	0.65
3:F:192:VAL:HG12	3:F:218:LEU:HD11	1.76	0.65
3:L:192:VAL:HG12	3:L:218:LEU:HD11	1.78	0.65
3:I:204:ILE:HG23	3:I:208:LEU:CD2	2.26	0.65
2:K:117:ASP:OD2	2:K:145:ALA:HB2	1.96	0.65
3:C:176:MET:HE1	3:C:207:LEU:HD22	1.77	0.65
2:E:122:TRP:HZ3	2:E:140:ILE:HG22	1.62	0.65
1:J:32:THR:HG22	1:J:34:GLU:H	1.61	0.65
3:C:43:THR:HG22	3:C:74:ARG:HE	1.61	0.65
3:I:32:ASP:HA	3:I:59:LYS:HE2	1.78	0.65
2:B:123:ASN:ND2	2:B:124:THR:H	1.95	0.65
1:D:143:ASN:HA	2:E:22:ASN:ND2	2.11	0.65
1:A:92:VAL:HG13	1:A:129:ARG:HG3	1.79	0.65
2:E:123:ASN:ND2	2:E:124:THR:H	1.95	0.65
2:H:46:GLU:HG3	2:H:79:LYS:HB3	1.77	0.65
2:B:49:PHE:HB3	2:B:77:LEU:HD12	1.79	0.65
2:K:62:ASN:O	2:K:64:LEU:HD22	1.97	0.65
1:A:143:ASN:ND2	2:B:25:PRO:HB3	2.12	0.65
2:H:123:ASN:ND2	2:H:124:THR:H	1.95	0.65
2:K:46:GLU:HG3	2:K:79:LYS:HB3	1.79	0.65
1:A:29:ARG:HD3	1:A:154:ASN:OD1	1.96	0.65
1:A:53:HIS:ND1	6:A:1269:HOH:O	2.28	0.65
2:B:62:ASN:O	2:B:64:LEU:HD22	1.97	0.65
3:F:200:ARG:HB3	3:F:201:PRO:CD	2.27	0.65
2:H:75:VAL:HG21	2:H:140:ILE:HD11	1.78	0.65
2:H:123:ASN:HD22	2:H:124:THR:H	1.45	0.64
3:I:20:ASP:O	3:I:22:LYS:N	2.31	0.64
3:C:200:ARG:HB3	3:C:201:PRO:CD	2.28	0.64
2:E:117:ASP:OD2	2:E:145:ALA:HB2	1.96	0.64
3:I:187:ARG:NH1	3:L:272:GLU:HG3	2.11	0.64
3:F:176:MET:CE	3:F:207:LEU:HB2	2.27	0.64
2:H:117:ASP:OD2	2:H:145:ALA:HB2	1.97	0.64
1:J:193:LEU:HD12	1:J:193:LEU:H	1.62	0.64
2:H:59:ALA:HB2	2:H:65:PRO:HA	1.80	0.64
2:B:59:ALA:HB2	2:B:65:PRO:HA	1.79	0.64
3:C:112:GLU:HB2	6:C:388:HOH:O	1.98	0.64
3:F:252:ASN:ND2	3:F:282:GLN:H	1.95	0.64
2:B:122:TRP:HZ3	2:B:140:ILE:HG22	1.62	0.63
2:B:46:GLU:HG3	2:B:79:LYS:HB3	1.80	0.63
3:C:204:ILE:HG23	3:C:208:LEU:CD2	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:192:VAL:HG12	3:C:218:LEU:HD11	1.80	0.63
2:H:167:LYS:N	2:H:167:LYS:HD2	2.13	0.63
3:C:32:ASP:HA	3:C:59:LYS:HE2	1.79	0.63
3:I:176:MET:HE1	3:I:207:LEU:HD22	1.78	0.63
3:L:112:GLU:HB2	6:L:423:HOH:O	1.98	0.63
6:D:2277:HOH:O	3:F:109:THR:CG2	2.47	0.63
1:A:169:ILE:HD12	2:B:33:LEU:HD12	1.81	0.63
1:D:92:VAL:HG13	1:D:129:ARG:HG3	1.81	0.63
3:L:200:ARG:HB3	3:L:201:PRO:CD	2.28	0.63
1:A:127:LYS:HB3	6:A:1262:HOH:O	1.98	0.63
1:G:13:LEU:HB2	1:G:85:CYS:SG	2.39	0.63
1:A:193:LEU:H	1:A:193:LEU:HD12	1.64	0.63
1:A:92:VAL:CG1	1:A:129:ARG:HG3	2.29	0.62
1:G:126:ILE:HD11	5:G:3250:GNP:N2	2.14	0.62
2:K:104:ILE:O	2:K:162:ILE:HD13	1.99	0.62
2:E:49:PHE:HB3	2:E:77:LEU:HD12	1.79	0.62
2:K:123:ASN:HD22	2:K:124:THR:H	1.47	0.62
2:E:46:GLU:HG3	2:E:79:LYS:HB3	1.80	0.62
1:G:153:SER:O	1:G:154:ASN:HB2	1.99	0.62
2:E:47:GLU:HA	2:E:78:LEU:HD23	1.82	0.62
1:A:153:SER:O	1:A:154:ASN:HB2	1.98	0.62
3:F:200:ARG:HB3	3:F:201:PRO:HD2	1.81	0.62
2:K:136:GLU:HG2	2:K:138:LEU:HD21	1.80	0.62
3:L:176:MET:HE1	3:L:207:LEU:HD22	1.80	0.62
1:A:32:THR:HG22	1:A:34:GLU:H	1.65	0.62
2:B:47:GLU:HA	2:B:78:LEU:HD23	1.81	0.62
2:K:47:GLU:HA	2:K:78:LEU:HD23	1.80	0.62
1:D:143:ASN:HD21	2:E:25:PRO:HB3	1.64	0.62
2:H:62:ASN:O	2:H:64:LEU:HD22	1.99	0.62
1:D:189:MET:HB2	1:D:193:LEU:HD22	1.82	0.62
1:J:153:SER:O	1:J:154:ASN:HB2	2.00	0.61
3:C:200:ARG:HB3	3:C:201:PRO:HD2	1.82	0.61
1:D:209:LEU:HD23	2:E:113:ASN:ND2	2.15	0.61
1:G:117:ILE:HB	1:G:144:LEU:HD22	1.83	0.61
3:C:193:LYS:N	6:C:445:HOH:O	2.27	0.61
2:B:136:GLU:HG2	2:B:138:LEU:HD21	1.81	0.61
3:I:112:GLU:HB2	6:I:425:HOH:O	2.00	0.61
1:J:77:ASP:OD2	1:J:110:ARG:NH2	2.34	0.61
1:J:169:ILE:HD12	2:K:33:LEU:HD12	1.83	0.61
3:F:111:GLN:O	3:F:115:ILE:HG13	2.01	0.61
2:H:136:GLU:HG2	2:H:138:LEU:HD21	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:144:ASN:HB2	2:E:146:GLU:HG3	1.83	0.61
2:K:92:ARG:HD2	6:K:202:HOH:O	2.00	0.61
1:D:126:ILE:HD11	5:D:2250:GNP:N2	2.15	0.61
3:F:176:MET:HE1	3:F:207:LEU:HD22	1.83	0.61
1:G:193:LEU:H	1:G:193:LEU:HD12	1.64	0.61
2:E:136:GLU:HG2	2:E:138:LEU:HD21	1.83	0.61
1:G:92:VAL:HG13	1:G:129:ARG:HG3	1.82	0.61
2:H:47:GLU:HA	2:H:78:LEU:HD23	1.82	0.61
1:D:92:VAL:CG1	1:D:129:ARG:HG3	2.30	0.61
3:L:335:GLY:O	3:L:336:GLU:HB2	1.99	0.61
2:K:122:TRP:HZ3	2:K:140:ILE:HG22	1.65	0.60
2:K:144:ASN:HB2	2:K:146:GLU:HG3	1.83	0.60
1:J:143:ASN:HA	2:K:22:ASN:HD22	1.64	0.60
2:B:144:ASN:HB2	2:B:146:GLU:HG3	1.83	0.60
1:D:117:ILE:HB	1:D:144:LEU:HD22	1.82	0.60
3:I:200:ARG:HB3	3:I:201:PRO:CD	2.31	0.60
2:K:49:PHE:HB3	2:K:77:LEU:HD12	1.83	0.60
2:H:144:ASN:HB2	2:H:146:GLU:HG3	1.84	0.60
1:A:117:ILE:HB	1:A:144:LEU:HD22	1.84	0.60
2:H:49:PHE:HB3	2:H:77:LEU:HD12	1.83	0.60
3:I:184:GLN:HE22	3:L:270:LYS:NZ	2.00	0.60
2:B:43:GLU:C	2:B:45:GLU:H	2.03	0.60
1:D:13:LEU:HD12	1:D:13:LEU:C	2.22	0.60
2:E:167:LYS:HD2	2:E:167:LYS:N	2.16	0.60
3:I:116:ASP:OD2	3:I:120:LYS:HE2	2.02	0.60
3:I:200:ARG:HB3	3:I:201:PRO:HD2	1.83	0.60
1:D:193:LEU:H	1:D:193:LEU:HD12	1.66	0.60
1:G:101:VAL:HB	1:G:102:PRO:HD3	1.84	0.59
2:H:122:TRP:HZ3	2:H:140:ILE:HG22	1.66	0.59
3:I:252:ASN:ND2	3:I:282:GLN:H	2.00	0.59
1:J:101:VAL:HB	1:J:102:PRO:HD3	1.84	0.59
1:A:168:LEU:HD22	2:B:30:ILE:HD12	1.84	0.59
2:K:123:ASN:ND2	2:K:124:THR:H	1.99	0.59
1:D:153:SER:O	1:D:154:ASN:HB2	2.01	0.59
3:L:200:ARG:HB3	3:L:201:PRO:HD2	1.85	0.59
3:L:252:ASN:ND2	3:L:282:GLN:H	2.01	0.59
1:A:189:MET:HB2	1:A:193:LEU:HD22	1.83	0.59
2:B:109:GLU:CD	2:B:109:GLU:H	2.06	0.59
2:E:43:GLU:C	2:E:45:GLU:H	2.05	0.59
2:K:109:GLU:CD	2:K:109:GLU:H	2.06	0.59
3:C:140:ALA:O	3:C:144:ARG:HG3	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:168:LEU:HD22	2:H:30:ILE:HD12	1.85	0.59
2:H:43:GLU:C	2:H:45:GLU:H	2.04	0.59
1:J:92:VAL:HG13	1:J:129:ARG:HG3	1.84	0.59
2:H:62:ASN:O	2:H:63:ASP:HB2	2.02	0.58
3:I:140:ALA:O	3:I:144:ARG:HG3	2.03	0.58
2:E:109:GLU:H	2:E:109:GLU:CD	2.06	0.58
1:D:169:ILE:HD12	2:E:33:LEU:HD12	1.85	0.58
3:F:116:ASP:OD2	3:F:120:LYS:HE2	2.03	0.58
3:C:192:VAL:CG1	3:C:218:LEU:HD11	2.33	0.58
3:F:335:GLY:O	3:F:336:GLU:HB2	2.02	0.58
1:J:189:MET:HB2	1:J:193:LEU:HD22	1.84	0.58
1:G:92:VAL:CG1	1:G:129:ARG:HG3	2.33	0.58
3:I:111:GLN:O	3:I:115:ILE:HG13	2.03	0.58
3:I:192:VAL:CG1	3:I:218:LEU:HD11	2.33	0.58
1:A:101:VAL:HB	1:A:102:PRO:HD3	1.84	0.58
1:G:189:MET:HB2	1:G:193:LEU:HD22	1.85	0.58
3:C:331:THR:HG21	1:J:142:LYS:HA	1.85	0.58
1:A:126:ILE:HD11	5:A:1250:GNP:N2	2.18	0.58
3:C:219:LYS:NZ	6:C:436:HOH:O	2.35	0.58
2:E:75:VAL:HG21	2:E:140:ILE:CD1	2.33	0.58
3:L:116:ASP:OD2	3:L:120:LYS:HE2	2.03	0.58
1:A:190:ASP:H	1:A:193:LEU:HD13	1.69	0.58
2:E:62:ASN:O	2:E:63:ASP:HB2	2.04	0.58
1:J:70:GLU:HA	6:L:411:HOH:O	2.03	0.58
2:K:59:ALA:HB2	2:K:66:GLU:H	1.69	0.58
3:L:18:THR:HG22	3:L:21:GLU:OE1	2.04	0.58
2:B:62:ASN:O	2:B:63:ASP:HB2	2.03	0.58
2:K:62:ASN:HB3	2:K:64:LEU:HD22	1.86	0.58
1:D:77:ASP:OD2	1:D:110:ARG:NH2	2.36	0.58
2:H:109:GLU:H	2:H:109:GLU:CD	2.06	0.58
1:J:56:ARG:NH1	2:K:33:LEU:O	2.36	0.58
2:B:75:VAL:HG21	2:B:140:ILE:CD1	2.34	0.57
3:I:344:GLU:HG2	3:I:345:GLU:N	2.19	0.57
3:C:112:GLU:CB	3:C:113:PRO:HD3	2.35	0.57
1:D:190:ASP:H	1:D:193:LEU:HD13	1.68	0.57
1:G:70:GLU:HA	6:I:391:HOH:O	2.04	0.57
1:J:92:VAL:CG1	1:J:129:ARG:HG3	2.34	0.57
3:F:192:VAL:CG1	3:F:218:LEU:HD11	2.34	0.57
3:L:112:GLU:CB	3:L:113:PRO:HD3	2.34	0.57
3:C:344:GLU:HG2	3:C:345:GLU:N	2.20	0.57
1:J:190:ASP:H	1:J:193:LEU:HD13	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:4250:GNP:O3G	6:J:4252:HOH:O	2.16	0.57
2:K:43:GLU:C	2:K:45:GLU:H	2.05	0.57
1:A:31:LEU:HB3	1:A:50:LEU:CD2	2.35	0.57
3:C:335:GLY:O	3:C:336:GLU:HB2	2.05	0.57
1:G:143:ASN:HA	2:H:22:ASN:ND2	2.20	0.57
2:K:62:ASN:O	2:K:63:ASP:HB2	2.04	0.57
3:L:344:GLU:HG2	3:L:345:GLU:N	2.19	0.57
2:K:86:ILE:HB	2:K:162:ILE:HD11	1.86	0.57
3:L:192:VAL:CG1	3:L:218:LEU:HD11	2.35	0.57
2:B:62:ASN:HB3	2:B:64:LEU:HD22	1.87	0.57
2:E:122:TRP:CZ3	2:E:140:ILE:HG22	2.40	0.57
2:H:63:ASP:C	2:H:64:LEU:HD13	2.26	0.57
3:F:112:GLU:CB	3:F:113:PRO:HD3	2.35	0.56
1:G:77:ASP:OD2	1:G:110:ARG:NH2	2.38	0.56
1:G:190:ASP:H	1:G:193:LEU:HD13	1.70	0.56
3:I:18:THR:HG22	3:I:21:GLU:CG	2.35	0.56
2:E:51:MET:HE3	2:E:147:ASN:HB3	1.87	0.56
1:J:117:ILE:HB	1:J:144:LEU:HD22	1.87	0.56
2:K:75:VAL:HG21	2:K:140:ILE:CD1	2.36	0.56
1:A:77:ASP:OD2	1:A:110:ARG:NH2	2.38	0.56
3:C:18:THR:HG22	3:C:21:GLU:CG	2.35	0.56
3:I:335:GLY:O	3:I:336:GLU:HB2	2.04	0.56
3:L:140:ALA:O	3:L:144:ARG:HG3	2.05	0.56
3:F:306:LEU:HD21	3:F:334:ARG:HD2	1.87	0.56
2:E:86:ILE:CB	2:E:162:ILE:HD11	2.28	0.56
3:L:137:GLN:HB2	6:L:414:HOH:O	2.06	0.56
1:G:31:LEU:HB3	1:G:50:LEU:CD2	2.36	0.56
3:C:165:ILE:HD13	6:C:445:HOH:O	2.05	0.55
1:J:168:LEU:HD22	2:K:30:ILE:HD12	1.87	0.55
3:F:140:ALA:O	3:F:144:ARG:HG3	2.06	0.55
2:B:63:ASP:C	2:B:64:LEU:HD13	2.27	0.55
2:E:153:THR:HG23	2:E:154:LYS:N	2.22	0.55
2:H:62:ASN:HB3	2:H:64:LEU:HD22	1.86	0.55
3:I:199:ILE:CG2	3:I:204:ILE:HD12	2.36	0.55
3:F:334:ARG:HG2	3:F:334:ARG:HH11	1.71	0.55
1:J:126:ILE:HD11	5:J:4250:GNP:N2	2.20	0.55
2:H:144:ASN:CB	2:H:146:GLU:HG3	2.37	0.55
3:I:112:GLU:CB	3:I:113:PRO:HD3	2.35	0.55
3:L:18:THR:HG22	3:L:21:GLU:CG	2.37	0.55
3:C:116:ASP:OD2	3:C:120:LYS:HE2	2.07	0.55
1:D:101:VAL:HB	1:D:102:PRO:HD3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:344:GLU:HG2	3:F:345:GLU:N	2.20	0.55
3:C:252:ASN:ND2	3:C:282:GLN:H	2.05	0.55
2:H:153:THR:HG23	2:H:154:LYS:N	2.22	0.55
2:B:59:ALA:HB2	2:B:66:GLU:H	1.72	0.55
2:E:59:ALA:HB2	2:E:66:GLU:H	1.72	0.55
2:B:122:TRP:CZ3	2:B:140:ILE:HG22	2.40	0.54
3:F:18:THR:HG22	3:F:21:GLU:CG	2.37	0.54
3:C:199:ILE:CG2	3:C:204:ILE:HD12	2.38	0.54
3:C:245:ASN:O	3:C:247:ARG:HD2	2.06	0.54
3:C:334:ARG:HG2	3:C:334:ARG:HH11	1.72	0.54
1:J:31:LEU:HB3	1:J:50:LEU:CD2	2.37	0.54
2:B:153:THR:HG23	2:B:154:LYS:N	2.23	0.54
2:E:112:PRO:HG3	2:E:120:TRP:HZ3	1.73	0.54
3:F:176:MET:CE	3:F:207:LEU:HD22	2.38	0.54
1:J:178:ALA:HB3	2:K:38:ILE:HD11	1.90	0.54
3:L:245:ASN:O	3:L:247:ARG:HD2	2.08	0.54
3:F:112:GLU:HA	3:F:112:GLU:OE1	2.07	0.54
1:A:13:LEU:C	1:A:13:LEU:HD12	2.28	0.54
1:A:141:LYS:HE3	1:A:142:LYS:HD2	1.90	0.54
1:J:13:LEU:HB2	1:J:85:CYS:SG	2.48	0.54
2:B:58:PHE:HB2	2:B:67:TRP:CZ3	2.43	0.54
2:B:49:PHE:CB	2:B:77:LEU:HD12	2.38	0.54
2:B:144:ASN:CB	2:B:146:GLU:HG3	2.38	0.54
1:D:141:LYS:HE3	1:D:142:LYS:HD2	1.90	0.54
1:D:168:LEU:HD22	2:E:30:ILE:HD12	1.89	0.54
3:L:199:ILE:CG2	3:L:204:ILE:HD12	2.38	0.54
3:C:183:PHE:HE1	3:C:207:LEU:HD11	1.72	0.54
2:E:62:ASN:HB3	2:E:64:LEU:HD22	1.89	0.54
1:G:141:LYS:HE3	1:G:142:LYS:HD2	1.90	0.54
3:I:334:ARG:HH11	3:I:334:ARG:HG2	1.73	0.54
3:F:261:ALA:CB	3:F:286:ILE:HG12	2.38	0.54
3:I:259:ARG:HH11	3:I:259:ARG:HB3	1.72	0.54
3:C:111:GLN:O	3:C:115:ILE:HG13	2.07	0.53
3:F:306:LEU:HD23	3:F:334:ARG:HH11	1.74	0.53
1:J:95:ARG:HB2	1:J:95:ARG:NH1	2.23	0.53
2:K:153:THR:HG23	2:K:154:LYS:N	2.22	0.53
2:E:144:ASN:CB	2:E:146:GLU:HG3	2.38	0.53
2:E:49:PHE:CB	2:E:77:LEU:HD12	2.38	0.53
1:D:13:LEU:HB2	1:D:85:CYS:SG	2.47	0.53
3:F:199:ILE:CG2	3:F:204:ILE:HD12	2.38	0.53
2:B:51:MET:HE3	2:B:147:ASN:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:59:ALA:HB2	2:H:66:GLU:H	1.73	0.53
6:A:1256:HOH:O	3:C:108:PRO:HD3	2.08	0.53
2:K:144:ASN:CB	2:K:146:GLU:HG3	2.39	0.53
2:B:104:ILE:O	2:B:162:ILE:HD13	2.09	0.53
3:C:18:THR:CG2	3:C:21:GLU:HG3	2.39	0.53
3:I:245:ASN:O	3:I:247:ARG:HD2	2.09	0.53
3:C:43:THR:HG21	3:C:72:THR:O	2.09	0.53
3:F:43:THR:CG2	3:F:72:THR:O	2.57	0.53
3:L:112:GLU:OE1	3:L:112:GLU:HA	2.08	0.53
2:B:123:ASN:ND2	2:B:124:THR:N	2.57	0.53
2:B:57:ARG:HG3	2:B:70:ARG:HD3	1.91	0.53
3:I:306:LEU:HD21	3:I:334:ARG:HD2	1.90	0.53
3:I:94:PRO:O	6:I:417:HOH:O	2.19	0.53
3:F:18:THR:HG22	3:F:21:GLU:OE1	2.08	0.53
1:G:190:ASP:N	1:G:191:PRO:CD	2.72	0.53
1:G:13:LEU:C	1:G:13:LEU:HD12	2.30	0.52
2:H:123:ASN:ND2	2:H:124:THR:N	2.57	0.52
2:K:63:ASP:C	2:K:64:LEU:HD13	2.29	0.52
3:L:111:GLN:O	3:L:115:ILE:HG13	2.10	0.52
3:L:259:ARG:HB3	3:L:259:ARG:HH11	1.74	0.52
2:B:164:GLU:O	2:B:165:ARG:C	2.47	0.52
1:G:209:LEU:HD23	2:H:113:ASN:ND2	2.24	0.52
3:F:245:ASN:O	3:F:247:ARG:HD2	2.08	0.52
3:I:176:MET:CE	3:I:207:LEU:HD22	2.40	0.52
3:I:266:ASP:O	3:I:269:SER:HB3	2.10	0.52
3:F:292:ARG:HG2	3:F:321:VAL:HG11	1.92	0.52
1:G:143:ASN:HD21	2:H:25:PRO:HB3	1.73	0.52
1:J:13:LEU:HD12	1:J:13:LEU:C	2.30	0.52
3:L:306:LEU:HD21	3:L:334:ARG:HD2	1.91	0.52
3:L:334:ARG:HG2	3:L:334:ARG:HH11	1.74	0.52
2:B:112:PRO:HG3	2:B:120:TRP:HZ3	1.74	0.52
3:F:43:THR:HG21	3:F:72:THR:O	2.10	0.52
1:J:190:ASP:N	1:J:191:PRO:CD	2.72	0.52
3:C:112:GLU:HA	3:C:112:GLU:OE1	2.09	0.52
1:J:163:TRP:CZ2	1:J:167:LYS:HE3	2.44	0.52
2:K:106:PRO:O	2:K:159:ARG:NE	2.43	0.52
1:D:31:LEU:HB3	1:D:50:LEU:CD2	2.39	0.52
2:E:63:ASP:C	2:E:64:LEU:HD13	2.30	0.52
1:G:188:VAL:C	1:G:189:MET:HG2	2.30	0.52
1:J:209:LEU:HD23	2:K:113:ASN:HD21	1.73	0.52
3:L:176:MET:CE	3:L:207:LEU:HD22	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:103:ASN:OD1	1:D:106:ARG:NH2	2.43	0.52
2:E:123:ASN:ND2	2:E:124:THR:N	2.57	0.52
2:H:64:LEU:HD13	2:H:64:LEU:N	2.24	0.52
3:I:43:THR:HG21	3:I:72:THR:O	2.10	0.52
3:L:204:ILE:HG23	3:L:208:LEU:HD23	1.91	0.52
2:K:51:MET:HE3	2:K:147:ASN:HB3	1.92	0.52
2:K:58:PHE:HB2	2:K:67:TRP:CZ3	2.44	0.52
3:F:120:LYS:HD3	3:L:318:GLU:HB3	1.92	0.52
3:L:43:THR:CG2	3:L:72:THR:O	2.58	0.52
1:A:190:ASP:N	1:A:191:PRO:CD	2.73	0.51
3:C:173:ASN:HD21	3:C:200:ARG:N	2.06	0.51
1:D:190:ASP:N	1:D:191:PRO:CD	2.72	0.51
2:E:58:PHE:HB2	2:E:67:TRP:CZ3	2.45	0.51
3:F:178:GLU:HB2	6:F:413:HOH:O	2.10	0.51
1:J:140:ARG:O	2:K:22:ASN:OD1	2.28	0.51
1:J:141:LYS:HE3	1:J:142:LYS:HD2	1.91	0.51
2:B:64:LEU:N	2:B:64:LEU:HD13	2.26	0.51
3:C:259:ARG:HB3	3:C:259:ARG:HH11	1.72	0.51
3:C:306:LEU:HD23	3:C:334:ARG:HH11	1.75	0.51
1:D:199:HIS:O	1:D:203:VAL:HG23	2.10	0.51
3:L:306:LEU:HD23	3:L:334:ARG:HH11	1.75	0.51
3:L:43:THR:HG21	3:L:72:THR:O	2.10	0.51
3:C:306:LEU:HD21	3:C:334:ARG:HD2	1.93	0.51
3:F:131:ASN:ND2	6:F:414:HOH:O	2.43	0.51
1:G:209:LEU:HD13	2:H:67:TRP:CG	2.44	0.51
3:I:43:THR:CG2	3:I:72:THR:O	2.58	0.51
2:K:112:PRO:HG3	2:K:120:TRP:HZ3	1.76	0.51
1:G:188:VAL:O	1:G:189:MET:O	2.27	0.51
2:H:112:PRO:HG3	2:H:120:TRP:HZ3	1.76	0.51
2:H:75:VAL:HG21	2:H:140:ILE:CD1	2.39	0.51
3:L:292:ARG:HG2	3:L:321:VAL:HG11	1.92	0.51
3:I:112:GLU:HA	3:I:112:GLU:OE1	2.10	0.51
3:I:306:LEU:HD23	3:I:334:ARG:HH11	1.74	0.51
3:C:204:ILE:HG23	3:C:208:LEU:HD23	1.92	0.51
3:F:204:ILE:HG23	3:F:208:LEU:HD23	1.92	0.51
1:G:190:ASP:OD2	1:G:194:ALA:HB2	2.10	0.51
3:L:242:SER:O	3:L:244:PRO:HD3	2.11	0.51
3:C:43:THR:CG2	3:C:72:THR:O	2.58	0.51
1:D:163:TRP:CZ2	1:D:167:LYS:HE3	2.45	0.51
1:J:188:VAL:O	1:J:189:MET:O	2.29	0.51
2:K:136:GLU:CG	2:K:138:LEU:HD21	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:143:ASN:CA	2:K:22:ASN:ND2	2.72	0.51
3:I:18:THR:HG22	3:I:21:GLU:OE1	2.10	0.51
3:I:20:ASP:O	3:I:21:GLU:HB2	2.11	0.51
3:C:18:THR:HG22	3:C:21:GLU:OE1	2.11	0.51
3:C:236:LEU:HD21	3:C:251:LEU:HD11	1.93	0.51
3:F:245:ASN:ND2	6:F:391:HOH:O	2.40	0.51
1:D:190:ASP:OD2	1:D:194:ALA:HB2	2.11	0.50
2:H:51:MET:HE3	2:H:147:ASN:HB3	1.93	0.50
6:G:3275:HOH:O	3:I:109:THR:CG2	2.59	0.50
3:I:261:ALA:CB	3:I:286:ILE:HG12	2.41	0.50
2:K:122:TRP:CZ3	2:K:140:ILE:HG22	2.45	0.50
1:J:190:ASP:OD2	1:J:194:ALA:HB2	2.10	0.50
3:C:294:LEU:O	3:C:298:ILE:HG13	2.11	0.50
3:F:259:ARG:HB3	3:F:259:ARG:HH11	1.73	0.50
1:A:188:VAL:C	1:A:189:MET:HG2	2.32	0.50
3:C:176:MET:CE	3:C:207:LEU:HD22	2.40	0.50
3:C:72:THR:HG23	6:C:389:HOH:O	2.12	0.50
1:A:12:LYS:HE3	1:A:64:TRP:CE2	2.46	0.50
2:B:78:LEU:O	2:B:86:ILE:HA	2.11	0.50
3:C:130:HIS:HE1	6:C:435:HOH:O	1.94	0.50
1:G:163:TRP:CZ2	1:G:167:LYS:HE3	2.47	0.50
1:G:199:HIS:O	1:G:203:VAL:HG23	2.11	0.50
5:J:4250:GNP:O1G	6:J:4252:HOH:O	2.17	0.50
1:A:209:LEU:HD23	2:B:113:ASN:HD21	1.76	0.50
1:D:95:ARG:NH1	1:D:95:ARG:HB2	2.26	0.50
1:J:199:HIS:O	1:J:203:VAL:HG23	2.11	0.50
2:K:123:ASN:ND2	2:K:124:THR:N	2.59	0.50
3:L:20:ASP:O	3:L:21:GLU:HB2	2.12	0.50
1:D:188:VAL:O	1:D:189:MET:O	2.29	0.50
2:H:78:LEU:O	2:H:86:ILE:HA	2.11	0.50
1:J:188:VAL:C	1:J:189:MET:HG2	2.33	0.50
3:C:100:ARG:HA	3:C:128:TYR:HB2	1.94	0.50
3:C:317:GLU:HB2	6:C:441:HOH:O	2.10	0.50
2:H:49:PHE:CB	2:H:77:LEU:HD12	2.41	0.50
1:J:32:THR:HG21	1:J:34:GLU:OE1	2.12	0.50
1:A:199:HIS:O	1:A:203:VAL:HG23	2.12	0.49
2:H:122:TRP:CZ3	2:H:140:ILE:HG22	2.45	0.49
2:H:57:ARG:HG3	2:H:70:ARG:HD3	1.93	0.49
1:A:143:ASN:HD21	2:B:25:PRO:HB3	1.75	0.49
3:C:19:GLU:C	3:C:20:ASP:O	2.50	0.49
3:C:326:ARG:NH2	6:C:442:HOH:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:195:VAL:HG22	3:F:224:GLN:HB3	1.95	0.49
2:H:38:ILE:HG13	2:H:38:ILE:O	2.12	0.49
3:I:295:LYS:HG3	3:I:325:ILE:HG13	1.94	0.49
3:L:294:LEU:O	3:L:298:ILE:HG13	2.12	0.49
1:D:188:VAL:C	1:D:189:MET:HG2	2.33	0.49
1:D:193:LEU:O	1:D:196:GLN:NE2	2.45	0.49
1:G:124:VAL:HG22	1:G:149:ILE:O	2.12	0.49
3:C:195:VAL:HG22	3:C:224:GLN:HB3	1.95	0.49
2:H:136:GLU:CG	2:H:138:LEU:HD21	2.42	0.49
3:I:183:PHE:HE1	3:I:207:LEU:HD11	1.77	0.49
3:I:292:ARG:HG2	3:I:321:VAL:HG11	1.94	0.49
3:L:18:THR:CG2	3:L:21:GLU:HG3	2.42	0.49
3:L:309:GLU:HA	3:L:338:ASP:OD1	2.11	0.49
1:A:190:ASP:OD2	1:A:194:ALA:HB2	2.12	0.49
3:C:128:TYR:CE2	3:C:165:ILE:HG13	2.47	0.49
2:E:78:LEU:O	2:E:86:ILE:HA	2.12	0.49
3:F:20:ASP:O	3:F:21:GLU:HB2	2.12	0.49
3:I:18:THR:CG2	3:I:21:GLU:HG3	2.41	0.49
1:J:143:ASN:HD21	2:K:25:PRO:HB3	1.76	0.49
2:K:57:ARG:HG3	2:K:70:ARG:HD3	1.94	0.49
3:C:242:SER:O	3:C:244:PRO:HD3	2.12	0.49
2:K:61:GLU:O	2:K:61:GLU:HG3	2.12	0.49
2:K:64:LEU:N	2:K:64:LEU:HD13	2.28	0.49
2:B:136:GLU:CG	2:B:138:LEU:HD21	2.41	0.49
2:B:61:GLU:HG3	2:B:61:GLU:O	2.13	0.49
3:C:20:ASP:O	3:C:21:GLU:HB2	2.13	0.49
1:G:95:ARG:HB2	1:G:95:ARG:NH1	2.28	0.49
2:H:61:GLU:HG3	2:H:61:GLU:O	2.13	0.49
1:A:188:VAL:O	1:A:189:MET:O	2.29	0.49
2:E:64:LEU:HD13	2:E:64:LEU:N	2.28	0.49
1:G:188:VAL:O	1:G:189:MET:HG2	2.13	0.49
1:G:10:GLN:HE21	1:G:60:LYS:HD2	1.78	0.49
3:I:326:ARG:NH2	6:I:430:HOH:O	2.40	0.49
2:K:49:PHE:CB	2:K:77:LEU:HD12	2.42	0.49
1:D:32:THR:HG21	1:D:34:GLU:OE1	2.12	0.49
1:G:193:LEU:O	1:G:196:GLN:NE2	2.46	0.49
1:G:213:ASP:OD2	2:H:141:ARG:NH1	2.38	0.49
2:H:58:PHE:HB2	2:H:67:TRP:CZ3	2.47	0.49
2:B:109:GLU:OE1	2:B:109:GLU:N	2.44	0.49
2:B:38:ILE:O	2:B:38:ILE:HG13	2.13	0.49
3:F:183:PHE:HE1	3:F:207:LEU:HD11	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:ASN:HA	2:B:22:ASN:ND2	2.28	0.48
1:D:13:LEU:HD12	1:D:14:VAL:N	2.28	0.48
1:A:202:GLU:C	1:A:204:ALA:H	2.15	0.48
2:B:109:GLU:CD	2:B:109:GLU:N	2.66	0.48
3:F:18:THR:CG2	3:F:21:GLU:HG3	2.42	0.48
3:I:204:ILE:HG23	3:I:208:LEU:HD23	1.95	0.48
2:K:78:LEU:O	2:K:86:ILE:HA	2.13	0.48
1:A:32:THR:HG21	1:A:34:GLU:OE1	2.13	0.48
1:D:125:ASP:OD2	1:D:126:ILE:HD12	2.14	0.48
1:G:202:GLU:C	1:G:204:ALA:H	2.16	0.48
2:H:58:PHE:HD2	2:H:67:TRP:CE2	2.32	0.48
1:A:125:ASP:OD2	1:A:126:ILE:HD12	2.13	0.48
2:E:61:GLU:O	2:E:61:GLU:HG3	2.13	0.48
1:G:81:ILE:HD13	1:G:82:GLN:HG3	1.95	0.48
3:I:199:ILE:HG22	3:I:204:ILE:HD12	1.96	0.48
3:L:236:LEU:HD21	3:L:251:LEU:HD11	1.95	0.48
1:D:189:MET:CB	1:D:193:LEU:HD22	2.43	0.48
1:G:32:THR:HG21	1:G:34:GLU:OE1	2.13	0.48
3:I:295:LYS:HG3	3:I:325:ILE:CG1	2.43	0.48
3:C:292:ARG:HG2	3:C:321:VAL:HG11	1.95	0.48
3:F:173:ASN:HD21	3:F:200:ARG:N	2.08	0.48
2:K:109:GLU:N	2:K:109:GLU:OE1	2.47	0.48
1:J:201:LEU:HG	2:K:111:LYS:HD3	1.94	0.48
1:D:10:GLN:HE21	1:D:60:LYS:HD2	1.79	0.48
3:I:259:ARG:CB	3:I:259:ARG:HH11	2.27	0.48
3:L:183:PHE:HE1	3:L:207:LEU:HD11	1.79	0.48
2:B:58:PHE:HD2	2:B:67:TRP:CE2	2.31	0.48
3:C:314:ARG:NH1	3:C:344:GLU:OE1	2.47	0.48
3:F:236:LEU:HD21	3:F:251:LEU:HD11	1.96	0.48
3:F:242:SER:O	3:F:244:PRO:HD3	2.14	0.48
3:I:303:PRO:O	3:I:334:ARG:NH2	2.47	0.48
2:K:49:PHE:HZ	2:K:51:MET:CE	2.26	0.48
2:K:58:PHE:HD2	2:K:67:TRP:CE2	2.31	0.48
3:L:128:TYR:CE2	3:L:165:ILE:HG13	2.49	0.48
3:C:259:ARG:CB	3:C:259:ARG:HH11	2.27	0.47
2:E:108:MET:O	2:E:159:ARG:HG3	2.14	0.47
2:H:109:GLU:OE1	2:H:109:GLU:N	2.45	0.47
3:I:19:GLU:C	3:I:20:ASP:O	2.48	0.47
1:A:189:MET:CB	1:A:193:LEU:HD22	2.44	0.47
1:D:178:ALA:O	1:D:179:MET:HB2	2.14	0.47
1:D:202:GLU:C	1:D:204:ALA:H	2.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:242:SER:O	3:I:244:PRO:HD3	2.14	0.47
2:B:40:THR:HB	2:B:43:GLU:OE2	2.14	0.47
3:I:122:THR:N	3:I:123:PRO:CD	2.77	0.47
1:J:13:LEU:HD12	1:J:14:VAL:N	2.29	0.47
1:A:193:LEU:O	1:A:196:GLN:NE2	2.46	0.47
3:I:322:VAL:HG12	3:I:326:ARG:NH1	2.29	0.47
3:L:18:THR:HG22	3:L:21:GLU:CD	2.34	0.47
3:L:261:ALA:CB	3:L:286:ILE:HG12	2.44	0.47
3:L:266:ASP:O	3:L:269:SER:HB3	2.14	0.47
3:C:309:GLU:HA	3:C:338:ASP:OD1	2.13	0.47
2:E:109:GLU:N	2:E:109:GLU:CD	2.67	0.47
3:I:100:ARG:HA	3:I:128:TYR:HB2	1.96	0.47
1:J:10:GLN:HE21	1:J:60:LYS:HD2	1.80	0.47
1:A:163:TRP:CZ2	1:A:167:LYS:HE3	2.49	0.47
1:A:95:ARG:HB2	1:A:95:ARG:NH1	2.30	0.47
3:F:19:GLU:C	3:F:20:ASP:O	2.52	0.47
3:F:303:PRO:O	3:F:334:ARG:NH2	2.48	0.47
1:J:178:ALA:O	1:J:179:MET:HB2	2.15	0.47
2:K:40:THR:HB	2:K:43:GLU:OE2	2.14	0.47
3:L:259:ARG:CB	3:L:259:ARG:HH11	2.27	0.47
1:A:13:LEU:HD12	1:A:14:VAL:N	2.30	0.47
1:A:16:VAL:HG13	1:A:17:GLY:N	2.30	0.47
3:C:322:VAL:HG12	3:C:326:ARG:NH1	2.30	0.47
1:D:189:MET:O	1:D:190:ASP:CB	2.63	0.47
1:D:81:ILE:HD13	1:D:82:GLN:HG3	1.96	0.47
2:E:136:GLU:CG	2:E:138:LEU:HD21	2.44	0.47
3:F:100:ARG:HA	3:F:128:TYR:HB2	1.96	0.47
3:F:122:THR:N	3:F:123:PRO:CD	2.78	0.47
1:J:189:MET:CB	1:J:193:LEU:HD22	2.45	0.47
2:E:49:PHE:HZ	2:E:51:MET:CE	2.28	0.47
3:F:259:ARG:CB	3:F:259:ARG:HH11	2.27	0.47
3:F:295:LYS:HG3	3:F:325:ILE:CG1	2.45	0.47
1:J:193:LEU:O	1:J:196:GLN:NE2	2.47	0.47
3:C:28:LEU:O	3:C:59:LYS:NZ	2.48	0.47
2:E:58:PHE:HD2	2:E:67:TRP:CE2	2.32	0.47
1:J:81:ILE:HD13	1:J:82:GLN:N	2.30	0.47
2:K:160:LYS:O	2:K:164:GLU:HG3	2.15	0.47
3:C:295:LYS:HG3	3:C:325:ILE:CG1	2.45	0.47
2:E:57:ARG:HG3	2:E:70:ARG:HD3	1.97	0.47
2:E:95:THR:O	2:E:96:LEU:HB2	2.14	0.47
3:L:100:ARG:HA	3:L:128:TYR:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:VAL:O	1:A:189:MET:HG2	2.14	0.47
3:C:122:THR:N	3:C:123:PRO:CD	2.78	0.47
3:C:144:ARG:HG2	3:C:178:GLU:CG	2.45	0.47
2:E:86:ILE:HB	2:E:162:ILE:CD1	2.32	0.47
3:I:144:ARG:HG2	3:I:178:GLU:CG	2.45	0.47
1:J:177:VAL:HG23	2:K:38:ILE:CD1	2.45	0.47
1:J:195:ALA:O	1:J:197:TYR:N	2.48	0.47
3:L:176:MET:CE	3:L:207:LEU:HD13	2.45	0.47
1:G:81:ILE:HD13	1:G:82:GLN:N	2.30	0.46
2:H:158:CYS:O	2:H:162:ILE:HG13	2.15	0.46
2:H:49:PHE:HZ	2:H:51:MET:CE	2.28	0.46
1:A:10:GLN:HE21	1:A:60:LYS:HD2	1.81	0.46
3:C:261:ALA:CB	3:C:286:ILE:HG12	2.45	0.46
3:C:266:ASP:O	3:C:269:SER:HB3	2.15	0.46
3:F:295:LYS:HG3	3:F:325:ILE:HG13	1.97	0.46
3:I:242:SER:C	3:I:244:PRO:HD3	2.35	0.46
1:J:202:GLU:C	1:J:204:ALA:H	2.18	0.46
3:L:19:GLU:C	3:L:20:ASP:O	2.52	0.46
1:D:188:VAL:O	1:D:189:MET:HG2	2.15	0.46
1:D:205:GLN:HE22	2:E:111:LYS:HE2	1.79	0.46
1:J:177:VAL:HG23	2:K:38:ILE:HD13	1.98	0.46
1:A:186:GLU:O	1:A:187:VAL:HB	2.16	0.46
3:F:144:ARG:HG2	3:F:178:GLU:CG	2.45	0.46
2:H:84:GLY:H	2:H:165:ARG:HH21	1.63	0.46
6:G:3275:HOH:O	3:I:107:GLY:HA3	2.14	0.46
3:I:195:VAL:HG22	3:I:224:GLN:HB3	1.97	0.46
3:I:236:LEU:HD21	3:I:251:LEU:HD11	1.97	0.46
3:L:195:VAL:HG22	3:L:224:GLN:HB3	1.97	0.46
2:E:118:ARG:HA	2:E:148:ALA:HB2	1.97	0.46
3:F:322:VAL:HG12	3:F:326:ARG:NH1	2.30	0.46
2:H:59:ALA:O	2:H:60:SER:CB	2.62	0.46
3:I:314:ARG:NH1	3:I:344:GLU:OE1	2.49	0.46
1:J:188:VAL:O	1:J:189:MET:HG2	2.14	0.46
2:K:59:ALA:O	2:K:60:SER:CB	2.63	0.46
3:C:183:PHE:CE1	3:C:207:LEU:HD11	2.50	0.46
3:F:314:ARG:NH1	3:F:344:GLU:OE1	2.49	0.46
3:L:122:THR:N	3:L:123:PRO:CD	2.79	0.46
2:B:63:ASP:C	2:B:65:PRO:HD3	2.36	0.46
1:G:186:GLU:O	1:G:187:VAL:HB	2.16	0.46
1:G:31:LEU:HB3	1:G:50:LEU:HD21	1.98	0.46
2:H:123:ASN:HD22	2:H:124:THR:N	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:144:ASN:HD22	2:H:147:ASN:HD21	1.64	0.46
3:L:322:VAL:HG12	3:L:326:ARG:NH1	2.31	0.46
3:C:4:PHE:HA	6:C:398:HOH:O	2.15	0.46
1:D:124:VAL:HG22	1:D:149:ILE:O	2.16	0.46
2:E:109:GLU:OE1	2:E:109:GLU:N	2.46	0.46
2:E:63:ASP:C	2:E:65:PRO:HD3	2.36	0.46
1:G:135:SER:O	1:G:137:VAL:HG23	2.16	0.46
2:H:49:PHE:O	2:H:76:LYS:HA	2.16	0.46
2:H:88:LEU:HD23	2:H:89:LEU:N	2.31	0.46
3:C:186:HIS:HD2	6:C:456:HOH:O	1.99	0.45
2:B:49:PHE:HZ	2:B:51:MET:CE	2.29	0.45
3:F:199:ILE:HG22	3:F:204:ILE:HD12	1.98	0.45
2:H:63:ASP:C	2:H:65:PRO:HD3	2.37	0.45
1:J:112:CYS:HB3	1:J:115:ILE:HD13	1.99	0.45
2:B:157:GLU:HA	2:B:160:LYS:HE2	1.97	0.45
2:B:59:ALA:O	2:B:60:SER:CB	2.63	0.45
3:C:18:THR:HG22	3:C:21:GLU:CD	2.37	0.45
1:D:81:ILE:HD13	1:D:82:GLN:N	2.32	0.45
3:F:18:THR:HG22	3:F:21:GLU:CD	2.37	0.45
1:G:112:CYS:HB3	1:G:115:ILE:HD13	1.98	0.45
1:J:169:ILE:HD12	2:K:33:LEU:CD1	2.45	0.45
1:J:183:ALA:HA	1:J:184:PRO:HD3	1.83	0.45
1:A:112:CYS:HB3	1:A:115:ILE:HD13	1.97	0.45
1:A:128:ASP:HB2	6:C:430:HOH:O	2.17	0.45
3:C:256:LEU:O	3:C:257:SER:CB	2.65	0.45
1:D:16:VAL:HG13	1:D:17:GLY:N	2.32	0.45
1:G:178:ALA:O	1:G:179:MET:HB2	2.16	0.45
1:D:112:CYS:HB3	1:D:115:ILE:HD13	1.98	0.45
1:D:186:GLU:O	1:D:187:VAL:HB	2.17	0.45
1:D:205:GLN:NE2	2:E:111:LYS:HE2	2.31	0.45
1:G:115:ILE:O	1:G:117:ILE:HG13	2.16	0.45
2:K:63:ASP:C	2:K:65:PRO:HD3	2.37	0.45
1:G:105:HIS:CD2	1:G:144:LEU:HD21	2.52	0.45
3:I:18:THR:HG22	3:I:21:GLU:CD	2.37	0.45
3:I:28:LEU:O	3:I:59:LYS:NZ	2.50	0.45
1:J:135:SER:O	1:J:137:VAL:HG23	2.16	0.45
1:J:209:LEU:HB3	2:K:141:ARG:NH2	2.31	0.45
1:A:135:SER:O	1:A:137:VAL:HG23	2.16	0.45
1:A:31:LEU:HB3	1:A:50:LEU:HD21	1.98	0.45
1:D:12:LYS:HE3	1:D:64:TRP:CE2	2.51	0.45
6:J:4278:HOH:O	3:L:109:THR:CG2	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:109:GLU:CD	2:H:109:GLU:N	2.66	0.45
1:J:93:THR:O	1:J:130:LYS:HD2	2.17	0.45
3:I:187:ARG:NH2	3:L:270:LYS:O	2.39	0.45
1:A:93:THR:HG21	1:A:126:ILE:HG21	1.99	0.45
1:J:103:ASN:OD1	1:J:106:ARG:NH2	2.50	0.45
3:L:256:LEU:O	3:L:257:SER:CB	2.65	0.45
1:A:195:ALA:O	1:A:197:TYR:N	2.50	0.45
2:K:118:ARG:HA	2:K:148:ALA:HB2	1.97	0.45
3:L:303:PRO:O	3:L:334:ARG:NH2	2.50	0.45
1:A:103:ASN:OD1	1:A:106:ARG:NH2	2.48	0.44
1:A:81:ILE:HD13	1:A:82:GLN:N	2.32	0.44
3:C:303:PRO:O	3:C:334:ARG:NH2	2.50	0.44
6:D:2277:HOH:O	3:F:107:GLY:HA3	2.17	0.44
2:K:38:ILE:O	2:K:38:ILE:HG13	2.16	0.44
3:L:18:THR:O	3:L:20:ASP:O	2.35	0.44
1:D:209:LEU:HD13	2:E:67:TRP:CG	2.51	0.44
2:E:149:GLN:O	2:E:153:THR:HG22	2.17	0.44
1:G:189:MET:CB	1:G:193:LEU:HD22	2.47	0.44
3:L:170:ARG:NH1	6:L:405:HOH:O	2.50	0.44
3:I:108:PRO:HD3	6:I:435:HOH:O	2.16	0.44
1:D:105:HIS:CD2	1:D:144:LEU:HD21	2.53	0.44
3:F:72:THR:HG22	6:F:406:HOH:O	2.16	0.44
1:A:178:ALA:O	1:A:179:MET:HB2	2.17	0.44
2:E:40:THR:HB	2:E:43:GLU:OE2	2.17	0.44
3:I:21:GLU:O	3:I:24:VAL:HB	2.18	0.44
3:L:314:ARG:NH1	3:L:344:GLU:OE1	2.50	0.44
3:L:295:LYS:HG3	3:L:325:ILE:CG1	2.47	0.44
3:L:295:LYS:HG3	3:L:325:ILE:HG13	2.00	0.44
1:A:202:GLU:C	1:A:204:ALA:N	2.70	0.44
2:B:118:ARG:HA	2:B:148:ALA:HB2	1.98	0.44
3:C:21:GLU:O	3:C:24:VAL:HB	2.17	0.44
1:D:115:ILE:O	1:D:117:ILE:HG13	2.18	0.44
3:I:173:ASN:HD21	3:I:200:ARG:N	2.10	0.44
1:J:186:GLU:O	1:J:187:VAL:HB	2.17	0.44
1:J:81:ILE:HD13	1:J:82:GLN:HG3	1.99	0.44
3:L:84:ARG:O	3:L:88:GLN:HB2	2.17	0.44
1:D:133:ALA:N	6:D:2269:HOH:O	2.37	0.44
1:D:135:SER:O	1:D:137:VAL:HG23	2.17	0.44
1:D:202:GLU:C	1:D:204:ALA:N	2.71	0.44
3:F:128:TYR:CE2	3:F:165:ILE:HG13	2.52	0.44
1:G:103:ASN:OD1	1:G:106:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:13:LEU:HD12	1:G:14:VAL:N	2.33	0.44
2:H:149:GLN:O	2:H:153:THR:HG22	2.17	0.44
3:I:96:LEU:O	3:I:121:HIS:HE1	2.01	0.44
3:F:250:GLY:HA2	3:F:280:ARG:HB2	2.00	0.44
1:G:125:ASP:OD2	1:G:126:ILE:HD12	2.17	0.44
1:J:124:VAL:HG22	1:J:149:ILE:O	2.18	0.44
1:A:105:HIS:CD2	1:A:144:LEU:HD21	2.53	0.44
2:B:149:GLN:O	2:B:153:THR:HG22	2.18	0.44
2:E:93:ASP:O	2:E:95:THR:N	2.43	0.44
2:H:70:ARG:HD2	2:H:70:ARG:HA	1.83	0.44
1:J:125:ASP:OD2	1:J:126:ILE:HD12	2.18	0.44
2:B:49:PHE:O	2:B:76:LYS:HA	2.17	0.43
1:D:159:LYS:HB2	1:D:160:PRO:HD3	2.00	0.43
3:I:294:LEU:O	3:I:298:ILE:HG13	2.18	0.43
1:J:31:LEU:HB3	1:J:50:LEU:HD21	1.99	0.43
2:K:49:PHE:O	2:K:76:LYS:HA	2.18	0.43
2:K:59:ALA:CB	2:K:65:PRO:HA	2.47	0.43
1:A:213:ASP:OD2	2:B:141:ARG:NH1	2.44	0.43
1:G:16:VAL:HG13	1:G:17:GLY:N	2.33	0.43
3:I:186:HIS:HD2	6:I:411:HOH:O	2.02	0.43
1:A:206:THR:O	2:B:114:ALA:HB2	2.17	0.43
3:C:199:ILE:HG22	3:C:204:ILE:HD12	1.98	0.43
1:D:195:ALA:O	1:D:197:TYR:N	2.51	0.43
1:G:202:GLU:C	1:G:204:ALA:N	2.71	0.43
1:J:178:ALA:O	1:J:179:MET:CB	2.66	0.43
1:J:30:HIS:HD2	6:J:4260:HOH:O	2.00	0.43
2:K:123:ASN:HD22	2:K:124:THR:N	2.14	0.43
3:C:252:ASN:ND2	3:C:280:ARG:HB3	2.33	0.43
3:F:309:GLU:HA	3:F:338:ASP:OD1	2.18	0.43
2:H:102:HIS:CE1	2:H:122:TRP:HE1	2.36	0.43
2:H:51:MET:HE3	2:H:142:PHE:CD1	2.54	0.43
1:D:178:ALA:O	1:D:179:MET:CB	2.66	0.43
2:E:57:ARG:HD3	2:E:136:GLU:OE2	2.18	0.43
2:E:49:PHE:O	2:E:76:LYS:HA	2.18	0.43
3:F:28:LEU:O	3:F:59:LYS:NZ	2.52	0.43
1:G:12:LYS:HE3	1:G:64:TRP:CE2	2.54	0.43
2:H:118:ARG:HA	2:H:148:ALA:HB2	2.00	0.43
3:I:206:HIS:HD2	6:I:439:HOH:O	2.01	0.43
1:A:16:VAL:CG1	1:A:17:GLY:N	2.81	0.43
3:C:165:ILE:CD1	6:C:445:HOH:O	2.64	0.43
2:E:38:ILE:O	2:E:38:ILE:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:59:ALA:O	2:E:60:SER:CB	2.62	0.43
3:F:21:GLU:O	3:F:24:VAL:HB	2.19	0.43
1:G:195:ALA:O	1:G:197:TYR:N	2.51	0.43
2:H:84:GLY:H	2:H:165:ARG:NH2	2.17	0.43
3:I:18:THR:O	3:I:20:ASP:O	2.36	0.43
2:K:102:HIS:HB3	2:K:127:ASP:HA	1.99	0.43
3:L:176:MET:HE3	3:L:207:LEU:HD13	1.99	0.43
1:A:67:ALA:HA	6:A:1252:HOH:O	2.18	0.43
2:B:102:HIS:HB3	2:B:127:ASP:HA	2.01	0.43
2:E:51:MET:HE2	2:E:142:PHE:CE1	2.54	0.43
2:E:58:PHE:O	2:E:59:ALA:C	2.57	0.43
3:I:176:MET:CE	3:I:207:LEU:HD13	2.49	0.43
2:K:80:HIS:O	2:K:83:LYS:O	2.37	0.43
3:L:344:GLU:CG	3:L:345:GLU:N	2.81	0.43
3:C:295:LYS:HG3	3:C:325:ILE:HG13	2.00	0.43
3:C:329:PHE:CG	3:C:335:GLY:HA3	2.53	0.43
3:I:309:GLU:HA	3:I:338:ASP:OD1	2.18	0.43
3:L:31:ASP:O	3:L:34:VAL:HG23	2.18	0.43
1:G:93:THR:HG21	1:G:126:ILE:HG21	2.00	0.43
2:H:95:THR:HG23	2:H:97:LYS:H	1.84	0.43
3:I:66:GLU:HG2	3:I:100:ARG:HD2	2.01	0.43
3:L:16:ILE:HG22	3:L:16:ILE:O	2.18	0.43
3:L:173:ASN:HD21	3:L:200:ARG:N	2.13	0.43
3:L:329:PHE:CG	3:L:335:GLY:HA3	2.54	0.43
3:C:274:ILE:HG22	3:C:276:LEU:H	1.84	0.43
6:G:3274:HOH:O	3:I:170:ARG:HG3	2.19	0.43
3:L:144:ARG:HG2	3:L:178:GLU:CG	2.48	0.43
2:B:51:MET:HE3	2:B:142:PHE:CD1	2.54	0.42
2:B:163:GLU:O	2:B:166:GLU:OE2	2.37	0.42
3:C:18:THR:HG22	3:C:21:GLU:HG3	2.00	0.42
3:F:207:LEU:HG	3:F:212:LEU:HD22	2.01	0.42
1:G:126:ILE:CD1	5:G:3250:GNP:N2	2.82	0.42
3:I:183:PHE:CE1	3:I:207:LEU:HD11	2.53	0.42
3:L:259:ARG:HB3	3:L:259:ARG:CZ	2.49	0.42
2:B:67:TRP:CH2	2:B:139:ALA:HB2	2.54	0.42
2:B:70:ARG:HD2	2:B:70:ARG:HA	1.86	0.42
3:C:339:GLU:HA	3:C:339:GLU:OE1	2.19	0.42
3:F:84:ARG:O	3:F:88:GLN:HB2	2.19	0.42
3:I:207:LEU:HG	3:I:212:LEU:HD22	2.01	0.42
3:I:339:GLU:OE1	3:I:339:GLU:HA	2.19	0.42
1:J:13:LEU:HD13	1:J:86:ALA:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:2277:HOH:O	3:F:109:THR:HG22	2.16	0.42
3:F:266:ASP:O	3:F:269:SER:HB3	2.20	0.42
2:H:144:ASN:HD22	2:H:147:ASN:ND2	2.17	0.42
2:K:149:GLN:O	2:K:153:THR:HG22	2.19	0.42
3:L:259:ARG:NH1	3:L:259:ARG:CB	2.78	0.42
1:G:202:GLU:HA	1:G:205:GLN:HG2	2.01	0.42
2:H:93:ASP:O	2:H:95:THR:N	2.45	0.42
3:I:18:THR:HG23	3:I:20:ASP:C	2.40	0.42
2:K:58:PHE:O	2:K:59:ALA:C	2.58	0.42
3:C:291:VAL:HG21	3:C:315:PHE:CD2	2.54	0.42
3:C:298:ILE:HD13	3:C:305:LEU:CD2	2.49	0.42
2:E:102:HIS:HB3	2:E:127:ASP:HA	2.02	0.42
2:E:80:HIS:O	2:E:83:LYS:O	2.37	0.42
3:F:339:GLU:OE1	3:F:339:GLU:HA	2.20	0.42
1:J:189:MET:O	1:J:190:ASP:CB	2.63	0.42
1:J:202:GLU:C	1:J:204:ALA:N	2.73	0.42
2:K:160:LYS:HG2	2:K:164:GLU:OE2	2.20	0.42
3:F:183:PHE:CE1	3:F:207:LEU:HD11	2.53	0.42
3:I:18:THR:HG23	3:I:20:ASP:O	2.20	0.42
3:L:252:ASN:ND2	3:L:280:ARG:HB3	2.35	0.42
2:B:102:HIS:CE1	2:B:122:TRP:HE1	2.37	0.42
1:A:177:VAL:HG23	2:B:38:ILE:CD1	2.49	0.42
2:E:88:LEU:HD23	2:E:89:LEU:N	2.35	0.42
3:F:344:GLU:CG	3:F:345:GLU:N	2.83	0.42
3:I:18:THR:HG22	3:I:21:GLU:HG3	2.01	0.42
3:I:344:GLU:CG	3:I:345:GLU:N	2.82	0.42
3:L:72:THR:HG23	6:L:409:HOH:O	2.18	0.42
1:A:178:ALA:O	1:A:179:MET:CB	2.67	0.42
1:D:171:ASP:OD1	1:D:173:ASN:N	2.49	0.42
3:I:66:GLU:OE1	3:I:100:ARG:HB2	2.20	0.42
2:K:102:HIS:CE1	2:K:122:TRP:HE1	2.37	0.42
2:B:59:ALA:CB	2:B:65:PRO:HA	2.48	0.42
2:E:164:GLU:O	2:E:165:ARG:C	2.58	0.42
3:F:231:LEU:HA	3:F:231:LEU:HD12	1.91	0.42
2:H:57:ARG:HD3	2:H:136:GLU:OE2	2.20	0.42
2:H:40:THR:HB	2:H:43:GLU:OE2	2.19	0.42
2:K:51:MET:HE3	2:K:142:PHE:CD1	2.55	0.42
1:A:124:VAL:HG22	1:A:149:ILE:O	2.19	0.41
2:B:84:GLY:H	2:B:165:ARG:NH2	2.17	0.41
2:B:33:LEU:HA	2:B:34:PRO:HD3	1.90	0.41
2:B:88:LEU:HD23	2:B:89:LEU:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:33:LEU:HA	2:H:34:PRO:HD3	1.89	0.41
1:J:205:GLN:OE1	2:K:111:LYS:HE2	2.20	0.41
2:K:70:ARG:HG2	2:K:70:ARG:HH11	1.86	0.41
3:F:294:LEU:O	3:F:298:ILE:HG13	2.20	0.41
3:I:256:LEU:O	3:I:257:SER:CB	2.69	0.41
2:K:93:ASP:O	2:K:95:THR:N	2.47	0.41
1:A:183:ALA:HA	1:A:184:PRO:HD3	1.83	0.41
1:D:143:ASN:HA	2:E:22:ASN:HD22	1.81	0.41
1:D:189:MET:CG	1:D:193:LEU:HD22	2.51	0.41
3:F:242:SER:C	3:F:244:PRO:HD3	2.41	0.41
1:J:137:VAL:O	1:J:140:ARG:HB2	2.20	0.41
3:I:238:ILE:HG21	3:L:238:ILE:HG21	2.02	0.41
1:A:81:ILE:HD13	1:A:82:GLN:HG3	2.01	0.41
3:C:96:LEU:O	3:C:121:HIS:HE1	2.03	0.41
3:C:138:ALA:O	3:C:142:ILE:HG12	2.21	0.41
3:C:146:LEU:HD12	3:C:146:LEU:HA	1.91	0.41
3:C:84:ARG:O	3:C:88:GLN:HB2	2.20	0.41
2:E:134:LYS:HA	2:E:135:PRO:HD3	1.96	0.41
2:H:167:LYS:HD2	2:H:167:LYS:H	1.85	0.41
2:H:46:GLU:O	2:H:47:GLU:CB	2.69	0.41
1:J:93:THR:HG21	1:J:126:ILE:HG21	2.02	0.41
3:L:18:THR:HG23	3:L:20:ASP:C	2.41	0.41
3:L:18:THR:HG23	3:L:20:ASP:O	2.20	0.41
2:B:123:ASN:HD22	2:B:124:THR:N	2.12	0.41
2:E:59:ALA:CB	2:E:65:PRO:HA	2.48	0.41
2:E:86:ILE:HD12	2:E:162:ILE:HD11	2.02	0.41
1:J:43:LEU:HD22	3:L:76:LYS:HA	2.02	0.41
3:C:231:LEU:HD12	3:C:231:LEU:HA	1.93	0.41
3:C:72:THR:HG22	6:C:427:HOH:O	2.20	0.41
1:D:16:VAL:CG1	1:D:17:GLY:N	2.83	0.41
2:E:144:ASN:HD22	2:E:147:ASN:HD21	1.69	0.41
1:D:177:VAL:HG23	2:E:38:ILE:CD1	2.50	0.41
2:E:46:GLU:HB3	2:E:47:GLU:H	1.69	0.41
3:F:96:LEU:O	3:F:121:HIS:HE1	2.04	0.41
3:L:99:VAL:HG12	3:L:124:LEU:CD1	2.50	0.41
3:L:329:PHE:CD2	3:L:335:GLY:HA3	2.56	0.41
1:A:189:MET:O	1:A:190:ASP:CB	2.62	0.41
2:B:144:ASN:HD22	2:B:147:ASN:HD21	1.69	0.41
3:F:91:LEU:HA	3:F:91:LEU:HD23	1.92	0.41
2:H:109:GLU:O	2:H:110:LEU:HD23	2.20	0.41
3:L:199:ILE:HG22	3:L:204:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:THR:HG23	2:B:97:LYS:H	1.86	0.41
2:E:113:ASN:O	2:E:114:ALA:C	2.58	0.41
1:G:137:VAL:O	1:G:140:ARG:HB2	2.20	0.41
2:H:113:ASN:O	2:H:114:ALA:C	2.58	0.41
1:J:202:GLU:HA	1:J:205:GLN:HG2	2.02	0.41
3:L:242:SER:C	3:L:244:PRO:HD3	2.40	0.41
1:A:137:VAL:O	1:A:140:ARG:HB2	2.21	0.41
2:B:57:ARG:HD3	2:B:136:GLU:OE2	2.21	0.41
3:C:170:ARG:HG2	6:C:412:HOH:O	2.21	0.41
3:C:242:SER:C	3:C:244:PRO:HD3	2.41	0.41
3:C:329:PHE:CD2	3:C:335:GLY:HA3	2.56	0.41
2:H:102:HIS:HB3	2:H:127:ASP:HA	2.02	0.41
2:H:67:TRP:CH2	2:H:139:ALA:HB2	2.56	0.41
2:K:144:ASN:HD22	2:K:147:ASN:HD21	1.68	0.41
3:C:317:GLU:CB	6:C:441:HOH:O	2.67	0.41
1:D:28:LYS:O	1:D:31:LEU:HD12	2.21	0.41
1:D:72:PHE:HE2	1:D:104:TRP:CD2	2.39	0.41
1:J:195:ALA:C	1:J:197:TYR:H	2.23	0.41
3:L:274:ILE:HG22	3:L:276:LEU:H	1.86	0.41
2:B:113:ASN:O	2:B:114:ALA:C	2.59	0.41
2:B:144:ASN:HD22	2:B:147:ASN:ND2	2.19	0.41
1:D:178:ALA:HB3	2:E:38:ILE:HD11	2.03	0.41
3:I:128:TYR:CE2	3:I:165:ILE:HG13	2.56	0.41
1:J:182:LEU:HD12	1:J:182:LEU:N	2.36	0.41
1:A:28:LYS:O	1:A:31:LEU:HD12	2.21	0.40
3:C:114:LEU:HD12	3:C:114:LEU:HA	1.94	0.40
1:D:13:LEU:HD13	1:D:86:ALA:HA	2.04	0.40
2:E:67:TRP:CH2	2:E:139:ALA:HB2	2.56	0.40
3:I:329:PHE:CG	3:I:335:GLY:HA3	2.56	0.40
1:J:146:TYR:CG	1:J:147:TYR:N	2.89	0.40
2:K:109:GLU:CD	2:K:109:GLU:N	2.67	0.40
3:L:183:PHE:CE1	3:L:207:LEU:HD11	2.56	0.40
2:B:46:GLU:HB3	2:B:47:GLU:H	1.69	0.40
3:F:146:LEU:HA	3:F:146:LEU:HD12	1.91	0.40
1:G:195:ALA:C	1:G:197:TYR:H	2.25	0.40
3:I:84:ARG:O	3:I:88:GLN:HB2	2.21	0.40
2:K:62:ASN:HB3	2:K:64:LEU:CD2	2.51	0.40
1:A:202:GLU:HA	1:A:205:GLN:HG2	2.03	0.40
1:D:31:LEU:HB3	1:D:50:LEU:HD21	2.04	0.40
3:I:114:LEU:HA	3:I:114:LEU:HD12	1.95	0.40
3:I:138:ALA:O	3:I:142:ILE:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:184:GLN:NE2	3:L:270:LYS:NZ	2.66	0.40
1:A:55:ASN:OD1	1:A:174:LEU:HD12	2.22	0.40
3:C:344:GLU:CG	3:C:345:GLU:N	2.83	0.40
2:E:123:ASN:HD22	2:E:124:THR:N	2.11	0.40
2:E:63:ASP:O	2:E:65:PRO:HD3	2.22	0.40
3:F:18:THR:HG22	3:F:21:GLU:HG3	2.02	0.40
3:I:231:LEU:HA	3:I:231:LEU:HD12	1.90	0.40
3:L:207:LEU:HG	3:L:212:LEU:HD22	2.04	0.40
3:C:18:THR:HG23	3:C:20:ASP:C	2.42	0.40
3:C:207:LEU:HG	3:C:212:LEU:HD22	2.03	0.40
3:C:259:ARG:CZ	3:C:259:ARG:HB3	2.51	0.40
2:E:70:ARG:HG2	2:E:70:ARG:HH11	1.87	0.40
3:F:334:ARG:CZ	3:F:334:ARG:HB3	2.52	0.40
1:G:13:LEU:HD13	1:G:86:ALA:HA	2.04	0.40
1:G:178:ALA:O	1:G:179:MET:CB	2.69	0.40
1:G:203:VAL:O	1:G:203:VAL:HG12	2.22	0.40
3:I:259:ARG:NH1	3:I:259:ARG:CB	2.80	0.40
3:C:331:THR:CG2	1:J:142:LYS:HA	2.50	0.40
1:J:202:GLU:O	1:J:206:THR:HG23	2.22	0.40
2:K:70:ARG:HA	2:K:70:ARG:HD2	1.82	0.40
3:L:21:GLU:O	3:L:24:VAL:HB	2.22	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	204/216 (94%)	174 (85%)	17 (8%)	13 (6%)	1	2
1	D	204/216 (94%)	176 (86%)	15 (7%)	13 (6%)	1	2
1	G	204/216 (94%)	174 (85%)	17 (8%)	13 (6%)	1	2
1	J	204/216 (94%)	175 (86%)	16 (8%)	13 (6%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	144/201 (72%)	121 (84%)	15 (10%)	8 (6%)	2	3
2	E	144/201 (72%)	119 (83%)	17 (12%)	8 (6%)	2	3
2	H	144/201 (72%)	121 (84%)	15 (10%)	8 (6%)	2	3
2	K	144/201 (72%)	121 (84%)	15 (10%)	8 (6%)	2	3
3	C	342/386 (89%)	301 (88%)	38 (11%)	3 (1%)	17	40
3	F	342/386 (89%)	302 (88%)	37 (11%)	3 (1%)	17	40
3	I	342/386 (89%)	305 (89%)	34 (10%)	3 (1%)	17	40
3	L	342/386 (89%)	305 (89%)	34 (10%)	3 (1%)	17	40
All	All	2760/3212 (86%)	2394 (87%)	270 (10%)	96 (4%)	3	8

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	ARG
1	A	179	MET
1	A	189	MET
1	A	190	ASP
1	A	191	PRO
2	B	45	GLU
2	B	46	GLU
2	B	59	ALA
2	B	60	SER
2	B	165	ARG
1	D	179	MET
1	D	189	MET
1	D	190	ASP
1	D	191	PRO
2	E	45	GLU
2	E	46	GLU
2	E	59	ALA
2	E	60	SER
2	E	165	ARG
1	G	106	ARG
1	G	179	MET
1	G	189	MET
1	G	190	ASP
1	G	191	PRO
2	H	45	GLU
2	H	46	GLU

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Mol	Chain	Res	Type
2	H	59	ALA
2	H	60	SER
2	H	165	ARG
1	J	106	ARG
1	J	179	MET
1	J	189	MET
1	J	190	ASP
1	J	191	PRO
2	K	45	GLU
2	K	46	GLU
2	K	59	ALA
2	K	60	SER
2	K	165	ARG
1	A	178	ALA
1	A	196	GLN
2	B	116	SER
1	D	106	ARG
1	D	178	ALA
1	D	196	GLN
2	E	116	SER
3	F	172	GLU
1	G	178	ALA
1	G	196	GLN
2	H	116	SER
1	J	178	ALA
1	J	196	GLN
1	A	194	ALA
3	C	172	GLU
1	D	194	ALA
2	E	47	GLU
1	G	194	ALA
2	H	47	GLU
3	I	172	GLU
1	J	194	ALA
2	K	47	GLU
2	K	116	SER
3	L	172	GLU
3	L	336	GLU
1	A	186	GLU
1	A	187	VAL
1	A	195	ALA
2	B	47	GLU

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Mol	Chain	Res	Type
3	C	336	GLU
1	D	186	GLU
1	D	187	VAL
1	D	195	ALA
3	F	336	GLU
1	G	186	GLU
1	G	187	VAL
1	G	195	ALA
3	I	336	GLU
1	J	186	GLU
1	J	195	ALA
1	A	188	VAL
1	D	188	VAL
1	D	210	PRO
1	G	188	VAL
1	G	210	PRO
1	J	187	VAL
1	J	188	VAL
1	J	210	PRO
1	A	210	PRO
2	H	65	PRO
2	B	65	PRO
2	K	65	PRO
2	E	65	PRO
3	C	16	ILE
3	F	16	ILE
3	I	16	ILE
3	L	16	ILE

### 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	178/185 (96%)	165 (93%)	13 (7%)	14	33
1	D	178/185 (96%)	165 (93%)	13 (7%)	14	33
1	G	178/185 (96%)	165 (93%)	13 (7%)	14	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	178/185 (96%)	166 (93%)	12 (7%)	16	37
2	B	131/176 (74%)	119 (91%)	12 (9%)	9	21
2	E	131/176 (74%)	119 (91%)	12 (9%)	9	21
2	H	131/176 (74%)	119 (91%)	12 (9%)	9	21
2	K	131/176 (74%)	119 (91%)	12 (9%)	9	21
3	C	295/334 (88%)	277 (94%)	18 (6%)	18	41
3	F	295/334 (88%)	277 (94%)	18 (6%)	18	41
3	I	295/334 (88%)	277 (94%)	18 (6%)	18	41
3	L	295/334 (88%)	277 (94%)	18 (6%)	18	41
All	All	2416/2780 (87%)	2245 (93%)	171 (7%)	14	34

All (171) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	16	VAL
1	A	28	LYS
1	A	31	LEU
1	A	81	ILE
1	A	97	THR
1	A	111	VAL
1	A	118	VAL
1	A	140	ARG
1	A	141	LYS
1	A	157	PHE
1	A	158	GLU
1	A	186	GLU
2	B	26	GLN
2	B	46	GLU
2	B	57	ARG
2	B	63	ASP
2	B	64	LEU
2	B	75	VAL
2	B	109	GLU
2	B	118	ARG
2	B	123	ASN
2	B	146	GLU
2	B	156	GLU
2	B	166	GLU

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Mol	Chain	Res	Type
3	C	19	GLU
3	C	29	LEU
3	C	43	THR
3	C	66	GLU
3	C	78	GLU
3	C	81	GLU
3	C	109	THR
3	C	112	GLU
3	C	114	LEU
3	C	146	LEU
3	C	192	VAL
3	C	196	GLN
3	C	208	LEU
3	C	212	LEU
3	C	247	ARG
3	C	278	THR
3	C	293	THR
3	C	296	THR
1	D	13	LEU
1	D	16	VAL
1	D	28	LYS
1	D	31	LEU
1	D	81	ILE
1	D	97	THR
1	D	111	VAL
1	D	118	VAL
1	D	140	ARG
1	D	141	LYS
1	D	157	PHE
1	D	158	GLU
1	D	186	GLU
2	E	26	GLN
2	E	46	GLU
2	E	57	ARG
2	E	63	ASP
2	E	64	LEU
2	E	75	VAL
2	E	109	GLU
2	E	118	ARG
2	E	123	ASN
2	E	146	GLU
2	E	156	GLU

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Mol	Chain	Res	Type
2	E	166	GLU
3	F	19	GLU
3	F	29	LEU
3	F	43	THR
3	F	66	GLU
3	F	78	GLU
3	F	81	GLU
3	F	109	THR
3	F	112	GLU
3	F	114	LEU
3	F	146	LEU
3	F	192	VAL
3	F	196	GLN
3	F	208	LEU
3	F	212	LEU
3	F	247	ARG
3	F	278	THR
3	F	293	THR
3	F	296	THR
1	G	13	LEU
1	G	16	VAL
1	G	28	LYS
1	G	31	LEU
1	G	81	ILE
1	G	97	THR
1	G	111	VAL
1	G	118	VAL
1	G	140	ARG
1	G	141	LYS
1	G	157	PHE
1	G	158	GLU
1	G	186	GLU
2	H	26	GLN
2	H	46	GLU
2	H	57	ARG
2	H	63	ASP
2	H	64	LEU
2	H	75	VAL
2	H	109	GLU
2	H	118	ARG
2	H	123	ASN
2	H	146	GLU

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Mol	Chain	Res	Type
2	H	156	GLU
2	H	166	GLU
3	I	19	GLU
3	I	29	LEU
3	I	43	THR
3	I	66	GLU
3	I	78	GLU
3	I	81	GLU
3	I	109	THR
3	I	112	GLU
3	I	114	LEU
3	I	146	LEU
3	I	192	VAL
3	I	196	GLN
3	I	208	LEU
3	I	212	LEU
3	I	247	ARG
3	I	278	THR
3	I	293	THR
3	I	296	THR
1	J	13	LEU
1	J	16	VAL
1	J	28	LYS
1	J	31	LEU
1	J	81	ILE
1	J	97	THR
1	J	118	VAL
1	J	140	ARG
1	J	141	LYS
1	J	157	PHE
1	J	158	GLU
1	J	186	GLU
2	K	26	GLN
2	K	46	GLU
2	K	57	ARG
2	K	63	ASP
2	K	64	LEU
2	K	75	VAL
2	K	109	GLU
2	K	118	ARG
2	K	123	ASN
2	K	146	GLU

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Mol	Chain	Res	Type
2	K	156	GLU
2	K	166	GLU
3	L	19	GLU
3	L	29	LEU
3	L	43	THR
3	L	66	GLU
3	L	78	GLU
3	L	81	GLU
3	L	109	THR
3	L	112	GLU
3	L	114	LEU
3	L	146	LEU
3	L	192	VAL
3	L	196	GLN
3	L	208	LEU
3	L	212	LEU
3	L	247	ARG
3	L	278	THR
3	L	293	THR
3	L	296	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (73) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	30	HIS
1	A	100	ASN
1	A	143	ASN
1	A	156	ASN
2	B	22	ASN
2	B	102	HIS
2	B	113	ASN
2	B	123	ASN
2	B	147	ASN
3	C	111	GLN
3	C	121	HIS
3	C	130	HIS
3	C	131	ASN
3	C	173	ASN
3	C	186	HIS
3	C	206	HIS
3	C	252	ASN

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Mol	Chain	Res	Type
1	D	10	GLN
1	D	30	HIS
1	D	143	ASN
1	D	156	ASN
2	E	22	ASN
2	E	102	HIS
2	E	113	ASN
2	E	123	ASN
2	E	147	ASN
3	F	111	GLN
3	F	121	HIS
3	F	130	HIS
3	F	131	ASN
3	F	173	ASN
3	F	186	HIS
3	F	206	HIS
3	F	245	ASN
3	F	252	ASN
1	G	10	GLN
1	G	30	HIS
1	G	100	ASN
1	G	143	ASN
1	G	156	ASN
2	H	22	ASN
2	H	102	HIS
2	H	113	ASN
2	H	123	ASN
2	H	147	ASN
3	I	111	GLN
3	I	121	HIS
3	I	130	HIS
3	I	131	ASN
3	I	147	GLN
3	I	173	ASN
3	I	184	GLN
3	I	186	HIS
3	I	252	ASN
1	J	10	GLN
1	J	30	HIS
1	J	100	ASN
1	J	143	ASN
1	J	156	ASN

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Mol	Chain	Res	Type
2	K	22	ASN
2	K	102	HIS
2	K	113	ASN
2	K	123	ASN
2	K	147	ASN
3	L	111	GLN
3	L	121	HIS
3	L	130	HIS
3	L	131	ASN
3	L	173	ASN
3	L	186	HIS
3	L	206	HIS
3	L	252	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z  > 2$
5	GNP	D	2250	4	28,34,34	2.19	7 (25%)	30,54,54	2.02	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GNP	J	4250	4	28,34,34	2.21	7 (25%)	30,54,54	1.96	8 (26%)
5	GNP	A	1250	4	28,34,34	2.18	7 (25%)	30,54,54	2.01	6 (20%)
5	GNP	G	3250	4	28,34,34	2.14	6 (21%)	30,54,54	1.98	6 (20%)

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
5	GNP	D	2250	4	-	5/17/38/38	0/3/3/3
5	GNP	J	4250	4	-	5/17/38/38	0/3/3/3
5	GNP	A	1250	4	-	5/17/38/38	0/3/3/3
5	GNP	G	3250	4	-	5/17/38/38	0/3/3/3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1250	GNP	C4-N9	-7.02	1.38	1.47
5	J	4250	GNP	C4-N9	-6.80	1.38	1.47
5	D	2250	GNP	C4-N9	-6.64	1.38	1.47
5	G	3250	GNP	C4-N9	-6.46	1.39	1.47
5	G	3250	GNP	C6-N1	4.30	1.40	1.33
5	J	4250	GNP	C6-N1	4.21	1.40	1.33
5	A	1250	GNP	C5-C6	-4.13	1.45	1.52
5	D	2250	GNP	PG-O2G	-4.11	1.45	1.56
5	D	2250	GNP	PB-O2B	-4.01	1.46	1.56
5	A	1250	GNP	PG-O2G	-3.95	1.46	1.56
5	G	3250	GNP	PG-O2G	-3.93	1.46	1.56
5	D	2250	GNP	C6-N1	3.93	1.39	1.33
5	G	3250	GNP	PB-O2B	-3.78	1.46	1.56
5	J	4250	GNP	PB-O2B	-3.74	1.46	1.56
5	G	3250	GNP	C5-C6	-3.71	1.46	1.52
5	J	4250	GNP	C5-C6	-3.53	1.46	1.52
5	J	4250	GNP	PB-O3A	3.51	1.63	1.59
5	A	1250	GNP	C6-N1	3.50	1.39	1.33
5	J	4250	GNP	PG-O2G	-3.44	1.47	1.56
5	D	2250	GNP	C5-C6	-3.32	1.47	1.52
5	A	1250	GNP	PB-O2B	-3.13	1.48	1.56
5	A	1250	GNP	PB-O3A	2.78	1.62	1.59
5	D	2250	GNP	PB-O3A	2.47	1.62	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	4250	GNP	C5-C4	-2.24	1.39	1.53
5	D	2250	GNP	C5-C4	-2.22	1.39	1.53
5	A	1250	GNP	C5-C4	-2.18	1.39	1.53
5	G	3250	GNP	C5-C4	-2.07	1.40	1.53

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	3250	GNP	C4-C5-N7	5.83	110.18	102.46
5	A	1250	GNP	C4-C5-N7	5.68	109.99	102.46
5	D	2250	GNP	C4-C5-N7	5.66	109.96	102.46
5	J	4250	GNP	C4-C5-N7	5.63	109.92	102.46
5	G	3250	GNP	C5-C6-N1	-4.63	112.48	118.19
5	D	2250	GNP	O6-C6-C5	4.62	129.29	119.86
5	A	1250	GNP	C5-C6-N1	-4.61	112.50	118.19
5	D	2250	GNP	C5-C6-N1	-4.55	112.58	118.19
5	A	1250	GNP	O6-C6-C5	4.48	129.01	119.86
5	J	4250	GNP	C5-C6-N1	-4.44	112.72	118.19
5	J	4250	GNP	O6-C6-C5	4.39	128.81	119.86
5	G	3250	GNP	O6-C6-C5	4.29	128.60	119.86
5	G	3250	GNP	O3G-PG-O1G	-3.58	104.46	113.45
5	A	1250	GNP	O3G-PG-O1G	-3.56	104.50	113.45
5	D	2250	GNP	O3G-PG-O1G	-3.47	104.72	113.45
5	D	2250	GNP	O6-C6-N1	-3.39	118.13	122.69
5	J	4250	GNP	O3G-PG-O1G	-3.18	105.45	113.45
5	J	4250	GNP	O6-C6-N1	-3.14	118.47	122.69
5	A	1250	GNP	O6-C6-N1	-3.13	118.49	122.69
5	G	3250	GNP	O6-C6-N1	-2.81	118.91	122.69
5	A	1250	GNP	O1G-PG-N3B	2.58	115.56	111.77
5	D	2250	GNP	O1G-PG-N3B	2.48	115.42	111.77
5	G	3250	GNP	O1G-PG-N3B	2.33	115.20	111.77
5	J	4250	GNP	O1G-PG-N3B	2.22	115.05	111.77
5	D	2250	GNP	O2G-PG-O1G	-2.17	108.00	113.45
5	J	4250	GNP	O1B-PB-N3B	2.11	114.88	111.77
5	J	4250	GNP	O2G-PG-O1G	-2.07	108.25	113.45

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	3250	GNP	PB-N3B-PG-O1G
5	G	3250	GNP	PG-N3B-PB-O1B

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Mol	Chain	Res	Type	Atoms
5	G	3250	GNP	PA-O3A-PB-O1B
5	G	3250	GNP	PA-O3A-PB-O2B
5	G	3250	GNP	C2'-C1'-N9-C4
5	D	2250	GNP	PB-N3B-PG-O1G
5	D	2250	GNP	PG-N3B-PB-O1B
5	D	2250	GNP	PA-O3A-PB-O1B
5	D	2250	GNP	PA-O3A-PB-O2B
5	D	2250	GNP	C2'-C1'-N9-C4
5	J	4250	GNP	PB-N3B-PG-O1G
5	J	4250	GNP	PG-N3B-PB-O1B
5	J	4250	GNP	PA-O3A-PB-O1B
5	J	4250	GNP	PA-O3A-PB-O2B
5	J	4250	GNP	C2'-C1'-N9-C4
5	A	1250	GNP	PB-N3B-PG-O1G
5	A	1250	GNP	PG-N3B-PB-O1B
5	A	1250	GNP	PA-O3A-PB-O1B
5	A	1250	GNP	PA-O3A-PB-O2B
5	A	1250	GNP	C2'-C1'-N9-C4

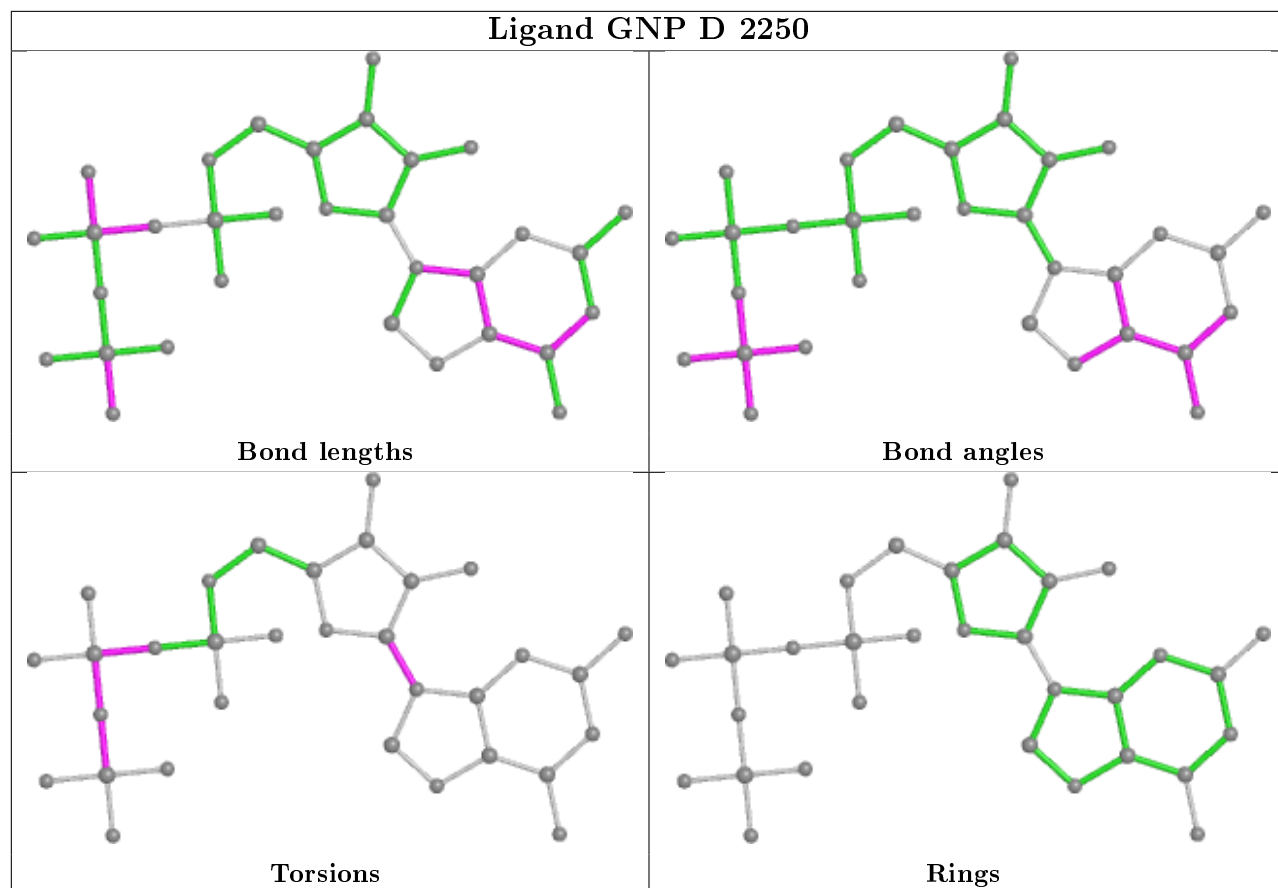
There are no ring outliers.

4 monomers are involved in 14 short contacts:

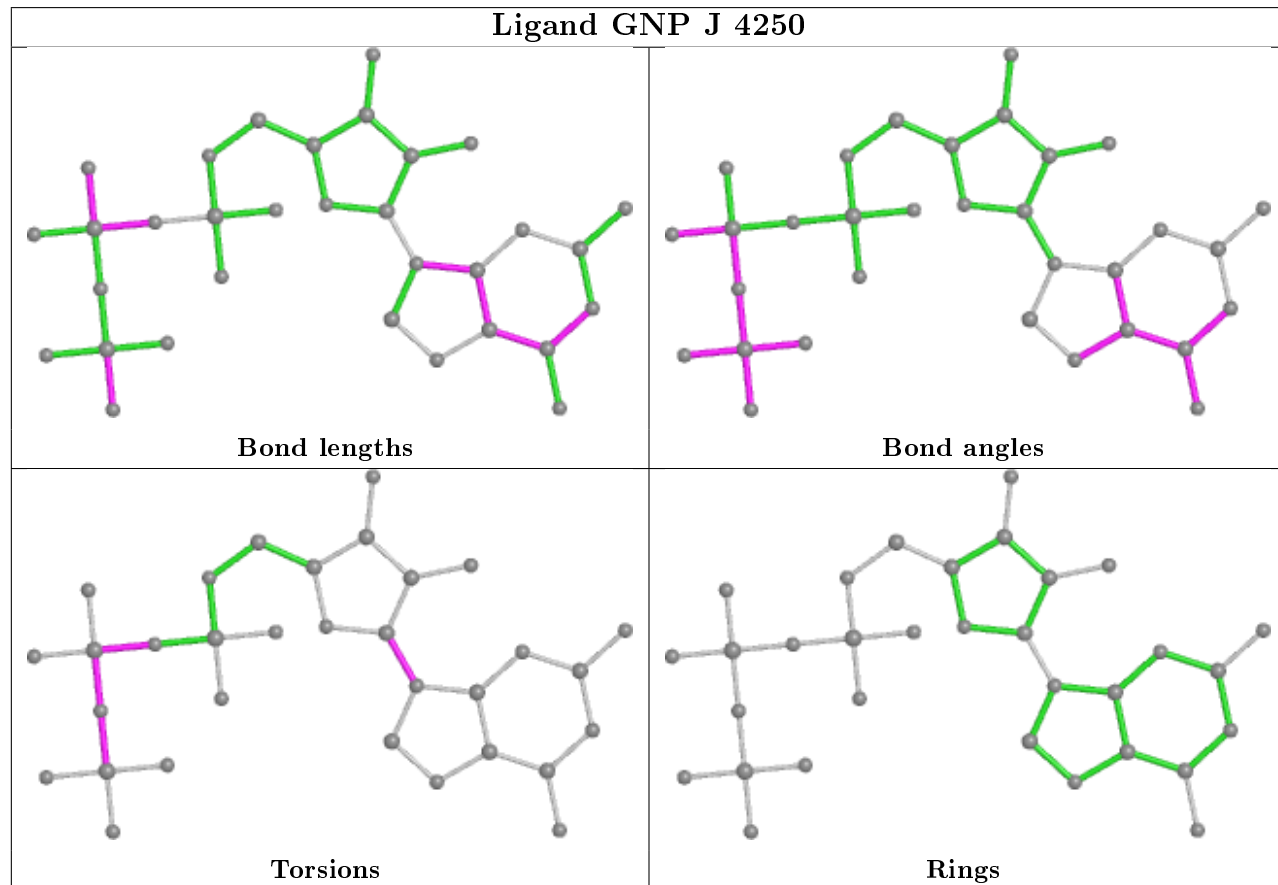
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	2250	GNP	3	0
5	J	4250	GNP	6	0
5	A	1250	GNP	2	0
5	G	3250	GNP	3	0

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.

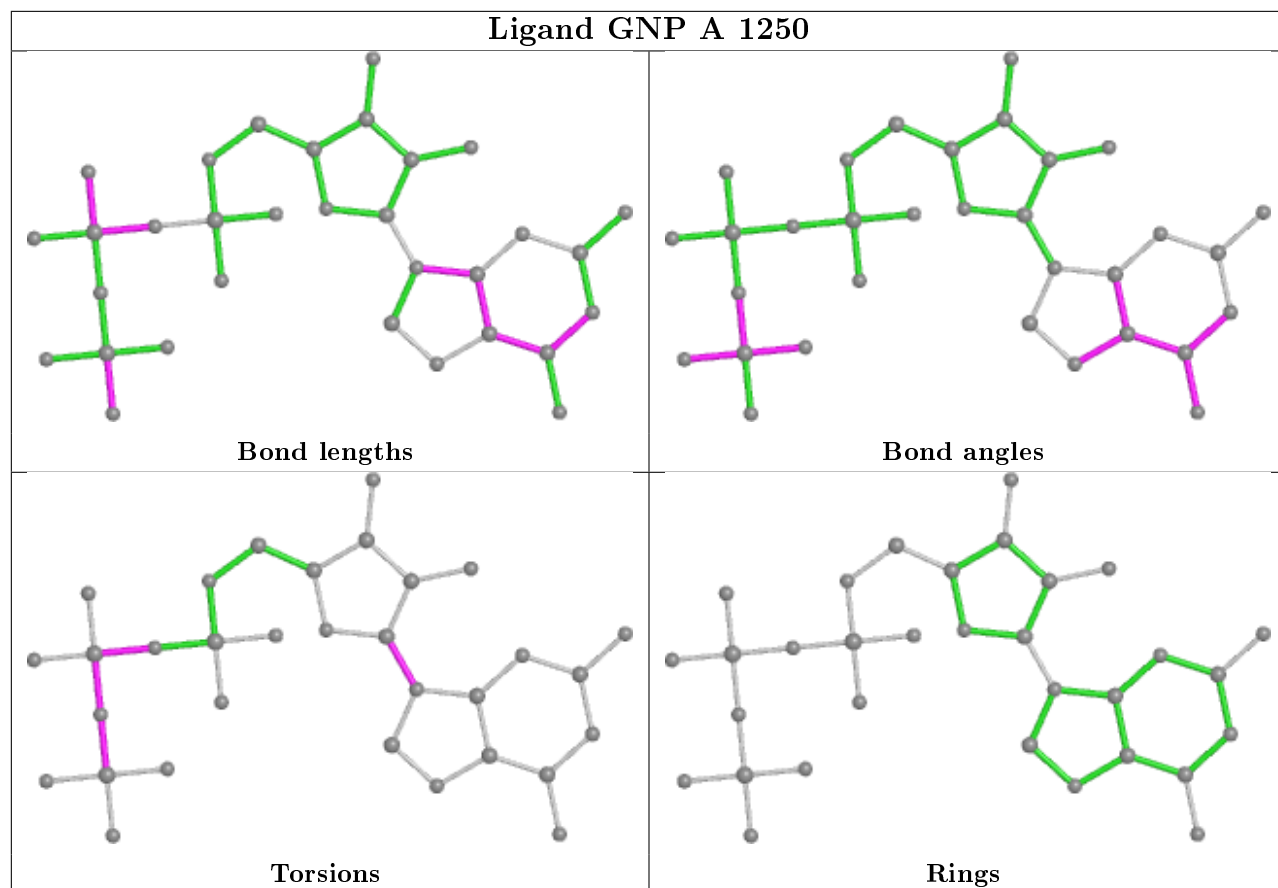
## Ligand GNP D 2250



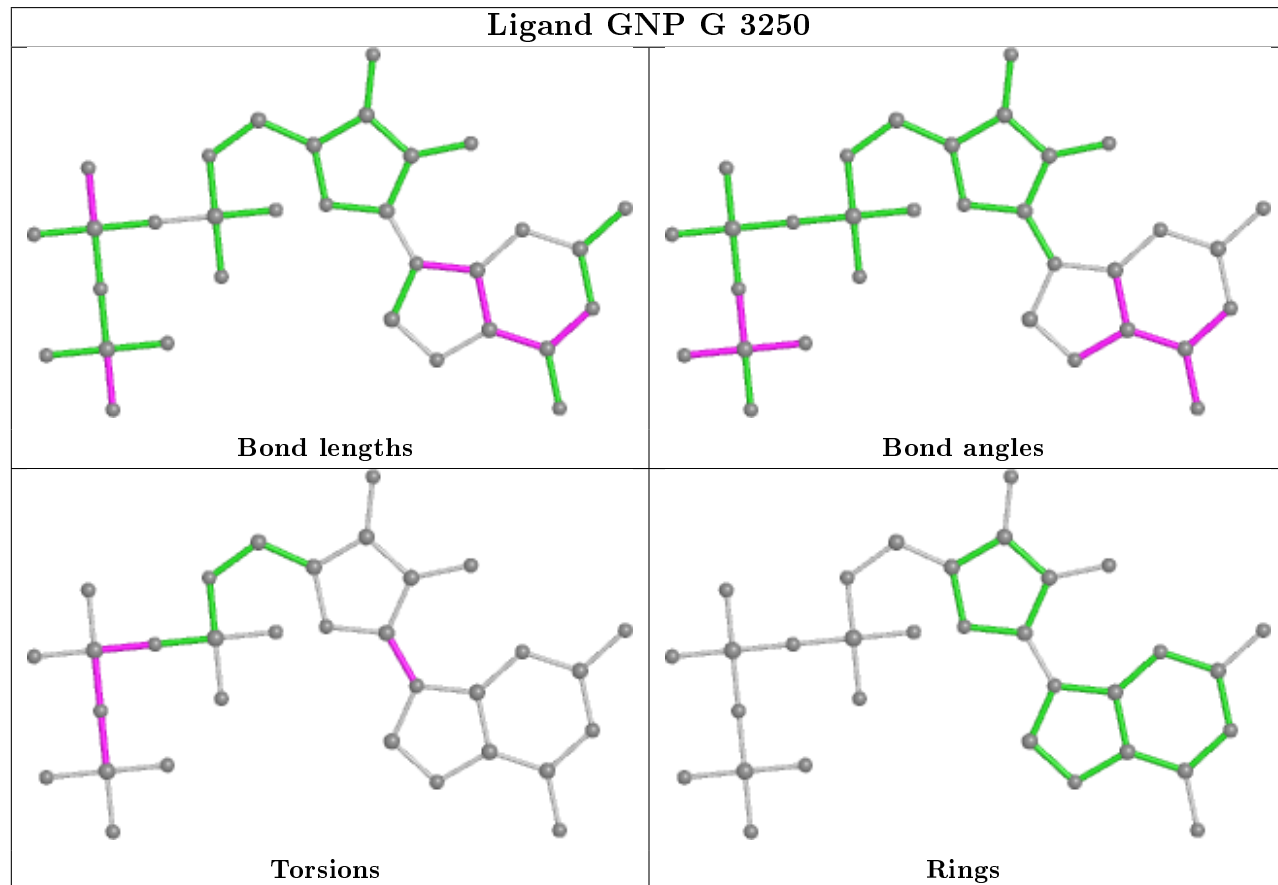
## Ligand GNP J 4250



## Ligand GNP A 1250



## Ligand GNP G 3250



## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	206/216 (95%)	0.36	23 (11%) 5 4	27, 46, 132, 170	0
1	D	206/216 (95%)	0.54	22 (10%) 6 4	21, 46, 146, 188	0
1	G	206/216 (95%)	0.44	23 (11%) 5 4	28, 49, 127, 168	0
1	J	206/216 (95%)	0.31	19 (9%) 9 7	24, 47, 117, 170	0
2	B	146/201 (72%)	0.73	24 (16%) 1 1	36, 72, 130, 159	0
2	E	146/201 (72%)	1.38	42 (28%) 0 0	41, 88, 138, 159	0
2	H	146/201 (72%)	0.96	24 (16%) 1 1	41, 71, 138, 176	0
2	K	146/201 (72%)	0.63	21 (14%) 2 1	28, 73, 126, 149	0
3	C	344/386 (89%)	-0.07	4 (1%) 79 80	21, 42, 76, 135	0
3	F	344/386 (89%)	-0.04	14 (4%) 37 36	24, 45, 83, 135	0
3	I	344/386 (89%)	-0.05	5 (1%) 73 76	23, 45, 81, 114	0
3	L	344/386 (89%)	0.02	10 (2%) 51 52	22, 45, 90, 143	0
All	All	2784/3212 (86%)	0.30	231 (8%) 11 9	21, 49, 120, 188	0

All (231) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	189	MET	14.5
1	D	191	PRO	12.0
1	D	192	ALA	11.8
1	G	192	ALA	10.9
1	D	188	VAL	10.5
2	H	63	ASP	10.3
1	G	191	PRO	10.2
1	D	187	VAL	10.1
1	A	190	ASP	9.2
1	D	190	ASP	8.2
1	D	195	ALA	8.0

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Mol	Chain	Res	Type	RSRZ
1	A	187	VAL	7.5
2	H	22	ASN	7.5
1	J	189	MET	7.4
2	B	63	ASP	7.4
1	A	192	ALA	7.4
1	D	194	ALA	7.3
2	E	107	MET	6.8
1	A	212	GLU	6.7
1	A	188	VAL	6.6
1	A	191	PRO	6.6
2	H	23	HIS	6.5
2	E	116	SER	6.3
1	J	190	ASP	6.3
1	G	197	TYR	6.2
1	A	197	TYR	6.1
3	F	20	ASP	6.0
1	G	199	HIS	5.9
1	D	193	LEU	5.9
2	E	63	ASP	5.8
2	E	61	GLU	5.8
1	A	194	ALA	5.7
1	D	197	TYR	5.7
1	D	141	LYS	5.6
1	G	186	GLU	5.6
2	B	23	HIS	5.5
2	E	117	ASP	5.3
1	A	186	GLU	5.2
1	A	193	LEU	5.2
2	B	65	PRO	5.2
2	H	116	SER	5.1
1	G	196	GLN	5.1
2	H	65	PRO	5.1
1	D	199	HIS	5.0
1	G	140	ARG	5.0
2	B	61	GLU	5.0
1	G	212	GLU	5.0
2	E	145	ALA	4.9
1	G	193	LEU	4.9
1	G	141	LYS	4.8
2	E	49	PHE	4.7
2	E	23	HIS	4.7
1	A	199	HIS	4.7

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Mol	Chain	Res	Type	RSRZ
1	G	195	ALA	4.6
2	H	37	GLU	4.5
2	K	61	GLU	4.5
2	E	160	LYS	4.5
2	E	22	ASN	4.4
2	H	64	LEU	4.3
2	H	61	GLU	4.2
1	D	186	GLU	4.2
2	E	82	GLU	4.2
1	A	141	LYS	4.2
1	J	191	PRO	4.1
1	D	198	GLU	4.1
1	A	195	ALA	4.1
1	J	192	ALA	4.0
1	D	212	GLU	4.0
2	E	115	GLY	4.0
2	H	82	GLU	3.9
3	I	334	ARG	3.9
2	B	64	LEU	3.8
2	E	167	LYS	3.8
2	K	115	GLY	3.8
3	I	345	GLU	3.8
1	J	193	LEU	3.8
1	A	189	MET	3.8
2	H	167	LYS	3.8
1	A	211	ASP	3.8
2	B	24	ASP	3.8
2	H	114	ALA	3.8
1	G	187	VAL	3.8
2	B	117	ASP	3.7
2	B	82	GLU	3.7
1	G	194	ALA	3.7
1	D	196	GLN	3.7
2	K	23	HIS	3.7
3	I	333	GLY	3.6
2	B	167	LYS	3.6
2	K	63	ASP	3.6
2	B	115	GLY	3.6
1	J	212	GLU	3.5
2	H	115	GLY	3.5
1	J	196	GLN	3.5
2	B	22	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
2	H	28	GLU	3.4
2	K	38	ILE	3.4
2	E	143	LEU	3.4
2	E	144	ASN	3.3
1	D	202	GLU	3.3
1	D	213	ASP	3.3
2	K	132	CYS	3.3
1	J	197	TYR	3.3
2	E	67	TRP	3.2
2	H	117	ASP	3.2
3	C	341	ASP	3.2
2	H	24	ASP	3.2
1	G	189	MET	3.2
2	E	46	GLU	3.2
1	G	190	ASP	3.2
3	F	31	ASP	3.2
1	G	211	ASP	3.1
3	F	32	ASP	3.1
2	E	62	ASN	3.1
2	B	45	GLU	3.1
3	F	345	GLU	3.1
2	B	28	GLU	3.1
3	L	345	GLU	3.1
1	A	213	ASP	3.1
1	A	202	GLU	3.1
2	B	166	GLU	3.0
2	E	65	PRO	3.0
2	E	140	ILE	3.0
2	E	45	GLU	3.0
2	B	26	GLN	3.0
2	B	140	ILE	3.0
1	G	213	ASP	2.9
2	E	149	GLN	2.9
2	B	37	GLU	2.9
2	E	66	GLU	2.9
2	K	64	LEU	2.9
1	A	140	ARG	2.9
2	E	165	ARG	2.9
3	C	310	LEU	2.9
3	L	20	ASP	2.9
3	L	52	LEU	2.8
2	E	163	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	198	GLU	2.8
1	J	195	ALA	2.8
3	C	230	HIS	2.8
3	F	19	GLU	2.8
2	K	145	ALA	2.8
2	H	140	ILE	2.7
2	E	132	CYS	2.7
2	K	114	ALA	2.7
1	D	211	ASP	2.7
1	G	144	LEU	2.7
2	H	164	GLU	2.7
2	K	62	ASN	2.7
1	J	188	VAL	2.7
1	J	200	ASP	2.7
2	K	117	ASP	2.7
1	A	209	LEU	2.7
2	B	163	GLU	2.7
2	B	59	ALA	2.6
2	E	121	VAL	2.6
2	K	82	GLU	2.6
2	H	160	LYS	2.6
3	F	157	ASN	2.6
1	G	198	GLU	2.6
2	E	108	MET	2.6
2	H	66	GLU	2.6
2	E	119	ALA	2.6
3	F	155	ALA	2.6
1	J	187	VAL	2.6
2	E	24	ASP	2.5
3	L	30	GLU	2.5
2	K	110	LEU	2.5
2	H	26	GLN	2.5
3	F	2	ALA	2.5
3	L	230	HIS	2.5
2	E	64	LEU	2.5
2	B	62	ASN	2.5
2	K	65	PRO	2.5
2	B	116	SER	2.5
2	E	84	GLY	2.5
1	A	137	VAL	2.5
1	J	211	ASP	2.4
1	J	199	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	G	188	VAL	2.4
2	K	144	ASN	2.4
2	K	84	GLY	2.4
1	J	186	GLU	2.4
2	E	38	ILE	2.4
2	K	166	GLU	2.4
1	J	134	LYS	2.3
3	L	320	ASP	2.3
3	F	30	GLU	2.3
3	L	327	GLU	2.3
1	G	185	PRO	2.3
1	J	67	ALA	2.3
2	E	28	GLU	2.3
2	E	146	GLU	2.3
2	H	163	GLU	2.3
3	L	32	ASP	2.3
2	H	145	ALA	2.3
3	F	333	GLY	2.3
2	H	45	GLU	2.3
3	F	67	PHE	2.2
2	E	60	SER	2.2
2	H	53	ALA	2.2
3	F	39	LEU	2.2
2	E	112	PRO	2.2
3	L	310	LEU	2.2
1	A	196	GLN	2.2
3	F	52	LEU	2.1
2	E	51	MET	2.1
2	B	60	SER	2.1
2	E	26	GLN	2.1
1	G	67	ALA	2.1
2	B	139	ALA	2.1
2	K	107	MET	2.1
1	J	213	ASP	2.1
3	C	19	GLU	2.1
1	D	206	THR	2.1
2	E	133	PRO	2.1
2	B	146	GLU	2.1
2	K	156	GLU	2.1
3	I	281	LEU	2.1
3	F	146	LEU	2.0
1	D	137	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	203	VAL	2.0
2	K	146	GLU	2.0
3	I	341	ASP	2.0
3	L	313	ASN	2.0
1	G	66	THR	2.0
1	J	206	THR	2.0
2	E	88	LEU	2.0
2	E	80	HIS	2.0
2	K	163	GLU	2.0
1	A	210	PRO	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

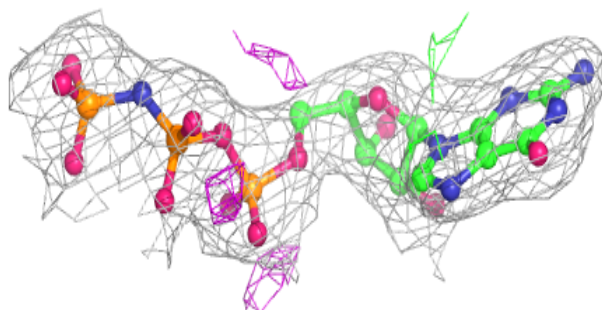
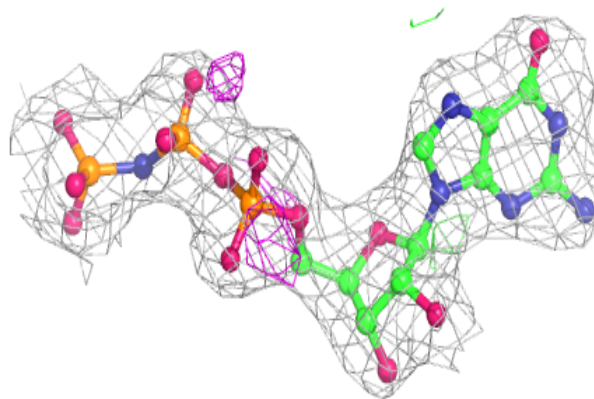
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	MG	D	2251	1/1	0.95	0.09	44,44,44,44	0
4	MG	G	3251	1/1	0.96	0.13	36,36,36,36	0
5	GNP	A	1250	32/32	0.96	0.13	37,37,37,37	0
5	GNP	G	3250	32/32	0.96	0.15	37,37,37,37	0
5	GNP	J	4250	32/32	0.97	0.13	36,36,36,36	0
4	MG	J	4251	1/1	0.98	0.08	44,44,44,44	0
5	GNP	D	2250	32/32	0.98	0.13	37,37,37,37	0
4	MG	A	1251	1/1	0.99	0.07	29,29,29,29	0

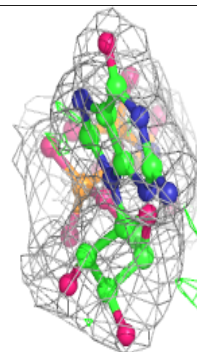
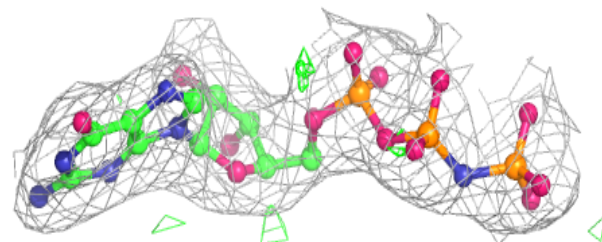
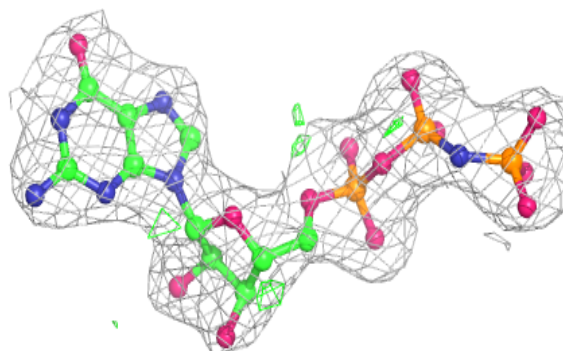
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around GNP A 1250:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

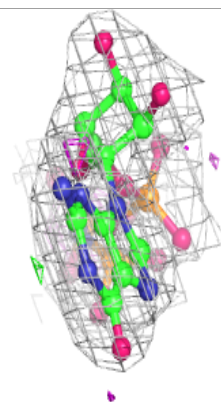
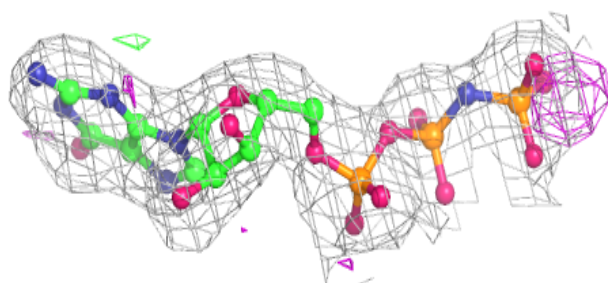
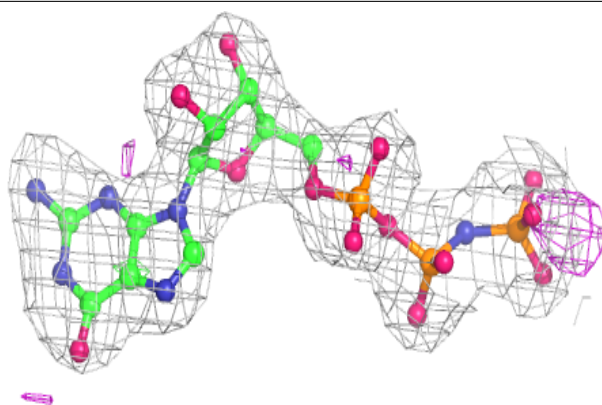
**Electron density around GNP G 3250:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

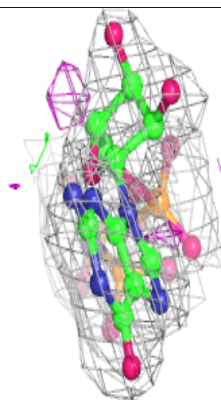
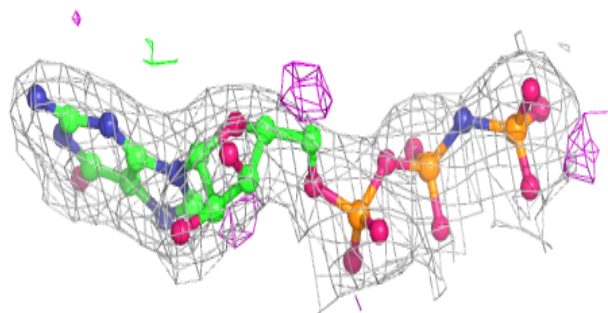
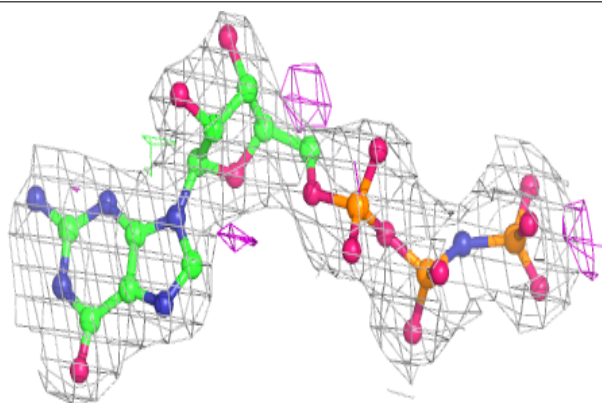


**Electron density around GNP J 4250:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around GNP D 2250:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers

There are no such residues in this entry.