



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:26 am GMT

PDB ID : 2D3B
Title : Crystal Structure of the Maize Glutamine Synthetase complexed with AMPPNP and Methionine sulfoximine
Authors : Unno, H.; Uchida, T.; Sugawara, H.; Kurisu, G.; Sugiyama, T.; Yamaya, T.; Sakakibara, H.; Hase, T.; Kusunoki, M.
Deposited on : 2005-09-26
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

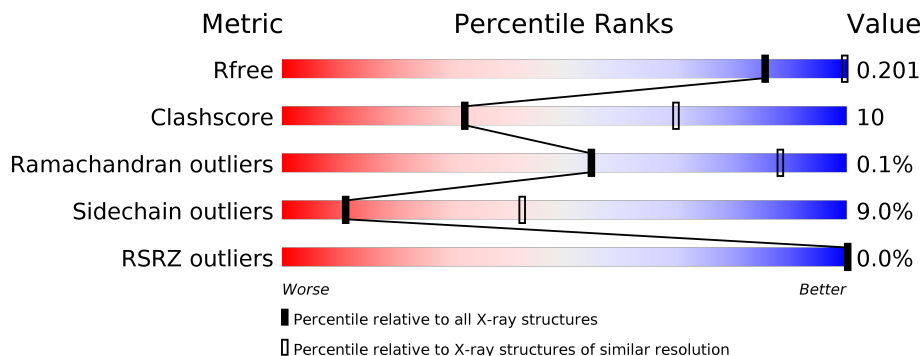
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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







Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1195 (3.60-3.40)
Clashscore	112137	1322 (3.60-3.40)
Ramachandran outliers	110173	1283 (3.60-3.40)
Sidechain outliers	110143	1284 (3.60-3.40)
RSRZ outliers	101464	1226 (3.60-3.40)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	356	<div> <div style="width: 79%;"></div> <div style="width: 17%;"></div> <div style="width: 4%;"></div> <div style="width: 2%;"></div> </div> <div>79% 17% . .</div>
1	B	356	<div> <div style="width: 79%;"></div> <div style="width: 17%;"></div> <div style="width: 4%;"></div> <div style="width: 2%;"></div> </div> <div>79% 17% . .</div>
1	C	356	<div> <div style="width: 76%;"></div> <div style="width: 19%;"></div> <div style="width: 4%;"></div> <div style="width: 2%;"></div> </div> <div>76% 19% . .</div>
1	D	356	<div> <div style="width: 76%;"></div> <div style="width: 19%;"></div> <div style="width: 4%;"></div> <div style="width: 2%;"></div> </div> <div>76% 19% . .</div>
1	E	356	<div> <div style="width: 76%;"></div> <div style="width: 21%;"></div> <div style="width: 4%;"></div> <div style="width: 2%;"></div> </div> <div>76% 21% . .</div>
1	F	356	<div> <div style="width: 76%;"></div> <div style="width: 20%;"></div> <div style="width: 4%;"></div> <div style="width: 2%;"></div> </div> <div>76% 20% . .</div>

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Mol	Chain	Length	Quality of chain
1	G	356	 74% 22% ..
1	H	356	 79% 17% ..
1	I	356	 79% 17% ..
1	J	356	 80% 16% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MSL	C	5002	-	-	X	-
3	MSL	C	5005	-	-	X	-
3	MSL	C	5007	-	-	X	-
4	ANP	A	6001	X	-	-	-
4	ANP	B	6002	X	-	-	-
4	ANP	C	6003	X	-	-	-
4	ANP	D	6004	X	-	-	-
4	ANP	E	6005	X	-	-	-
4	ANP	F	6006	X	-	-	-
4	ANP	G	6007	X	-	-	-
4	ANP	H	6008	X	-	-	-
4	ANP	I	6009	X	-	-	-
4	ANP	J	6010	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 28277 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 glutamine synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	B	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	C	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	D	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	E	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	F	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	G	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	H	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	I	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			
1	J	353	Total	C	N	O	S	0	0	0
			2745	1739	470	525	11			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

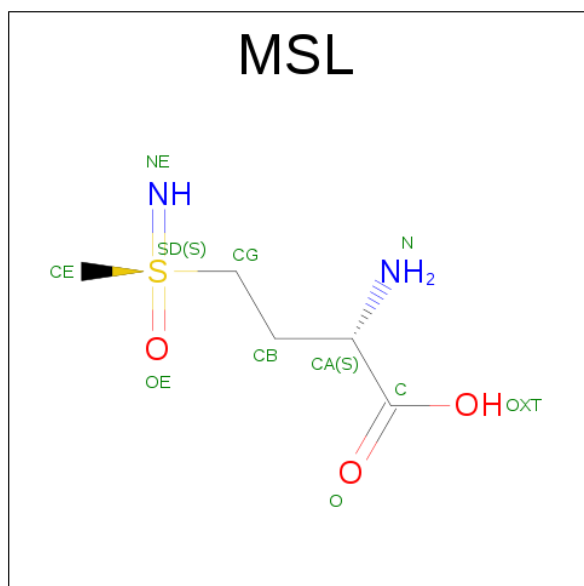
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	3	Total	Mn	0	0
			3	3		
2	J	3	Total	Mn	0	0
			3	3		
2	D	3	Total	Mn	0	0
			3	3		
2	E	3	Total	Mn	0	0
			3	3		

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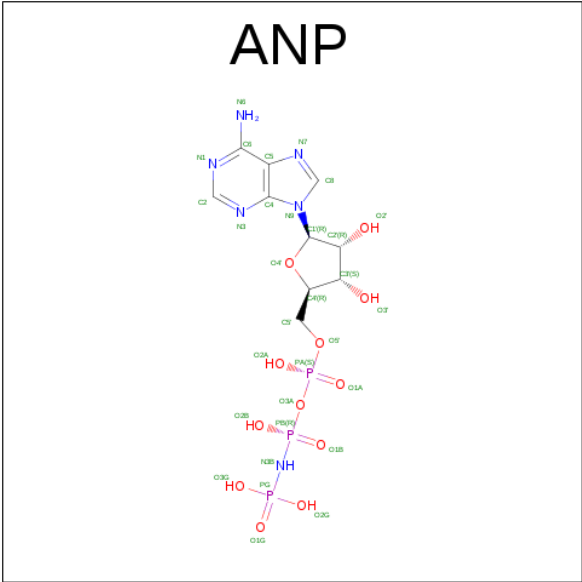
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	3	Total	Mn	0	0
			3	3		
2	B	3	Total	Mn	0	0
			3	3		
2	I	3	Total	Mn	0	0
			3	3		
2	C	3	Total	Mn	0	0
			3	3		
2	A	3	Total	Mn	0	0
			3	3		
2	F	3	Total	Mn	0	0
			3	3		

- Molecule 3 is (2S)-2-AMINO-4-(METHYLSULFONIMIDOYL)BUTANOIC ACID (three-letter code: MSL) (formula: C₅H₁₂N₂O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	10	Total	C	N	O	S	0	0
			110	50	20	30	10		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	F	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	G	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	H	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	I	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	J	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	32	Total	O	0	0
			32	32		
5	B	36	Total	O	0	0
			36	36		

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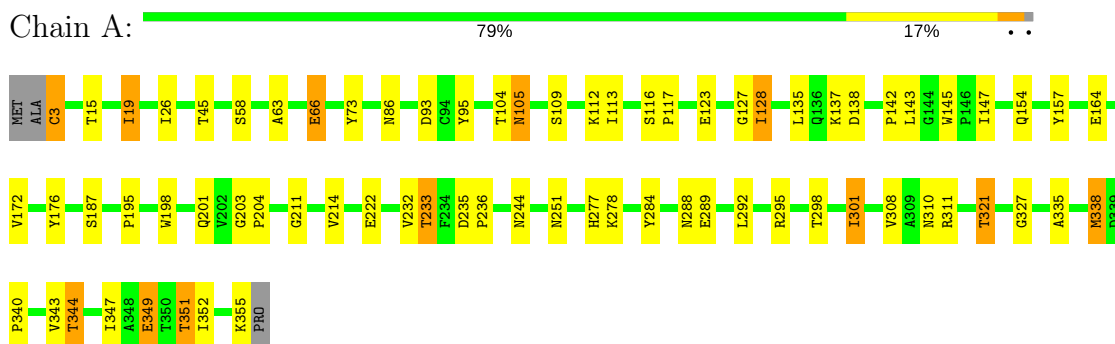
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	40	Total 40	O 40	0	0
5	D	42	Total 42	O 42	0	0
5	E	41	Total 41	O 41	0	0
5	F	39	Total 39	O 39	0	0
5	G	40	Total 40	O 40	0	0
5	H	32	Total 32	O 32	0	0
5	I	37	Total 37	O 37	0	0
5	J	38	Total 38	O 38	0	0

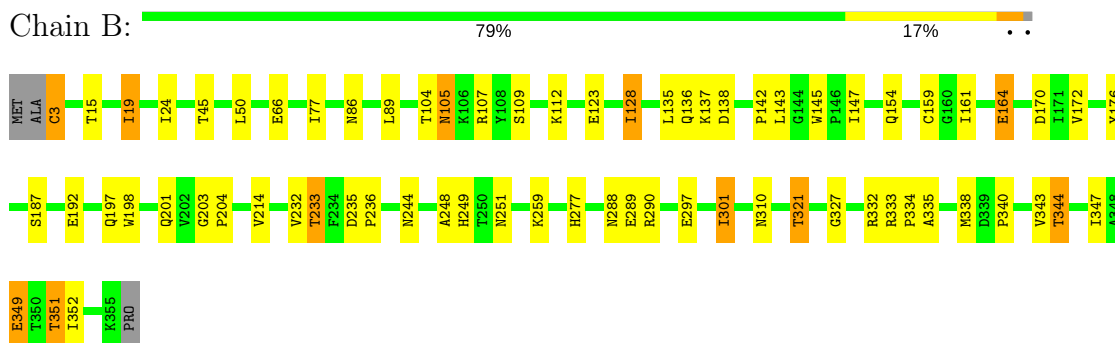
3 Residue-property plots [i](#)

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.

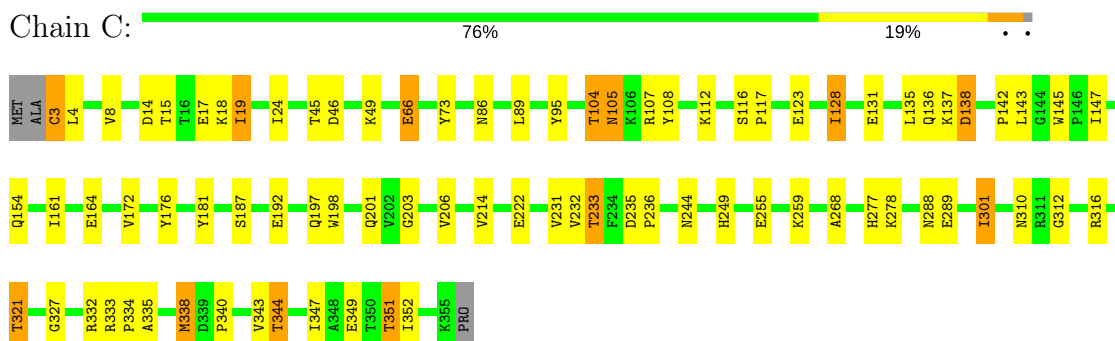
- Molecule 1: glutamine synthetase



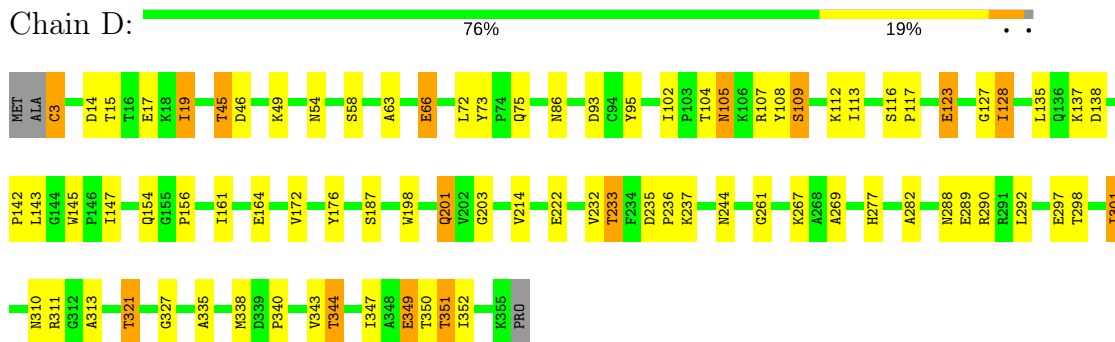
- Molecule 1: glutamine synthetase



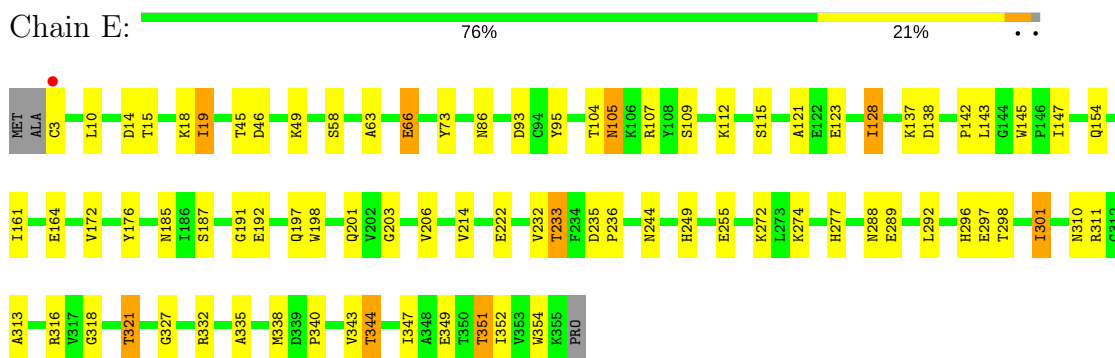
- Molecule 1: glutamine synthetase



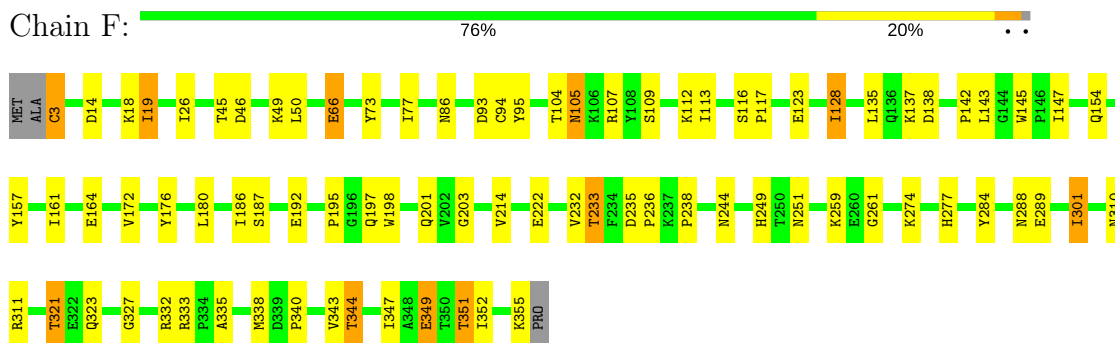
- Molecule 1: glutamine synthetase



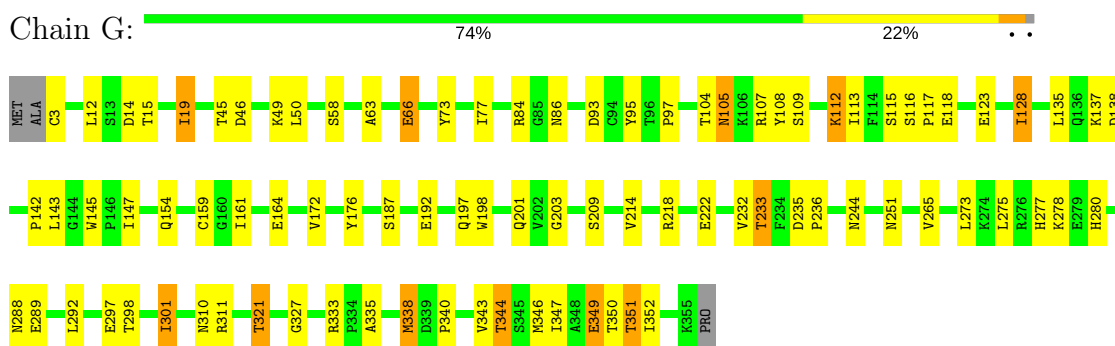
- Molecule 1: glutamine synthetase




- Molecule 1: glutamine synthetase

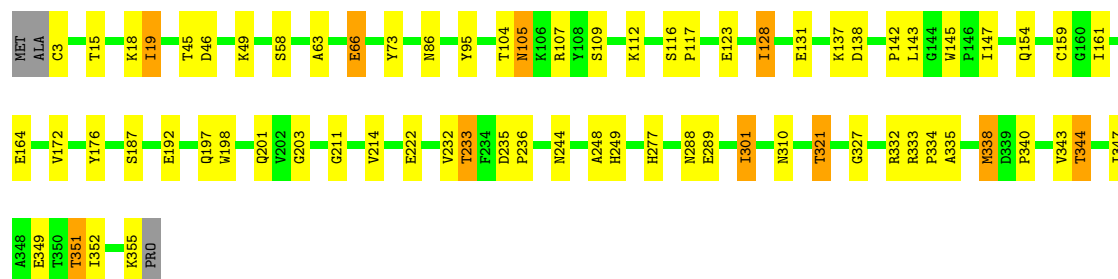


- Molecule 1: glutamine synthetase




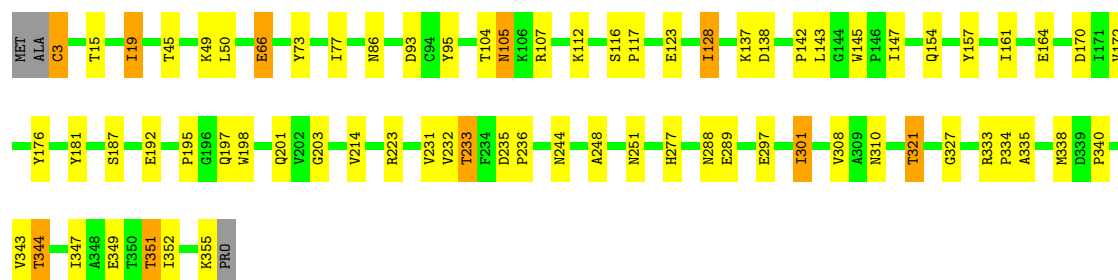
- Molecule 1: glutamine synthetase

Chain H:  79% 17% ..




- Molecule 1: glutamine synthetase

Chain I:  79% 17% ..



- Molecule 1: glutamine synthetase

Chain J:  80% 16% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.88Å 190.94Å 117.90Å 90.00° 101.23° 90.00°	Depositor
Resolution (Å)	33.50 – 3.50 33.50 – 3.50	Depositor EDS
% Data completeness (in resolution range)	83.1 (33.50-3.50) 83.1 (33.50-3.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 3.47Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.166 , 0.209 0.159 , 0.201	Depositor DCC
R_{free} test set	2227 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	86.0	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	28277	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MSL, ANP, MN

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	0.67	0/2819	0.70	0/3834
1	B	0.69	1/2819 (0.0%)	0.70	0/3834
1	C	0.67	0/2819	0.70	0/3834
1	D	0.75	0/2819	0.72	0/3834
1	E	0.71	0/2819	0.70	0/3834
1	F	0.73	0/2819	0.72	0/3834
1	G	0.74	1/2819 (0.0%)	0.71	1/3834 (0.0%)
1	H	0.70	1/2819 (0.0%)	0.70	0/3834
1	I	0.66	0/2819	0.69	0/3834
1	J	0.67	0/2819	0.70	0/3834
All	All	0.70	3/28190 (0.0%)	0.70	1/38340 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	159	CYS	CB-SG	-5.96	1.72	1.81
1	H	159	CYS	CB-SG	-5.62	1.72	1.81
1	G	159	CYS	CB-SG	-5.14	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	218	ARG	NE-CZ-NH2	-5.24	117.68	120.30

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	2745	0	2653	48	0
1	B	2745	0	2653	49	0
1	C	2745	0	2653	59	0
1	D	2745	0	2653	73	0
1	E	2745	0	2653	57	0
1	F	2745	0	2653	64	0
1	G	2745	0	2653	63	0
1	H	2745	0	2653	45	0
1	I	2745	0	2653	48	0
1	J	2745	0	2653	43	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	3	0	0	0	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	3	0	0	0	0
3	C	110	0	100	37	0
4	A	31	0	10	7	0
4	B	31	0	11	3	0
4	C	31	0	10	4	0
4	D	31	0	11	6	0
4	E	31	0	11	6	0
4	F	31	0	11	4	0
4	G	31	0	10	4	0
4	H	31	0	10	3	0
4	I	31	0	10	3	0
4	J	31	0	10	3	0
5	A	32	0	0	7	0
5	B	36	0	0	11	0
5	C	40	0	0	12	0
5	D	42	0	0	27	0
5	E	41	0	0	14	0
5	F	39	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	40	0	0	19	0
5	H	32	0	0	9	0
5	I	37	0	0	7	0
5	J	38	0	0	11	0
All	All	28277	0	26734	546	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 10.

All (546) 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:G:12:LEU:HD23	5:G:6047:HOH:O	1.47	1.11
3:C:5010:MSL:NE	4:H:6008:ANP:PG	2.25	1.09
1:E:354:TRP:HA	5:E:6026:HOH:O	1.56	1.05
1:G:346:MET:SD	5:G:6041:HOH:O	2.14	1.03
1:E:255:GLU:HG2	5:E:6019:HOH:O	1.58	1.02
1:H:344:THR:HG21	5:H:6034:HOH:O	1.59	0.98
1:E:154:GLN:HE22	1:E:244:ASN:H	1.08	0.97
1:E:296:HIS:HD2	5:E:6033:HOH:O	1.46	0.97
1:I:154:GLN:HE22	1:I:244:ASN:H	1.08	0.97
1:F:128:ILE:HG21	5:F:6034:HOH:O	1.67	0.95
1:F:154:GLN:HE22	1:F:244:ASN:H	1.12	0.95
1:D:154:GLN:HE22	1:D:244:ASN:H	1.13	0.94
1:B:154:GLN:HE22	1:B:244:ASN:H	1.15	0.93
1:D:73:TYR:HB2	5:D:6032:HOH:O	1.69	0.92
1:J:154:GLN:HE22	1:J:244:ASN:H	1.13	0.92
1:C:154:GLN:HE22	1:C:244:ASN:H	1.07	0.91
1:E:185:ASN:HB2	5:E:6036:HOH:O	1.68	0.91
1:H:154:GLN:HE22	1:H:244:ASN:H	1.14	0.90
1:E:274:LYS:HE3	5:E:6025:HOH:O	1.70	0.90
1:A:154:GLN:HE22	1:A:244:ASN:H	1.19	0.89
1:H:321:THR:HB	1:H:327:GLY:HA3	1.55	0.88
1:D:282:ALA:HB3	5:D:6022:HOH:O	1.75	0.87
1:G:154:GLN:HE22	1:G:244:ASN:H	1.19	0.86
1:D:350:THR:HG22	5:D:6024:HOH:O	1.73	0.86
1:D:72:LEU:HG	5:D:6046:HOH:O	1.74	0.86
1:C:259:LYS:HB3	5:C:6028:HOH:O	1.76	0.85
1:D:95:TYR:HE1	5:D:6032:HOH:O	1.59	0.85
1:F:107:ARG:HG2	5:F:6016:HOH:O	1.76	0.84
1:G:280:HIS:HA	5:G:6041:HOH:O	1.76	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:259:LYS:HD2	5:C:6025:HOH:O	1.78	0.83
1:D:321:THR:HB	1:D:327:GLY:HA3	1.59	0.82
1:C:268:ALA:HB1	5:C:6031:HOH:O	1.80	0.82
1:E:321:THR:HB	1:E:327:GLY:HA3	1.61	0.82
1:G:275:LEU:CD2	5:G:6028:HOH:O	2.26	0.82
1:A:321:THR:HB	1:A:327:GLY:HA3	1.61	0.82
1:F:321:THR:HB	1:F:327:GLY:HA3	1.61	0.82
1:G:321:THR:HB	1:G:327:GLY:HA3	1.59	0.81
1:E:19:ILE:HD11	1:E:86:ASN:HB2	1.59	0.81
1:I:321:THR:HB	1:I:327:GLY:HA3	1.61	0.80
1:B:19:ILE:HD11	1:B:86:ASN:HB2	1.62	0.80
1:B:321:THR:HB	1:B:327:GLY:HA3	1.63	0.80
1:F:261:GLY:HA2	5:F:6011:HOH:O	1.82	0.80
1:J:19:ILE:HD11	1:J:86:ASN:HB2	1.64	0.79
5:B:6034:HOH:O	1:C:8:VAL:HG21	1.79	0.79
1:C:321:THR:HB	1:C:327:GLY:HA3	1.61	0.79
1:G:19:ILE:HD11	1:G:86:ASN:HB2	1.61	0.79
1:H:49:LYS:HG2	5:H:6027:HOH:O	1.83	0.79
1:D:93:ASP:HB3	5:D:6032:HOH:O	1.84	0.78
1:D:73:TYR:CB	5:D:6032:HOH:O	2.29	0.78
1:A:19:ILE:HD11	1:A:86:ASN:HB2	1.67	0.77
1:J:321:THR:HB	1:J:327:GLY:HA3	1.67	0.77
1:I:19:ILE:HD11	1:I:86:ASN:HB2	1.66	0.76
3:C:5007:MSL:HG3	1:F:332:ARG:HH22	1.51	0.76
1:D:19:ILE:HD11	1:D:86:ASN:HB2	1.68	0.75
1:F:259:LYS:HD2	5:F:6008:HOH:O	1.88	0.74
1:F:19:ILE:HD11	1:F:86:ASN:HB2	1.70	0.74
1:E:296:HIS:CD2	5:E:6033:HOH:O	2.27	0.74
3:C:5010:MSL:NE	4:H:6008:ANP:O1G	2.16	0.74
1:G:275:LEU:HD23	5:G:6028:HOH:O	1.87	0.73
1:D:311:ARG:NH1	4:D:6004:ANP:O1G	2.21	0.73
1:H:19:ILE:HD11	1:H:86:ASN:HB2	1.71	0.73
4:A:6001:ANP:PG	3:C:5001:MSL:NE	2.62	0.73
1:G:128:ILE:HG12	1:G:214:VAL:HG21	1.70	0.72
1:D:123:GLU:HA	5:D:6015:HOH:O	1.90	0.72
1:D:54:ASN:HA	5:D:6046:HOH:O	1.89	0.71
1:D:45:THR:HG22	5:D:6034:HOH:O	1.89	0.71
1:J:223:ARG:NH1	5:J:6024:HOH:O	2.23	0.71
1:C:128:ILE:HG12	1:C:214:VAL:HG21	1.73	0.70
1:B:344:THR:HG21	5:B:6009:HOH:O	1.90	0.70
1:D:105:ASN:HD22	1:D:105:ASN:C	1.94	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:18:LYS:HE2	5:I:6021:HOH:O	1.92	0.70
1:A:128:ILE:HG12	1:A:214:VAL:HG21	1.73	0.70
1:A:311:ARG:NH1	4:A:6001:ANP:O1G	2.24	0.70
1:J:320:GLU:HB3	5:J:6019:HOH:O	1.92	0.70
1:C:19:ILE:HD11	1:C:86:ASN:HB2	1.74	0.69
3:C:5009:MSL:HG3	1:J:297:GLU:OE2	1.92	0.69
1:E:128:ILE:HG12	1:E:214:VAL:HG21	1.74	0.69
1:D:66:GLU:HA	1:E:310:ASN:OD1	1.92	0.69
1:A:3:CYS:HB3	5:E:6009:HOH:O	1.93	0.68
1:D:95:TYR:CE1	5:D:6032:HOH:O	2.38	0.68
1:J:128:ILE:HG12	1:J:214:VAL:HG21	1.76	0.68
1:I:128:ILE:HG12	1:I:214:VAL:HG21	1.74	0.68
1:F:66:GLU:HA	1:I:310:ASN:OD1	1.93	0.68
1:D:237:LYS:HE2	5:D:6009:HOH:O	1.93	0.67
1:G:118:GLU:HG3	5:G:6021:HOH:O	1.94	0.67
1:D:128:ILE:HG12	1:D:214:VAL:HG21	1.78	0.66
1:G:123:GLU:HG3	5:G:6016:HOH:O	1.95	0.66
1:H:355:LYS:C	5:H:6009:HOH:O	2.33	0.66
1:B:332:ARG:HH22	3:C:5002:MSL:HG3	1.61	0.66
1:D:203:GLY:HA2	4:D:6004:ANP:O3'	1.95	0.66
1:I:105:ASN:HD22	1:I:105:ASN:C	1.97	0.66
1:D:277:HIS:HE1	1:D:301:ILE:O	1.79	0.65
1:F:128:ILE:HG12	1:F:214:VAL:HG21	1.78	0.65
1:G:107:ARG:HG2	5:G:6019:HOH:O	1.95	0.65
3:C:5004:MSL:NE	4:D:6004:ANP:PG	2.69	0.65
1:J:355:LYS:HB2	5:J:6033:HOH:O	1.97	0.65
1:G:112:LYS:HD3	5:G:6031:HOH:O	1.97	0.65
1:A:347:ILE:O	1:A:351:THR:HB	1.97	0.65
1:J:338:MET:HG3	1:J:343:VAL:HG21	1.77	0.65
1:F:347:ILE:O	1:F:351:THR:HB	1.97	0.64
1:B:154:GLN:HB2	5:B:6026:HOH:O	1.96	0.64
1:E:115:SER:HB3	5:E:6016:HOH:O	1.95	0.64
1:C:278:LYS:HD3	5:C:6029:HOH:O	1.96	0.64
1:F:154:GLN:HB2	5:F:6013:HOH:O	1.96	0.64
1:F:351:THR:HG22	1:F:352:ILE:HG13	1.80	0.64
3:C:5008:MSL:HG3	1:I:297:GLU:OE2	1.96	0.64
1:D:338:MET:HG3	1:D:343:VAL:HG21	1.80	0.64
3:C:5006:MSL:HG3	1:G:297:GLU:OE2	1.98	0.64
1:H:347:ILE:O	1:H:351:THR:HB	1.98	0.64
1:G:275:LEU:HD21	5:G:6028:HOH:O	1.89	0.64
3:C:5007:MSL:HB2	1:F:249:HIS:CE1	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:LEU:HB3	5:C:6019:HOH:O	1.98	0.63
1:F:340:PRO:O	1:F:344:THR:HB	1.99	0.63
1:F:94:CYS:N	5:F:6010:HOH:O	2.31	0.63
1:E:351:THR:HG22	1:E:352:ILE:HG13	1.81	0.63
1:B:105:ASN:HD22	1:B:105:ASN:C	2.02	0.62
1:E:105:ASN:C	1:E:105:ASN:HD22	2.03	0.62
1:H:277:HIS:HE1	1:H:301:ILE:O	1.82	0.62
1:E:347:ILE:O	1:E:351:THR:HB	1.99	0.62
1:F:310:ASN:OD1	1:G:66:GLU:HA	1.99	0.62
1:H:128:ILE:HG12	1:H:214:VAL:HG21	1.81	0.62
1:C:105:ASN:HD22	1:C:105:ASN:C	2.00	0.62
1:J:105:ASN:HD22	1:J:105:ASN:C	2.02	0.62
1:B:249:HIS:CE1	3:C:5002:MSL:HB2	2.35	0.62
1:H:203:GLY:HA2	4:H:6008:ANP:O3'	2.00	0.62
1:E:338:MET:HG3	1:E:343:VAL:HG21	1.82	0.62
1:J:277:HIS:HE1	1:J:301:ILE:O	1.82	0.62
1:D:3:CYS:HB3	5:D:6017:HOH:O	2.00	0.61
1:F:251:ASN:ND2	4:F:6006:ANP:H5'2	2.15	0.61
3:C:5006:MSL:NE	4:G:6007:ANP:PG	2.74	0.61
1:B:351:THR:HG22	1:B:352:ILE:HG13	1.83	0.61
1:G:347:ILE:O	1:G:351:THR:HB	2.00	0.61
1:B:277:HIS:HE1	1:B:301:ILE:O	1.83	0.61
1:D:347:ILE:O	1:D:351:THR:HB	2.01	0.61
5:H:6016:HOH:O	1:I:3:CYS:HB3	2.00	0.61
1:C:154:GLN:HE22	1:C:244:ASN:N	1.90	0.61
1:E:277:HIS:HE1	1:E:301:ILE:O	1.84	0.61
1:G:105:ASN:HD22	1:G:105:ASN:C	2.05	0.60
1:A:172:VAL:HG21	1:A:198:TRP:CD2	2.36	0.60
1:A:340:PRO:O	1:A:344:THR:HB	2.01	0.60
1:D:267:LYS:HD3	5:D:6020:HOH:O	2.01	0.60
1:B:338:MET:HG3	1:B:343:VAL:HG21	1.84	0.60
1:G:277:HIS:HE1	1:G:301:ILE:O	1.84	0.60
1:D:172:VAL:HG21	1:D:198:TRP:CD2	2.37	0.60
1:B:128:ILE:HG12	1:B:214:VAL:HG21	1.82	0.60
1:C:310:ASN:OD1	1:E:66:GLU:HA	2.01	0.60
1:F:3:CYS:HB3	5:J:6048:HOH:O	2.01	0.60
3:C:5005:MSL:OE	4:E:6005:ANP:O3G	2.20	0.60
1:G:273:LEU:HA	5:G:6036:HOH:O	2.02	0.60
1:G:73:TYR:CD2	1:G:95:TYR:CE1	2.89	0.60
1:A:278:LYS:HB2	5:A:6011:HOH:O	2.02	0.59
1:D:17:GLU:HG2	5:D:6030:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:310:ASN:OD1	1:J:66:GLU:HA	2.02	0.59
3:C:5004:MSL:HG3	1:D:297:GLU:OE2	2.02	0.59
1:F:203:GLY:HA2	4:F:6006:ANP:O3'	2.02	0.59
3:C:5009:MSL:NE	4:J:6010:ANP:PG	2.76	0.59
1:B:170:ASP:HA	5:B:6034:HOH:O	2.02	0.59
1:D:105:ASN:C	1:D:105:ASN:ND2	2.56	0.59
1:D:123:GLU:HG2	5:D:6015:HOH:O	2.01	0.59
1:A:277:HIS:HE1	1:A:301:ILE:O	1.85	0.59
1:B:204:PRO:HD2	5:B:6028:HOH:O	2.02	0.58
1:J:203:GLY:HA2	4:J:6010:ANP:O3'	2.03	0.58
1:C:347:ILE:O	1:C:351:THR:HB	2.03	0.58
1:F:277:HIS:HE1	1:F:301:ILE:O	1.87	0.58
1:C:277:HIS:HE1	1:C:301:ILE:O	1.86	0.58
1:H:338:MET:HG3	1:H:343:VAL:HG21	1.85	0.58
1:B:340:PRO:O	1:B:344:THR:HB	2.04	0.58
1:E:187:SER:HB3	1:E:203:GLY:HA3	1.84	0.58
1:E:187:SER:HB3	1:E:203:GLY:CA	2.34	0.58
1:H:340:PRO:O	1:H:344:THR:HB	2.03	0.58
1:F:274:LYS:HE2	5:F:6041:HOH:O	2.04	0.57
1:I:154:GLN:HE22	1:I:244:ASN:N	1.91	0.57
1:C:351:THR:HG22	1:C:352:ILE:HG13	1.85	0.57
1:I:66:GLU:HA	1:J:310:ASN:OD1	2.03	0.57
1:B:347:ILE:O	1:B:351:THR:HB	2.04	0.57
1:D:269:ALA:HA	5:D:6006:HOH:O	2.04	0.57
1:F:105:ASN:HD22	1:F:105:ASN:C	2.08	0.57
1:J:347:ILE:O	1:J:351:THR:HB	2.05	0.57
1:I:105:ASN:ND2	1:I:105:ASN:C	2.58	0.57
1:A:105:ASN:C	1:A:105:ASN:HD22	2.07	0.57
1:F:172:VAL:HG21	1:F:198:TRP:CD2	2.39	0.57
1:J:351:THR:HG22	1:J:352:ILE:HG13	1.85	0.57
1:A:351:THR:HG22	1:A:352:ILE:HG13	1.87	0.57
1:A:204:PRO:HD3	4:A:6001:ANP:O2'	2.05	0.57
1:I:351:THR:HG22	1:I:352:ILE:HG13	1.87	0.57
1:I:355:LYS:HB3	5:I:6022:HOH:O	2.04	0.57
1:J:172:VAL:HG21	1:J:198:TRP:CD2	2.39	0.57
1:C:73:TYR:CD2	1:C:95:TYR:CE1	2.93	0.57
1:G:340:PRO:O	1:G:344:THR:HB	2.04	0.57
1:B:172:VAL:HG21	1:B:198:TRP:CD2	2.39	0.57
1:I:347:ILE:O	1:I:351:THR:HB	2.05	0.57
1:C:172:VAL:HG21	1:C:198:TRP:CD2	2.40	0.56
1:F:187:SER:HB3	1:F:203:GLY:HA3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:187:SER:HB3	1:F:203:GLY:CA	2.35	0.56
1:J:172:VAL:HG13	5:J:6011:HOH:O	2.04	0.56
1:B:19:ILE:HD11	1:B:86:ASN:CB	2.34	0.56
3:C:5005:MSL:HB2	1:E:249:HIS:CE1	2.40	0.56
1:E:154:GLN:HE22	1:E:244:ASN:N	1.91	0.56
1:J:19:ILE:HD11	1:J:86:ASN:CB	2.34	0.56
1:C:187:SER:HB3	1:C:203:GLY:CA	2.36	0.56
1:B:310:ASN:OD1	1:C:66:GLU:HA	2.05	0.56
1:I:187:SER:HB3	1:I:203:GLY:CA	2.35	0.56
1:J:340:PRO:O	1:J:344:THR:HB	2.05	0.56
1:G:338:MET:HG3	1:G:343:VAL:HG21	1.88	0.56
1:I:355:LYS:HB2	5:I:6029:HOH:O	2.06	0.56
1:E:311:ARG:NH1	4:E:6005:ANP:O3G	2.38	0.56
1:G:172:VAL:HG21	1:G:198:TRP:CD2	2.41	0.56
1:G:311:ARG:NH1	4:G:6007:ANP:O1G	2.39	0.56
1:D:351:THR:HG22	1:D:352:ILE:HG13	1.87	0.56
1:G:310:ASN:OD1	1:H:66:GLU:HA	2.06	0.56
1:C:131:GLU:OE1	3:C:5003:MSL:HB3	2.06	0.55
1:H:351:THR:HG22	1:H:352:ILE:HG13	1.88	0.55
1:G:278:LYS:HB2	5:G:6014:HOH:O	2.05	0.55
1:D:187:SER:HB3	1:D:203:GLY:CA	2.37	0.55
1:E:19:ILE:HD11	1:E:86:ASN:CB	2.35	0.55
1:H:105:ASN:HD22	1:H:105:ASN:C	2.08	0.55
1:I:338:MET:HG3	1:I:343:VAL:HG21	1.88	0.55
1:A:3:CYS:HA	5:A:6012:HOH:O	2.04	0.55
1:H:172:VAL:HG21	1:H:198:TRP:CD2	2.41	0.55
1:C:187:SER:HB3	1:C:203:GLY:HA3	1.88	0.55
1:F:154:GLN:NE2	1:F:244:ASN:H	1.95	0.55
1:G:251:ASN:ND2	4:G:6007:ANP:H5'2	2.22	0.55
1:J:10:LEU:HD23	5:J:6031:HOH:O	2.06	0.55
1:C:105:ASN:C	1:C:105:ASN:ND2	2.60	0.55
1:I:277:HIS:HE1	1:I:301:ILE:O	1.90	0.55
1:A:63:ALA:HA	5:A:6031:HOH:O	2.06	0.55
1:A:310:ASN:OD1	1:B:66:GLU:HA	2.07	0.55
1:C:338:MET:HG3	1:C:343:VAL:HG21	1.88	0.55
1:D:187:SER:HB3	1:D:203:GLY:HA3	1.89	0.55
1:E:172:VAL:HG21	1:E:198:TRP:CD2	2.42	0.55
1:C:312:GLY:N	5:C:6030:HOH:O	2.39	0.54
1:I:340:PRO:O	1:I:344:THR:HB	2.07	0.54
1:C:3:CYS:HB3	5:C:6015:HOH:O	2.08	0.54
1:I:170:ASP:HB2	5:I:6046:HOH:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:137:LYS:O	1:G:138:ASP:HB2	2.07	0.54
1:A:73:TYR:CD2	1:A:95:TYR:CE1	2.95	0.54
1:D:340:PRO:O	1:D:344:THR:HB	2.07	0.54
1:E:105:ASN:ND2	1:E:105:ASN:C	2.61	0.54
1:I:19:ILE:HD11	1:I:86:ASN:CB	2.35	0.54
1:A:137:LYS:O	1:A:138:ASP:HB2	2.07	0.54
1:A:26:ILE:N	5:A:6007:HOH:O	2.35	0.54
1:B:161:ILE:HD12	1:C:222:GLU:HB3	1.89	0.54
1:G:115:SER:HB3	5:G:6027:HOH:O	2.07	0.54
1:H:137:LYS:O	1:H:138:ASP:HB2	2.08	0.54
1:E:316:ARG:NH1	4:E:6005:ANP:O1B	2.27	0.53
1:C:340:PRO:O	1:C:344:THR:HB	2.09	0.53
3:C:5008:MSL:NE	4:I:6009:ANP:PG	2.82	0.53
1:B:105:ASN:ND2	1:B:105:ASN:C	2.61	0.53
1:A:66:GLU:HA	1:D:310:ASN:OD1	2.08	0.53
1:J:187:SER:HB3	1:J:203:GLY:HA3	1.90	0.53
1:G:187:SER:HB3	1:G:203:GLY:CA	2.38	0.53
1:F:26:ILE:HG21	5:F:6042:HOH:O	2.07	0.53
1:D:19:ILE:HD11	1:D:86:ASN:CB	2.36	0.53
1:E:105:ASN:HD22	1:E:107:ARG:H	1.55	0.53
1:I:49:LYS:HE2	5:I:6036:HOH:O	2.08	0.52
1:I:137:LYS:O	1:I:138:ASP:HB2	2.09	0.52
1:J:187:SER:HB3	1:J:203:GLY:CA	2.40	0.52
1:C:137:LYS:O	1:C:138:ASP:HB2	2.10	0.52
1:I:172:VAL:HG21	1:I:198:TRP:CD2	2.45	0.52
3:C:5003:MSL:OE	4:C:6003:ANP:O1G	2.27	0.52
1:G:209:SER:HA	5:G:6013:HOH:O	2.09	0.52
1:G:351:THR:HG22	1:G:352:ILE:HG13	1.92	0.52
1:H:321:THR:CB	1:H:327:GLY:HA3	2.35	0.52
1:G:19:ILE:HD11	1:G:86:ASN:CB	2.36	0.52
1:H:142:PRO:HB2	1:H:145:TRP:CD1	2.45	0.52
1:J:105:ASN:ND2	1:J:105:ASN:C	2.62	0.52
1:A:19:ILE:HD11	1:A:86:ASN:CB	2.39	0.52
1:F:19:ILE:HD11	1:F:86:ASN:CB	2.37	0.52
1:G:105:ASN:HD22	1:G:107:ARG:H	1.57	0.52
1:A:338:MET:HG3	1:A:343:VAL:HG21	1.92	0.51
1:E:203:GLY:HA2	4:E:6005:ANP:O3'	2.11	0.51
1:D:105:ASN:HD22	1:D:107:ARG:H	1.58	0.51
1:E:236:PRO:HB3	1:E:335:ALA:HB1	1.91	0.51
1:E:318:GLY:HA3	5:E:6020:HOH:O	2.09	0.51
1:F:311:ARG:NH1	4:F:6006:ANP:O1G	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:142:PRO:HB2	1:I:145:TRP:CD1	2.45	0.51
1:E:105:ASN:ND2	1:E:107:ARG:H	2.08	0.51
1:F:338:MET:HG3	1:F:343:VAL:HG21	1.92	0.51
1:F:50:LEU:HD11	1:F:77:ILE:HD11	1.92	0.51
1:H:142:PRO:HB2	1:H:145:TRP:CG	2.46	0.51
1:E:206:VAL:CG1	5:E:6022:HOH:O	2.58	0.51
1:I:187:SER:HB3	1:I:203:GLY:HA3	1.93	0.51
1:H:192:GLU:HB3	1:H:197:GLN:HE21	1.75	0.51
1:A:295:ARG:HG3	5:A:6009:HOH:O	2.10	0.51
1:J:105:ASN:HD22	1:J:107:ARG:H	1.58	0.51
1:B:233:THR:HB	1:B:235:ASP:H	1.77	0.50
1:D:73:TYR:CD2	5:D:6032:HOH:O	2.55	0.50
1:I:142:PRO:HB2	1:I:145:TRP:CG	2.46	0.50
1:I:73:TYR:CD2	1:I:95:TYR:CE1	2.99	0.50
1:A:105:ASN:C	1:A:105:ASN:ND2	2.65	0.50
1:A:142:PRO:HB2	1:A:145:TRP:CD1	2.47	0.50
1:J:137:LYS:O	1:J:138:ASP:HB2	2.11	0.50
1:I:157:TYR:CD1	1:I:195:PRO:HD3	2.47	0.50
1:A:187:SER:HB3	1:A:203:GLY:HA3	1.93	0.50
1:E:137:LYS:O	1:E:138:ASP:HB2	2.12	0.50
1:G:50:LEU:HD11	1:G:77:ILE:HD11	1.94	0.49
1:H:105:ASN:C	1:H:105:ASN:ND2	2.65	0.49
1:G:236:PRO:HB3	1:G:335:ALA:HB1	1.94	0.49
1:C:192:GLU:HB3	1:C:197:GLN:HE21	1.76	0.49
1:C:203:GLY:HA2	4:C:6003:ANP:O3'	2.13	0.49
1:D:236:PRO:HB3	1:D:335:ALA:HB1	1.94	0.49
1:H:187:SER:HB3	1:H:203:GLY:CA	2.42	0.49
1:A:187:SER:HB3	1:A:203:GLY:CA	2.43	0.49
1:C:105:ASN:HD22	1:C:107:ARG:H	1.60	0.49
1:E:154:GLN:NE2	1:E:244:ASN:H	1.92	0.49
1:F:274:LYS:CE	5:F:6041:HOH:O	2.61	0.49
1:G:105:ASN:C	1:G:105:ASN:ND2	2.65	0.49
1:E:121:ALA:HA	5:E:6027:HOH:O	2.11	0.49
1:I:251:ASN:ND2	4:I:6009:ANP:H5'2	2.27	0.49
1:G:115:SER:CB	5:G:6027:HOH:O	2.61	0.49
1:H:161:ILE:HD12	1:J:222:GLU:HB3	1.95	0.49
1:B:135:LEU:HD23	1:B:142:PRO:HA	1.95	0.49
1:D:222:GLU:HB3	1:E:161:ILE:HD12	1.94	0.49
1:A:58:SER:HA	1:A:63:ALA:O	2.12	0.48
1:C:236:PRO:HB3	1:C:335:ALA:HB1	1.95	0.48
1:F:105:ASN:ND2	1:F:105:ASN:C	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:259:LYS:HD2	5:B:6016:HOH:O	2.12	0.48
1:E:142:PRO:HB2	1:E:145:TRP:CD1	2.48	0.48
1:F:128:ILE:HD13	1:F:338:MET:HE3	1.95	0.48
1:G:233:THR:HB	1:G:235:ASP:H	1.78	0.48
1:B:137:LYS:O	1:B:138:ASP:HB2	2.14	0.48
1:D:109:SER:HB2	5:D:6005:HOH:O	2.12	0.48
1:D:58:SER:HA	1:D:63:ALA:O	2.14	0.48
1:I:105:ASN:HD22	1:I:107:ARG:H	1.61	0.48
1:B:297:GLU:OE2	3:C:5002:MSL:HG2	2.14	0.48
1:E:142:PRO:HB2	1:E:145:TRP:CG	2.48	0.48
1:F:73:TYR:CD2	1:F:95:TYR:CE1	3.02	0.48
1:J:303:THR:HG21	5:J:6045:HOH:O	2.13	0.48
1:D:113:ILE:HD13	1:D:349:GLU:HG3	1.95	0.48
1:E:73:TYR:CD2	1:E:95:TYR:CE1	3.01	0.48
1:G:187:SER:HB3	1:G:203:GLY:HA3	1.94	0.48
1:G:273:LEU:HD23	5:G:6036:HOH:O	2.14	0.48
1:A:203:GLY:HA2	4:A:6001:ANP:O3'	2.14	0.48
1:F:142:PRO:HB2	1:F:145:TRP:CG	2.49	0.48
1:A:251:ASN:ND2	4:A:6001:ANP:H5'2	2.29	0.48
1:H:236:PRO:HB3	1:H:335:ALA:HB1	1.96	0.48
1:A:142:PRO:HB2	1:A:145:TRP:CG	2.49	0.47
1:D:203:GLY:HA2	4:D:6004:ANP:HO3'	1.79	0.47
1:D:128:ILE:HD13	1:D:338:MET:HE3	1.96	0.47
4:A:6001:ANP:O1G	3:C:5001:MSL:NE	2.48	0.47
1:C:233:THR:HB	1:C:235:ASP:H	1.79	0.47
1:H:332:ARG:HD3	5:H:6035:HOH:O	2.14	0.47
1:B:187:SER:HB3	1:B:203:GLY:CA	2.44	0.47
1:F:137:LYS:O	1:F:138:ASP:HB2	2.14	0.47
1:J:157:TYR:CD1	1:J:195:PRO:HD3	2.49	0.47
1:B:142:PRO:HB2	1:B:145:TRP:CD1	2.50	0.47
1:B:251:ASN:ND2	4:B:6002:ANP:H5'2	2.29	0.47
1:C:255:GLU:HG2	5:C:6042:HOH:O	2.13	0.47
1:E:340:PRO:O	1:E:344:THR:HB	2.14	0.47
3:C:5007:MSL:OE	4:F:6006:ANP:O1G	2.33	0.47
1:H:333:ARG:N	1:H:334:PRO:CD	2.77	0.47
1:J:105:ASN:ND2	1:J:107:ARG:H	2.13	0.47
1:A:292:LEU:HD23	1:A:298:THR:HB	1.96	0.47
1:D:142:PRO:HB2	1:D:145:TRP:CD1	2.50	0.47
1:E:233:THR:HB	1:E:235:ASP:H	1.80	0.47
1:F:18:LYS:O	1:F:19:ILE:HD12	2.15	0.47
1:G:105:ASN:ND2	1:G:107:ARG:H	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:142:PRO:HB2	1:G:145:TRP:CD1	2.50	0.47
1:J:236:PRO:HB3	1:J:335:ALA:HB1	1.97	0.47
1:G:265:VAL:HG12	5:G:6011:HOH:O	2.15	0.47
1:J:320:GLU:HB2	5:J:6039:HOH:O	2.15	0.47
1:A:236:PRO:HB3	1:A:335:ALA:HB1	1.95	0.47
1:D:261:GLY:HA2	5:D:6010:HOH:O	2.14	0.47
1:G:135:LEU:HD23	1:G:142:PRO:HA	1.97	0.47
1:H:19:ILE:HD11	1:H:86:ASN:CB	2.43	0.47
1:H:73:TYR:CD2	1:H:95:TYR:CE1	3.03	0.47
1:C:206:VAL:HG22	5:C:6022:HOH:O	2.15	0.46
1:C:104:THR:HA	5:C:6006:HOH:O	2.14	0.46
1:B:192:GLU:HB3	1:B:197:GLN:HE21	1.80	0.46
1:C:105:ASN:HD21	1:C:108:TYR:H	1.63	0.46
1:C:161:ILE:HD12	1:E:222:GLU:HB3	1.97	0.46
3:C:5007:MSL:HG3	1:F:332:ARG:NH2	2.27	0.46
1:F:222:GLU:HB3	1:I:161:ILE:HD12	1.98	0.46
1:I:233:THR:HB	1:I:235:ASP:H	1.81	0.46
1:J:233:THR:HB	1:J:235:ASP:H	1.81	0.46
1:C:17:GLU:HA	5:C:6035:HOH:O	2.15	0.46
1:B:187:SER:HB2	5:B:6028:HOH:O	2.15	0.46
1:C:249:HIS:CE1	3:C:5003:MSL:HB2	2.50	0.46
1:H:49:LYS:NZ	5:H:6039:HOH:O	2.47	0.46
1:E:206:VAL:HG13	5:E:6022:HOH:O	2.14	0.46
1:D:201:GLN:HG2	4:D:6004:ANP:O2A	2.16	0.46
1:H:187:SER:HB3	1:H:203:GLY:HA3	1.98	0.46
1:E:192:GLU:HB3	1:E:197:GLN:HE21	1.81	0.46
1:C:19:ILE:HD11	1:C:86:ASN:CB	2.44	0.46
1:D:142:PRO:HB2	1:D:145:TRP:CG	2.51	0.46
1:F:142:PRO:HB2	1:F:145:TRP:CD1	2.51	0.45
1:I:236:PRO:HB3	1:I:335:ALA:HB1	1.98	0.45
1:F:301:ILE:HG13	1:F:301:ILE:H	1.52	0.45
1:G:203:GLY:HA2	4:G:6007:ANP:O3'	2.16	0.45
1:I:105:ASN:ND2	1:I:107:ARG:H	2.14	0.45
1:I:192:GLU:HB3	1:I:197:GLN:HE21	1.82	0.45
1:D:116:SER:HA	1:D:117:PRO:HD3	1.82	0.45
1:F:236:PRO:HB3	1:F:335:ALA:HB1	1.99	0.45
1:B:105:ASN:HD22	1:B:107:ARG:H	1.65	0.45
4:B:6002:ANP:PG	3:C:5002:MSL:NE	2.89	0.45
1:D:105:ASN:ND2	1:D:107:ARG:H	2.14	0.45
1:F:161:ILE:HD12	1:G:222:GLU:HB3	1.98	0.45
1:C:105:ASN:ND2	1:C:108:TYR:H	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:10:LEU:HA	5:E:6013:HOH:O	2.17	0.45
1:F:46:ASP:HB3	1:F:49:LYS:HD3	1.99	0.45
1:F:73:TYR:HB2	1:F:93:ASP:HB3	1.97	0.45
1:G:49:LYS:HE2	5:G:6025:HOH:O	2.16	0.45
1:A:295:ARG:HD2	5:A:6013:HOH:O	2.17	0.45
1:E:46:ASP:HB3	1:E:49:LYS:HD3	1.97	0.45
1:C:277:HIS:CD2	1:C:333:ARG:HH11	2.35	0.44
3:C:5005:MSL:NE	4:E:6005:ANP:PG	2.90	0.44
1:D:105:ASN:ND2	1:D:108:TYR:H	2.15	0.44
1:G:301:ILE:HG13	1:G:301:ILE:H	1.48	0.44
1:I:355:LYS:HG2	5:I:6044:HOH:O	2.16	0.44
1:C:24:ILE:HD11	1:C:89:LEU:HD22	2.00	0.44
1:D:46:ASP:HB3	1:D:49:LYS:HD3	1.98	0.44
1:F:355:LYS:HB3	5:F:6014:HOH:O	2.16	0.44
1:E:18:LYS:O	1:E:19:ILE:HD12	2.17	0.44
1:F:93:ASP:HB3	1:F:95:TYR:HE1	1.83	0.44
3:C:5009:MSL:OE	4:J:6010:ANP:O1G	2.35	0.44
1:A:284:TYR:CD2	1:A:343:VAL:HG22	2.53	0.44
1:C:136:GLN:HB3	5:C:6009:HOH:O	2.17	0.44
3:C:5005:MSL:OE	1:E:311:ARG:HD3	2.18	0.44
3:C:5003:MSL:NE	4:C:6003:ANP:PG	2.90	0.44
1:D:73:TYR:CD2	1:D:95:TYR:CE1	3.06	0.44
1:G:73:TYR:HB2	1:G:93:ASP:HB3	1.98	0.44
1:H:233:THR:HB	1:H:235:ASP:H	1.83	0.44
1:H:355:LYS:HB3	5:H:6009:HOH:O	2.16	0.44
1:D:72:LEU:CG	5:D:6046:HOH:O	2.48	0.44
1:J:292:LEU:HD23	1:J:298:THR:HB	2.00	0.44
1:F:135:LEU:HD23	1:F:142:PRO:HA	2.00	0.44
1:I:73:TYR:HB2	1:I:93:ASP:HB3	2.00	0.44
1:J:324:ASN:CB	5:J:6034:HOH:O	2.64	0.44
1:A:157:TYR:CD1	1:A:195:PRO:HD3	2.53	0.44
1:B:187:SER:HB3	1:B:203:GLY:HA3	1.99	0.43
1:D:105:ASN:HD21	1:D:108:TYR:H	1.66	0.43
3:C:5005:MSL:HG3	1:E:332:ARG:HH22	1.83	0.43
1:A:172:VAL:HG21	1:A:198:TRP:CE3	2.54	0.43
1:B:154:GLN:NE2	1:B:244:ASN:H	1.98	0.43
1:C:116:SER:HA	1:C:117:PRO:HD3	1.85	0.43
1:E:310:ASN:HD22	1:E:313:ALA:HB2	1.83	0.43
1:F:233:THR:HB	1:F:235:ASP:H	1.83	0.43
1:G:142:PRO:HB2	1:G:145:TRP:CG	2.53	0.43
1:A:73:TYR:HB2	1:A:93:ASP:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:TYR:CE2	1:A:343:VAL:HG22	2.54	0.43
1:D:233:THR:HB	1:D:235:ASP:H	1.84	0.43
1:J:58:SER:HA	1:J:63:ALA:O	2.19	0.43
1:D:310:ASN:HD22	1:D:313:ALA:HB2	1.82	0.43
1:E:272:LYS:HA	5:E:6035:HOH:O	2.19	0.43
5:F:6037:HOH:O	1:G:97:PRO:HG2	2.19	0.43
1:I:116:SER:HA	1:I:117:PRO:HD3	1.86	0.43
1:B:301:ILE:H	1:B:301:ILE:HG13	1.53	0.43
1:B:3:CYS:N	5:B:6032:HOH:O	2.52	0.43
1:F:113:ILE:HD13	1:F:349:GLU:HG3	1.99	0.43
1:C:316:ARG:NH1	4:C:6003:ANP:O1B	2.43	0.43
1:D:127:GLY:HA3	4:D:6004:ANP:O4'	2.19	0.43
1:D:93:ASP:CB	5:D:6032:HOH:O	2.55	0.43
3:C:5007:MSL:CB	1:F:249:HIS:CE1	3.01	0.43
1:G:113:ILE:HD13	1:G:349:GLU:HG3	2.01	0.43
1:G:192:GLU:HB3	1:G:197:GLN:HE21	1.84	0.43
1:H:46:ASP:HB3	1:H:49:LYS:HD3	2.01	0.43
1:B:154:GLN:HE22	1:B:244:ASN:N	1.98	0.42
1:A:211:GLY:HA2	1:A:340:PRO:HB2	2.01	0.42
1:G:116:SER:HA	1:G:117:PRO:HD3	1.80	0.42
1:H:18:LYS:O	1:H:19:ILE:HD12	2.20	0.42
1:D:235:ASP:OD2	1:D:290:ARG:NH2	2.52	0.42
1:E:93:ASP:HB3	1:E:95:TYR:HE1	1.84	0.42
1:H:116:SER:HA	1:H:117:PRO:HD3	1.76	0.42
1:I:50:LEU:HD11	1:I:77:ILE:HD11	2.00	0.42
1:B:333:ARG:N	1:B:334:PRO:CD	2.82	0.42
1:C:333:ARG:N	1:C:334:PRO:CD	2.82	0.42
1:F:157:TYR:CD1	1:F:195:PRO:HD3	2.54	0.42
1:F:180:LEU:HG	1:F:186:ILE:CG2	2.49	0.42
1:F:277:HIS:CD2	1:F:333:ARG:HH11	2.38	0.42
1:E:58:SER:HA	1:E:63:ALA:O	2.19	0.42
4:B:6002:ANP:O1G	3:C:5002:MSL:OE	2.38	0.42
1:C:135:LEU:HD23	1:C:142:PRO:HA	2.02	0.42
1:B:249:HIS:HE1	3:C:5002:MSL:HB2	1.82	0.42
1:F:116:SER:HA	1:F:117:PRO:HD3	1.82	0.42
1:G:105:ASN:ND2	1:G:108:TYR:H	2.17	0.42
1:H:131:GLU:HG2	1:H:192:GLU:HG3	2.02	0.42
1:H:58:SER:HA	1:H:63:ALA:O	2.20	0.42
1:B:235:ASP:OD2	1:B:290:ARG:NH2	2.53	0.42
1:D:102:ILE:HD11	5:D:6039:HOH:O	2.19	0.42
1:D:156:PRO:HB3	5:D:6008:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:45:THR:CG2	5:D:6034:HOH:O	2.56	0.42
1:I:181:TYR:CD2	1:I:181:TYR:C	2.93	0.42
1:I:333:ARG:N	1:I:334:PRO:CD	2.83	0.42
1:J:324:ASN:CA	5:J:6034:HOH:O	2.68	0.42
1:B:349:GLU:HB3	5:B:6027:HOH:O	2.18	0.42
1:D:172:VAL:HG21	1:D:198:TRP:CE3	2.54	0.42
1:G:350:THR:HG21	5:G:6036:HOH:O	2.20	0.42
1:B:142:PRO:HB2	1:B:145:TRP:CG	2.54	0.42
1:H:105:ASN:HD22	1:H:107:ARG:H	1.67	0.42
1:H:355:LYS:CB	5:H:6009:HOH:O	2.68	0.42
1:C:105:ASN:ND2	1:C:107:ARG:H	2.17	0.41
1:D:292:LEU:HD23	1:D:298:THR:HB	2.02	0.41
1:J:142:PRO:HB2	1:J:145:TRP:CD1	2.55	0.41
1:J:18:LYS:O	1:J:19:ILE:HD12	2.20	0.41
1:A:116:SER:HA	1:A:117:PRO:HD3	1.87	0.41
1:A:135:LEU:HD23	1:A:142:PRO:HA	2.02	0.41
5:B:6034:HOH:O	1:C:8:VAL:CG2	2.54	0.41
1:G:161:ILE:HD12	1:H:222:GLU:HB3	2.02	0.41
1:I:308:VAL:HG22	5:I:6041:HOH:O	2.20	0.41
1:B:164:GLU:HG3	1:C:231:VAL:HG22	2.01	0.41
1:D:123:GLU:CG	5:D:6015:HOH:O	2.64	0.41
1:D:137:LYS:O	1:D:138:ASP:HB2	2.20	0.41
1:I:203:GLY:HA2	4:I:6009:ANP:O3'	2.19	0.41
1:B:136:GLN:HB3	5:B:6018:HOH:O	2.20	0.41
1:I:231:VAL:HG22	1:J:164:GLU:HG3	2.02	0.41
1:C:332:ARG:HH22	3:C:5003:MSL:HG3	1.85	0.41
3:C:5005:MSL:NE	4:E:6005:ANP:O1G	2.54	0.41
3:C:5005:MSL:CE	1:E:297:GLU:OE2	2.69	0.41
1:C:142:PRO:HB2	1:C:145:TRP:CD1	2.56	0.41
1:C:46:ASP:HB3	1:C:49:LYS:HD3	2.03	0.41
1:E:191:GLY:HA2	1:E:198:TRP:CE3	2.56	0.41
1:B:24:ILE:HD11	1:B:89:LEU:HD22	2.02	0.41
1:C:142:PRO:HB2	1:C:145:TRP:CG	2.56	0.41
1:C:18:LYS:O	1:C:19:ILE:HD12	2.20	0.41
1:A:222:GLU:HB3	1:D:161:ILE:HD12	2.01	0.41
1:F:128:ILE:O	1:F:128:ILE:HG13	2.21	0.41
1:G:277:HIS:CD2	1:G:333:ARG:HH11	2.38	0.41
1:G:46:ASP:HB3	1:G:49:LYS:HD3	2.03	0.41
1:J:302:ASN:HA	5:J:6028:HOH:O	2.21	0.41
1:B:236:PRO:HB3	1:B:335:ALA:HB1	2.03	0.41
1:D:75:GLN:NE2	5:D:6032:HOH:O	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ALA:HB1	1:B:338:MET:HE3	2.03	0.41
1:F:284:TYR:CD2	1:F:343:VAL:HG22	2.56	0.41
1:I:223:ARG:HH11	1:I:223:ARG:HD2	1.71	0.41
1:I:248:ALA:HB1	1:I:338:MET:HE1	2.04	0.41
3:C:5007:MSL:HB2	1:F:249:HIS:HE1	1.84	0.40
1:A:233:THR:HB	1:A:235:ASP:H	1.86	0.40
1:D:135:LEU:HD23	1:D:142:PRO:HA	2.03	0.40
1:J:277:HIS:CD2	1:J:333:ARG:HH11	2.39	0.40
1:J:46:ASP:HB3	1:J:49:LYS:HD3	2.02	0.40
1:B:50:LEU:HD11	1:B:77:ILE:HD11	2.03	0.40
1:E:292:LEU:HD23	1:E:298:THR:HB	2.02	0.40
1:F:192:GLU:HB3	1:F:197:GLN:HE21	1.87	0.40
1:G:292:LEU:HD23	1:G:298:THR:HB	2.03	0.40
1:G:58:SER:HA	1:G:63:ALA:O	2.21	0.40
1:H:211:GLY:HA2	1:H:340:PRO:HB2	2.02	0.40
1:A:127:GLY:HA3	4:A:6001:ANP:O4'	2.21	0.40
1:A:308:VAL:N	5:A:6028:HOH:O	2.48	0.40
1:A:113:ILE:HD13	1:A:349:GLU:HG3	2.02	0.40
1:C:181:TYR:CD2	1:C:181:TYR:C	2.95	0.40
1:D:154:GLN:HE22	1:D:244:ASN:N	1.96	0.40
1:F:105:ASN:HD22	1:F:107:ARG:H	1.68	0.40
1:F:323:GLN:HG2	5:F:6035:HOH:O	2.22	0.40
1:H:105:ASN:ND2	1:H:107:ARG:H	2.20	0.40
1:H:248:ALA:O	1:H:249:HIS:C	2.60	0.40
5:H:6015:HOH:O	1:I:3:CYS:HA	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	351/356 (99%)	331 (94%)	20 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	351/356 (99%)	331 (94%)	20 (6%)	0	100	100
1	C	351/356 (99%)	334 (95%)	16 (5%)	1 (0%)	44	80
1	D	351/356 (99%)	333 (95%)	18 (5%)	0	100	100
1	E	351/356 (99%)	328 (93%)	23 (7%)	0	100	100
1	F	351/356 (99%)	331 (94%)	20 (6%)	0	100	100
1	G	351/356 (99%)	332 (95%)	18 (5%)	1 (0%)	44	80
1	H	351/356 (99%)	334 (95%)	17 (5%)	0	100	100
1	I	351/356 (99%)	330 (94%)	21 (6%)	0	100	100
1	J	351/356 (99%)	332 (95%)	19 (5%)	0	100	100
All	All	3510/3560 (99%)	3316 (94%)	192 (6%)	2 (0%)	55	88

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	84	ARG
1	C	138	ASP

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	288/290 (99%)	261 (91%)	27 (9%)	10	40
1	B	288/290 (99%)	264 (92%)	24 (8%)	13	46
1	C	288/290 (99%)	262 (91%)	26 (9%)	11	42
1	D	288/290 (99%)	262 (91%)	26 (9%)	11	42
1	E	288/290 (99%)	262 (91%)	26 (9%)	11	42
1	F	288/290 (99%)	262 (91%)	26 (9%)	11	42
1	G	288/290 (99%)	262 (91%)	26 (9%)	11	42
1	H	288/290 (99%)	262 (91%)	26 (9%)	11	42
1	I	288/290 (99%)	264 (92%)	24 (8%)	13	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	288/290 (99%)	261 (91%)	27 (9%)	10	40
All	All	2880/2900 (99%)	2622 (91%)	258 (9%)	11	42

All (258) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	CYS
1	A	15	THR
1	A	19	ILE
1	A	45	THR
1	A	66	GLU
1	A	104	THR
1	A	105	ASN
1	A	109	SER
1	A	112	LYS
1	A	123	GLU
1	A	128	ILE
1	A	143	LEU
1	A	147	ILE
1	A	164	GLU
1	A	176	TYR
1	A	201	GLN
1	A	232	VAL
1	A	233	THR
1	A	288	ASN
1	A	289	GLU
1	A	301	ILE
1	A	321	THR
1	A	338	MET
1	A	344	THR
1	A	349	GLU
1	A	351	THR
1	A	355	LYS
1	B	3	CYS
1	B	15	THR
1	B	19	ILE
1	B	45	THR
1	B	104	THR
1	B	105	ASN
1	B	109	SER
1	B	112	LYS
1	B	123	GLU

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Mol	Chain	Res	Type
1	B	128	ILE
1	B	143	LEU
1	B	147	ILE
1	B	164	GLU
1	B	176	TYR
1	B	201	GLN
1	B	232	VAL
1	B	233	THR
1	B	288	ASN
1	B	289	GLU
1	B	301	ILE
1	B	321	THR
1	B	344	THR
1	B	349	GLU
1	B	351	THR
1	C	3	CYS
1	C	14	ASP
1	C	15	THR
1	C	19	ILE
1	C	45	THR
1	C	66	GLU
1	C	104	THR
1	C	105	ASN
1	C	112	LYS
1	C	123	GLU
1	C	128	ILE
1	C	143	LEU
1	C	147	ILE
1	C	164	GLU
1	C	176	TYR
1	C	201	GLN
1	C	232	VAL
1	C	233	THR
1	C	288	ASN
1	C	289	GLU
1	C	301	ILE
1	C	321	THR
1	C	338	MET
1	C	344	THR
1	C	349	GLU
1	C	351	THR
1	D	3	CYS

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Mol	Chain	Res	Type
1	D	14	ASP
1	D	15	THR
1	D	19	ILE
1	D	45	THR
1	D	66	GLU
1	D	104	THR
1	D	105	ASN
1	D	109	SER
1	D	112	LYS
1	D	123	GLU
1	D	128	ILE
1	D	143	LEU
1	D	147	ILE
1	D	164	GLU
1	D	176	TYR
1	D	201	GLN
1	D	232	VAL
1	D	233	THR
1	D	288	ASN
1	D	289	GLU
1	D	301	ILE
1	D	321	THR
1	D	344	THR
1	D	349	GLU
1	D	351	THR
1	E	3	CYS
1	E	14	ASP
1	E	15	THR
1	E	19	ILE
1	E	45	THR
1	E	66	GLU
1	E	104	THR
1	E	105	ASN
1	E	109	SER
1	E	112	LYS
1	E	123	GLU
1	E	128	ILE
1	E	143	LEU
1	E	147	ILE
1	E	164	GLU
1	E	176	TYR
1	E	201	GLN

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Mol	Chain	Res	Type
1	E	232	VAL
1	E	233	THR
1	E	288	ASN
1	E	289	GLU
1	E	301	ILE
1	E	321	THR
1	E	344	THR
1	E	349	GLU
1	E	351	THR
1	F	3	CYS
1	F	14	ASP
1	F	19	ILE
1	F	45	THR
1	F	66	GLU
1	F	104	THR
1	F	105	ASN
1	F	109	SER
1	F	112	LYS
1	F	123	GLU
1	F	128	ILE
1	F	143	LEU
1	F	147	ILE
1	F	164	GLU
1	F	176	TYR
1	F	201	GLN
1	F	232	VAL
1	F	233	THR
1	F	238	PRO
1	F	288	ASN
1	F	289	GLU
1	F	301	ILE
1	F	321	THR
1	F	344	THR
1	F	349	GLU
1	F	351	THR
1	G	3	CYS
1	G	14	ASP
1	G	15	THR
1	G	19	ILE
1	G	45	THR
1	G	66	GLU
1	G	104	THR

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Mol	Chain	Res	Type
1	G	105	ASN
1	G	109	SER
1	G	112	LYS
1	G	128	ILE
1	G	143	LEU
1	G	147	ILE
1	G	164	GLU
1	G	176	TYR
1	G	201	GLN
1	G	232	VAL
1	G	233	THR
1	G	288	ASN
1	G	289	GLU
1	G	301	ILE
1	G	321	THR
1	G	338	MET
1	G	344	THR
1	G	349	GLU
1	G	351	THR
1	H	3	CYS
1	H	15	THR
1	H	19	ILE
1	H	45	THR
1	H	66	GLU
1	H	104	THR
1	H	105	ASN
1	H	109	SER
1	H	112	LYS
1	H	123	GLU
1	H	128	ILE
1	H	143	LEU
1	H	147	ILE
1	H	164	GLU
1	H	176	TYR
1	H	201	GLN
1	H	232	VAL
1	H	233	THR
1	H	288	ASN
1	H	289	GLU
1	H	301	ILE
1	H	321	THR
1	H	338	MET

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Mol	Chain	Res	Type
1	H	344	THR
1	H	349	GLU
1	H	351	THR
1	I	3	CYS
1	I	15	THR
1	I	19	ILE
1	I	45	THR
1	I	66	GLU
1	I	104	THR
1	I	105	ASN
1	I	112	LYS
1	I	123	GLU
1	I	128	ILE
1	I	143	LEU
1	I	147	ILE
1	I	164	GLU
1	I	176	TYR
1	I	201	GLN
1	I	232	VAL
1	I	233	THR
1	I	288	ASN
1	I	289	GLU
1	I	301	ILE
1	I	321	THR
1	I	344	THR
1	I	349	GLU
1	I	351	THR
1	J	3	CYS
1	J	15	THR
1	J	19	ILE
1	J	45	THR
1	J	66	GLU
1	J	104	THR
1	J	105	ASN
1	J	109	SER
1	J	112	LYS
1	J	123	GLU
1	J	128	ILE
1	J	143	LEU
1	J	147	ILE
1	J	164	GLU
1	J	176	TYR

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Mol	Chain	Res	Type
1	J	201	GLN
1	J	232	VAL
1	J	233	THR
1	J	238	PRO
1	J	288	ASN
1	J	289	GLU
1	J	301	ILE
1	J	321	THR
1	J	338	MET
1	J	344	THR
1	J	349	GLU
1	J	351	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	154	GLN
1	A	190	ASN
1	A	197	GLN
1	A	201	GLN
1	A	251	ASN
1	A	277	HIS
1	A	288	ASN
1	A	324	ASN
1	B	105	ASN
1	B	154	GLN
1	B	190	ASN
1	B	197	GLN
1	B	201	GLN
1	B	249	HIS
1	B	251	ASN
1	B	277	HIS
1	B	288	ASN
1	B	324	ASN
1	C	105	ASN
1	C	154	GLN
1	C	190	ASN
1	C	197	GLN
1	C	201	GLN
1	C	277	HIS
1	C	288	ASN

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Mol	Chain	Res	Type
1	C	296	HIS
1	C	324	ASN
1	D	105	ASN
1	D	154	GLN
1	D	190	ASN
1	D	197	GLN
1	D	201	GLN
1	D	277	HIS
1	D	288	ASN
1	D	296	HIS
1	D	324	ASN
1	E	105	ASN
1	E	154	GLN
1	E	190	ASN
1	E	197	GLN
1	E	201	GLN
1	E	251	ASN
1	E	277	HIS
1	E	288	ASN
1	E	296	HIS
1	E	324	ASN
1	F	105	ASN
1	F	154	GLN
1	F	190	ASN
1	F	197	GLN
1	F	201	GLN
1	F	249	HIS
1	F	251	ASN
1	F	277	HIS
1	F	288	ASN
1	F	296	HIS
1	F	324	ASN
1	G	75	GLN
1	G	105	ASN
1	G	154	GLN
1	G	190	ASN
1	G	197	GLN
1	G	201	GLN
1	G	251	ASN
1	G	277	HIS
1	G	288	ASN
1	G	296	HIS

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Mol	Chain	Res	Type
1	G	324	ASN
1	H	105	ASN
1	H	154	GLN
1	H	190	ASN
1	H	197	GLN
1	H	201	GLN
1	H	251	ASN
1	H	277	HIS
1	H	288	ASN
1	H	296	HIS
1	H	324	ASN
1	I	105	ASN
1	I	154	GLN
1	I	190	ASN
1	I	197	GLN
1	I	201	GLN
1	I	251	ASN
1	I	277	HIS
1	I	288	ASN
1	I	296	HIS
1	I	324	ASN
1	J	105	ASN
1	J	154	GLN
1	J	190	ASN
1	J	197	GLN
1	J	201	GLN
1	J	277	HIS
1	J	288	ASN
1	J	296	HIS
1	J	324	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 50 ligands modelled in this entry, 30 are monoatomic - leaving 20 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	ANP	A	6001	2	29,33,33	2.53	11 (37%)	28,52,52	4.01	17 (60%)
4	ANP	B	6002	2	29,33,33	2.70	12 (41%)	28,52,52	4.47	14 (50%)
3	MSL	C	5001	2	4,10,10	4.85	2 (50%)	3,14,14	1.88	2 (66%)
3	MSL	C	5002	2	4,10,10	5.31	1 (25%)	3,14,14	8.29	1 (33%)
3	MSL	C	5003	2	4,10,10	5.18	1 (25%)	3,14,14	3.40	2 (66%)
3	MSL	C	5004	2	4,10,10	5.45	1 (25%)	3,14,14	2.98	3 (100%)
3	MSL	C	5005	2	4,10,10	4.89	1 (25%)	3,14,14	2.48	2 (66%)
3	MSL	C	5006	2	4,10,10	5.44	2 (50%)	3,14,14	2.17	2 (66%)
3	MSL	C	5007	2	4,10,10	4.98	2 (50%)	3,14,14	6.90	3 (100%)
3	MSL	C	5008	2	4,10,10	5.51	1 (25%)	3,14,14	1.26	0
3	MSL	C	5009	2	4,10,10	4.76	1 (25%)	3,14,14	3.16	2 (66%)
3	MSL	C	5010	2	4,10,10	5.20	1 (25%)	3,14,14	5.63	2 (66%)
4	ANP	C	6003	2	29,33,33	2.47	10 (34%)	28,52,52	4.43	15 (53%)
4	ANP	D	6004	2	29,33,33	2.92	10 (34%)	28,52,52	4.39	17 (60%)
4	ANP	E	6005	2	29,33,33	2.88	12 (41%)	28,52,52	4.81	18 (64%)
4	ANP	F	6006	2	29,33,33	2.92	13 (44%)	28,52,52	3.65	15 (53%)
4	ANP	G	6007	2	29,33,33	2.43	11 (37%)	28,52,52	3.61	14 (50%)
4	ANP	H	6008	2	29,33,33	2.52	13 (44%)	28,52,52	4.74	16 (57%)
4	ANP	I	6009	2	29,33,33	2.60	10 (34%)	28,52,52	3.73	15 (53%)
4	ANP	J	6010	2	29,33,33	2.56	12 (41%)	28,52,52	4.01	16 (57%)

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	ANP	A	6001	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	B	6002	2	2/2/7/8	1/13/38/38	0/3/3/3
3	MSL	C	5001	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5002	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5003	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5004	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5005	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5006	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5007	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5008	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5009	2	-	0/5/10/10	0/0/0/0
3	MSL	C	5010	2	-	0/5/10/10	0/0/0/0
4	ANP	C	6003	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	D	6004	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	E	6005	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	F	6006	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	G	6007	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	H	6008	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	I	6009	2	2/2/7/8	0/13/38/38	0/3/3/3
4	ANP	J	6010	2	2/2/7/8	0/13/38/38	0/3/3/3

All (127) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	5008	MSL	CG-SD	-10.83	1.67	1.79
3	C	5004	MSL	CG-SD	-10.74	1.67	1.79
3	C	5002	MSL	CG-SD	-10.47	1.67	1.79
3	C	5006	MSL	CG-SD	-10.37	1.67	1.79
3	C	5003	MSL	CG-SD	-10.23	1.67	1.79
3	C	5010	MSL	CG-SD	-10.22	1.67	1.79
3	C	5005	MSL	CG-SD	-9.63	1.68	1.79
3	C	5007	MSL	CG-SD	-9.60	1.68	1.79
3	C	5009	MSL	CG-SD	-9.35	1.68	1.79
3	C	5001	MSL	CG-SD	-9.18	1.68	1.79
4	H	6008	ANP	C5'-C4'	-6.16	1.32	1.51
4	F	6006	ANP	C5'-C4'	-5.97	1.32	1.51
4	G	6007	ANP	C5'-C4'	-5.94	1.32	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	6001	ANP	C5'-C4'	-5.88	1.33	1.51
4	D	6004	ANP	C5'-C4'	-5.88	1.33	1.51
4	I	6009	ANP	C5'-C4'	-5.73	1.33	1.51
4	E	6005	ANP	C5'-C4'	-5.71	1.33	1.51
4	B	6002	ANP	C5'-C4'	-5.31	1.34	1.51
4	J	6010	ANP	C5'-C4'	-5.11	1.35	1.51
4	C	6003	ANP	C5'-C4'	-5.06	1.35	1.51
4	G	6007	ANP	PB-O2B	-4.51	1.44	1.56
4	B	6002	ANP	PB-O2B	-4.44	1.44	1.56
4	H	6008	ANP	PG-O3G	-4.04	1.45	1.56
4	H	6008	ANP	PB-O2B	-3.90	1.46	1.56
4	A	6001	ANP	C8-N7	-3.87	1.27	1.34
4	E	6005	ANP	C8-N7	-3.75	1.27	1.34
4	I	6009	ANP	C8-N7	-3.69	1.27	1.34
4	C	6003	ANP	PB-O2B	-3.65	1.46	1.56
4	C	6003	ANP	C8-N7	-3.60	1.27	1.34
4	D	6004	ANP	C8-N7	-3.53	1.28	1.34
4	A	6001	ANP	PB-O2B	-3.44	1.47	1.56
4	J	6010	ANP	C8-N7	-3.35	1.28	1.34
4	G	6007	ANP	C8-N7	-3.33	1.28	1.34
4	B	6002	ANP	C8-N7	-3.30	1.28	1.34
4	F	6006	ANP	C8-N7	-3.28	1.28	1.34
4	J	6010	ANP	PB-O2B	-3.11	1.48	1.56
4	I	6009	ANP	PB-O2B	-3.06	1.48	1.56
4	H	6008	ANP	C8-N7	-2.97	1.29	1.34
4	E	6005	ANP	PB-O2B	-2.88	1.48	1.56
4	E	6005	ANP	PG-O3G	-2.65	1.49	1.56
4	B	6002	ANP	PG-O3G	-2.64	1.49	1.56
4	H	6008	ANP	O3'-C3'	-2.56	1.37	1.43
4	F	6006	ANP	PB-O2B	-2.44	1.50	1.56
4	A	6001	ANP	PB-N3B	-2.42	1.56	1.63
4	G	6007	ANP	PB-N3B	-2.32	1.57	1.63
4	A	6001	ANP	O3'-C3'	-2.20	1.37	1.43
4	B	6002	ANP	O3'-C3'	-2.20	1.37	1.43
4	D	6004	ANP	PG-O3G	-2.15	1.50	1.56
4	J	6010	ANP	O3'-C3'	-2.07	1.38	1.43
4	G	6007	ANP	PG-O3G	-2.05	1.51	1.56
4	E	6005	ANP	C2'-C3'	2.10	1.59	1.53
4	H	6008	ANP	PA-O5'	2.16	1.68	1.59
3	C	5007	MSL	CB-CG	2.17	1.54	1.52
4	G	6007	ANP	C2'-C3'	2.19	1.59	1.53
4	F	6006	ANP	O5'-C5'	2.21	1.53	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	6007	ANP	PG-O1G	2.22	1.48	1.46
4	A	6001	ANP	O5'-C5'	2.23	1.53	1.44
4	D	6004	ANP	O5'-C5'	2.25	1.53	1.44
4	F	6006	ANP	PA-O1A	2.26	1.59	1.50
4	H	6008	ANP	C2'-C3'	2.29	1.59	1.53
4	G	6007	ANP	PG-N3B	2.29	1.69	1.63
4	F	6006	ANP	PG-O3G	2.36	1.63	1.56
4	F	6006	ANP	PB-O1B	2.36	1.48	1.46
4	C	6003	ANP	PG-N3B	2.37	1.69	1.63
4	J	6010	ANP	PB-O1B	2.38	1.48	1.46
4	J	6010	ANP	PA-O5'	2.47	1.69	1.59
4	C	6003	ANP	PA-O5'	2.53	1.69	1.59
4	J	6010	ANP	C2'-C3'	2.55	1.60	1.53
4	J	6010	ANP	O5'-C5'	2.61	1.55	1.44
4	F	6006	ANP	PG-O1G	2.64	1.49	1.46
4	C	6003	ANP	C2-N3	2.66	1.36	1.32
4	H	6008	ANP	O5'-C5'	2.70	1.55	1.44
4	I	6009	ANP	PG-N3B	2.72	1.70	1.63
4	B	6002	ANP	O5'-C5'	2.72	1.55	1.44
4	A	6001	ANP	PG-N3B	2.74	1.70	1.63
4	I	6009	ANP	C2'-C3'	2.75	1.60	1.53
4	C	6003	ANP	O5'-C5'	2.76	1.55	1.44
3	C	5001	MSL	CB-CG	2.81	1.55	1.52
4	H	6008	ANP	C4-N3	2.83	1.39	1.35
3	C	5006	MSL	CB-CG	2.84	1.55	1.52
4	B	6002	ANP	PG-N3B	2.98	1.71	1.63
4	E	6005	ANP	PB-O1B	3.13	1.49	1.46
4	D	6004	ANP	PG-N3B	3.13	1.71	1.63
4	H	6008	ANP	PG-N3B	3.19	1.71	1.63
4	B	6002	ANP	PB-O1B	3.46	1.50	1.46
4	I	6009	ANP	PG-O1G	3.48	1.50	1.46
4	F	6006	ANP	C2-N1	3.52	1.40	1.33
4	G	6007	ANP	C4-N3	3.63	1.40	1.35
4	H	6008	ANP	PB-O1B	3.63	1.50	1.46
4	E	6005	ANP	C2-N1	3.65	1.40	1.33
4	B	6002	ANP	PB-O3A	3.72	1.63	1.59
4	B	6002	ANP	C2-N1	3.74	1.40	1.33
4	E	6005	ANP	PG-N3B	3.78	1.73	1.63
4	A	6001	ANP	C2-N1	3.79	1.41	1.33
4	H	6008	ANP	C2-N1	3.83	1.41	1.33
4	G	6007	ANP	C2-N1	3.85	1.41	1.33
4	I	6009	ANP	C2-N1	3.85	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	6004	ANP	C2-N1	3.97	1.41	1.33
4	E	6005	ANP	C4-N3	4.09	1.41	1.35
4	C	6003	ANP	C2-N1	4.18	1.41	1.33
4	A	6001	ANP	C4-N3	4.21	1.41	1.35
4	I	6009	ANP	PB-O1B	4.32	1.51	1.46
4	D	6004	ANP	PB-O1B	4.34	1.51	1.46
4	A	6001	ANP	PG-O1G	4.36	1.51	1.46
4	E	6005	ANP	PG-O1G	4.49	1.51	1.46
4	J	6010	ANP	C2-N1	4.52	1.42	1.33
4	J	6010	ANP	C4-N3	4.57	1.42	1.35
4	J	6010	ANP	O2'-C2'	4.77	1.53	1.43
4	F	6006	ANP	C4-N3	4.81	1.42	1.35
4	F	6006	ANP	O2'-C2'	4.82	1.54	1.43
4	H	6008	ANP	O2'-C2'	4.82	1.54	1.43
4	I	6009	ANP	C4-N3	4.83	1.42	1.35
4	D	6004	ANP	C4-N3	4.87	1.42	1.35
4	D	6004	ANP	O2'-C2'	4.87	1.54	1.43
4	E	6005	ANP	O2'-C2'	4.94	1.54	1.43
4	C	6003	ANP	O2'-C2'	4.97	1.54	1.43
4	A	6001	ANP	O2'-C2'	4.98	1.54	1.43
4	I	6009	ANP	O2'-C2'	5.26	1.55	1.43
4	B	6002	ANP	O2'-C2'	5.43	1.55	1.43
4	J	6010	ANP	PG-N3B	5.46	1.77	1.63
4	G	6007	ANP	O2'-C2'	5.55	1.55	1.43
4	C	6003	ANP	C4-N3	5.55	1.43	1.35
4	B	6002	ANP	C4-N3	5.73	1.44	1.35
4	F	6006	ANP	PG-O2G	6.02	1.73	1.56
4	F	6006	ANP	PB-O3A	7.00	1.67	1.59
4	E	6005	ANP	PB-O3A	7.66	1.68	1.59
4	D	6004	ANP	PB-O3A	8.42	1.69	1.59

All (176) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	6002	ANP	C4'-O4'-C1'	-16.53	92.17	109.77
4	E	6005	ANP	C4'-O4'-C1'	-15.74	93.02	109.77
4	D	6004	ANP	C4'-O4'-C1'	-14.94	93.87	109.77
4	H	6008	ANP	C4'-O4'-C1'	-14.76	94.06	109.77
4	C	6003	ANP	C4'-O4'-C1'	-14.72	94.10	109.77
4	A	6001	ANP	C4'-O4'-C1'	-13.85	95.02	109.77
4	E	6005	ANP	C2'-C3'-C4'	-11.77	79.70	102.62
4	J	6010	ANP	C4'-O4'-C1'	-11.35	97.68	109.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	6008	ANP	C2'-C3'-C4'	-11.30	80.62	102.62
4	G	6007	ANP	C4'-O4'-C1'	-11.28	97.76	109.77
4	C	6003	ANP	C2'-C3'-C4'	-11.01	81.18	102.62
4	I	6009	ANP	C4'-O4'-C1'	-10.56	98.53	109.77
4	J	6010	ANP	C2'-C3'-C4'	-10.49	82.19	102.62
4	F	6006	ANP	C4'-O4'-C1'	-10.41	98.69	109.77
4	D	6004	ANP	C2'-C3'-C4'	-10.18	82.79	102.62
3	C	5010	MSL	OE-SD-CG	-9.43	101.12	108.37
4	B	6002	ANP	C2'-C3'-C4'	-9.27	84.57	102.62
4	F	6006	ANP	C2'-C3'-C4'	-8.99	85.11	102.62
4	I	6009	ANP	C2'-C3'-C4'	-8.78	85.51	102.62
4	A	6001	ANP	C2'-C3'-C4'	-8.37	86.32	102.62
4	G	6007	ANP	C2'-C3'-C4'	-7.43	88.14	102.62
3	C	5007	MSL	OE-SD-CE	-7.04	97.94	109.14
4	H	6008	ANP	O2'-C2'-C3'	-6.66	90.51	111.83
4	B	6002	ANP	O2'-C2'-C3'	-5.57	93.98	111.83
4	H	6008	ANP	N6-C6-N1	-5.48	107.90	118.77
4	E	6005	ANP	O2'-C2'-C3'	-5.25	95.00	111.83
3	C	5003	MSL	OE-SD-CE	-4.94	101.27	109.14
4	A	6001	ANP	O2'-C2'-C3'	-4.83	96.37	111.83
4	D	6004	ANP	O1B-PB-N3B	-4.79	104.62	111.79
4	C	6003	ANP	O2'-C2'-C3'	-4.74	96.64	111.83
4	B	6002	ANP	O5'-PA-O1A	-4.36	91.64	109.25
4	D	6004	ANP	O2'-C2'-C3'	-4.27	98.16	111.83
4	G	6007	ANP	O2'-C2'-C3'	-4.19	98.42	111.83
4	A	6001	ANP	O1B-PB-N3B	-4.11	105.64	111.79
4	H	6008	ANP	O3G-PG-O1G	-4.03	103.17	113.41
3	C	5004	MSL	OE-SD-CE	-3.69	103.27	109.14
4	I	6009	ANP	O2'-C2'-C3'	-3.59	100.34	111.83
4	A	6001	ANP	O5'-PA-O1A	-3.53	95.00	109.25
4	F	6006	ANP	O2'-C2'-C3'	-3.40	100.93	111.83
4	J	6010	ANP	O2'-C2'-C3'	-3.34	101.14	111.83
4	E	6005	ANP	PA-O3A-PB	-3.31	120.69	132.38
4	H	6008	ANP	O2'-C2'-C1'	-3.28	101.35	111.61
4	E	6005	ANP	O5'-PA-O1A	-3.25	96.15	109.25
4	F	6006	ANP	O1B-PB-N3B	-3.21	106.99	111.79
4	C	6003	ANP	N6-C6-N1	-3.19	112.44	118.77
4	J	6010	ANP	O5'-PA-O1A	-3.17	96.45	109.25
4	J	6010	ANP	O3G-PG-O1G	-3.16	105.38	113.41
4	C	6003	ANP	O2G-PG-O1G	-3.16	105.38	113.41
3	C	5005	MSL	OE-SD-CG	-3.14	105.95	108.37
4	F	6006	ANP	O5'-PA-O1A	-3.12	96.67	109.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	6004	ANP	PA-O3A-PB	-3.08	121.50	132.38
4	D	6004	ANP	O5'-PA-O1A	-2.98	97.24	109.25
4	G	6007	ANP	O3G-PG-O1G	-2.97	105.87	113.41
4	J	6010	ANP	O4'-C4'-C3'	-2.97	99.27	105.17
4	C	6003	ANP	O4'-C4'-C3'	-2.95	99.30	105.17
3	C	5009	MSL	OE-SD-CE	-2.91	104.50	109.14
4	D	6004	ANP	N6-C6-N1	-2.78	113.25	118.77
4	E	6005	ANP	O1B-PB-N3B	-2.77	107.64	111.79
4	B	6002	ANP	O3G-PG-O1G	-2.74	106.44	113.41
4	H	6008	ANP	O4'-C4'-C3'	-2.72	99.75	105.17
4	I	6009	ANP	O1B-PB-N3B	-2.64	107.84	111.79
4	J	6010	ANP	O1B-PB-N3B	-2.59	107.92	111.79
3	C	5001	MSL	OE-SD-CG	-2.44	106.49	108.37
4	I	6009	ANP	N6-C6-N1	-2.43	113.94	118.77
4	D	6004	ANP	O4'-C4'-C3'	-2.42	100.35	105.17
4	G	6007	ANP	O5'-PA-O1A	-2.41	99.54	109.25
4	E	6005	ANP	N6-C6-N1	-2.28	114.24	118.77
4	A	6001	ANP	O2'-C2'-C1'	-2.28	104.48	111.61
3	C	5006	MSL	OE-SD-CE	-2.28	105.51	109.14
4	D	6004	ANP	O3G-PG-O1G	-2.26	107.67	113.41
4	H	6008	ANP	PA-O3A-PB	-2.24	124.47	132.38
4	G	6007	ANP	N6-C6-N1	-2.24	114.33	118.77
4	A	6001	ANP	N6-C6-N1	-2.23	114.34	118.77
4	E	6005	ANP	O3G-PG-O1G	-2.23	107.75	113.41
4	G	6007	ANP	PA-O3A-PB	-2.21	124.59	132.38
4	E	6005	ANP	O3G-PG-O2G	-2.20	101.51	107.69
4	F	6006	ANP	N6-C6-N1	-2.17	114.45	118.77
4	C	6003	ANP	PA-O3A-PB	-2.09	124.99	132.38
4	E	6005	ANP	O4'-C4'-C3'	-2.09	101.01	105.17
4	I	6009	ANP	O4'-C4'-C3'	-2.05	101.09	105.17
4	D	6004	ANP	O3'-C3'-C2'	2.01	118.26	111.83
4	F	6006	ANP	C1'-N9-C4	2.03	130.15	126.64
3	C	5001	MSL	CE-SD-CG	2.08	112.97	105.21
4	F	6006	ANP	O4'-C4'-C5'	2.12	116.56	109.40
4	E	6005	ANP	C1'-N9-C4	2.13	130.31	126.64
4	F	6006	ANP	O3A-PB-N3B	2.15	112.56	106.59
4	A	6001	ANP	O3'-C3'-C2'	2.15	118.73	111.83
3	C	5010	MSL	OE-SD-CE	2.18	112.60	109.14
4	B	6002	ANP	O3'-C3'-C2'	2.19	118.85	111.83
3	C	5004	MSL	CE-SD-CG	2.19	113.41	105.21
4	G	6007	ANP	C1'-N9-C4	2.27	130.56	126.64
4	I	6009	ANP	O3'-C3'-C4'	2.31	117.84	111.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	6001	ANP	O1G-PG-N3B	2.32	115.25	111.79
4	J	6010	ANP	O3'-C3'-C2'	2.36	119.38	111.83
4	A	6001	ANP	C1'-N9-C4	2.49	130.94	126.64
4	A	6001	ANP	O2B-PB-O1B	2.59	115.25	109.87
3	C	5006	MSL	OE-SD-CG	2.59	110.36	108.37
4	A	6001	ANP	O3'-C3'-C4'	2.64	118.80	111.09
4	C	6003	ANP	C4-C5-N7	2.70	112.02	109.41
4	E	6005	ANP	O3A-PB-N3B	2.72	114.14	106.59
4	D	6004	ANP	O3'-C3'-C4'	2.76	119.14	111.09
3	C	5005	MSL	CE-SD-CG	2.78	115.59	105.21
4	I	6009	ANP	O3'-C3'-C2'	2.79	120.76	111.83
3	C	5007	MSL	CE-SD-CG	2.80	115.67	105.21
4	D	6004	ANP	O1G-PG-N3B	2.80	115.98	111.79
4	H	6008	ANP	O3'-C3'-C4'	2.81	119.30	111.09
4	H	6008	ANP	O2G-PG-O1G	2.81	120.55	113.41
3	C	5004	MSL	OE-SD-CG	2.87	110.58	108.37
4	A	6001	ANP	O3A-PB-N3B	2.87	114.56	106.59
4	F	6006	ANP	O2B-PB-O1B	2.92	115.94	109.87
4	D	6004	ANP	C4-C5-N7	3.19	112.49	109.41
3	C	5003	MSL	CE-SD-CG	3.21	117.21	105.21
4	B	6002	ANP	O2B-PB-O1B	3.23	116.59	109.87
4	G	6007	ANP	O4'-C4'-C5'	3.25	120.38	109.40
4	G	6007	ANP	O3'-C3'-C4'	3.25	120.58	111.09
4	H	6008	ANP	N3-C2-N1	3.27	131.70	128.86
4	B	6002	ANP	C5-C6-N6	3.42	127.45	120.47
4	E	6005	ANP	O3'-C3'-C4'	3.45	121.16	111.09
4	F	6006	ANP	O3'-C3'-C4'	3.52	121.36	111.09
4	J	6010	ANP	O3'-C3'-C4'	3.53	121.41	111.09
4	B	6002	ANP	O3'-C3'-C4'	3.54	121.41	111.09
4	G	6007	ANP	C4-C5-N7	3.55	112.84	109.41
4	J	6010	ANP	O3A-PB-N3B	3.57	116.50	106.59
4	H	6008	ANP	O2B-PB-O1B	3.58	117.31	109.87
4	I	6009	ANP	O4'-C4'-C5'	3.68	121.84	109.40
4	E	6005	ANP	O4'-C4'-C5'	3.69	121.86	109.40
4	J	6010	ANP	O4'-C4'-C5'	3.77	122.14	109.40
4	I	6009	ANP	O1G-PG-N3B	3.77	117.43	111.79
4	A	6001	ANP	O4'-C4'-C5'	3.81	122.27	109.40
4	E	6005	ANP	C4-C5-N7	3.81	113.09	109.41
4	J	6010	ANP	O2B-PB-O1B	3.84	117.85	109.87
4	C	6003	ANP	O3'-C3'-C4'	3.84	122.31	111.09
4	J	6010	ANP	C1'-N9-C4	3.86	133.30	126.64
4	D	6004	ANP	O4'-C4'-C5'	3.88	122.50	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	6010	ANP	C4-C5-N7	3.90	113.18	109.41
4	I	6009	ANP	C4-C5-N7	3.92	113.20	109.41
4	C	6003	ANP	C1'-N9-C4	3.99	133.53	126.64
4	I	6009	ANP	C5-C6-N6	4.09	128.81	120.47
4	B	6002	ANP	C1'-N9-C4	4.10	133.72	126.64
4	A	6001	ANP	C4-C5-N7	4.15	113.42	109.41
4	C	6003	ANP	O2B-PB-O1B	4.15	118.51	109.87
4	F	6006	ANP	C4-C5-N7	4.17	113.44	109.41
4	B	6002	ANP	C4-C5-N7	4.19	113.46	109.41
4	B	6002	ANP	O4'-C4'-C5'	4.21	123.61	109.40
4	B	6002	ANP	O3A-PB-N3B	4.22	118.30	106.59
4	C	6003	ANP	O4'-C4'-C5'	4.27	123.83	109.40
4	F	6006	ANP	C5-C6-N6	4.32	129.27	120.47
4	C	6003	ANP	O1G-PG-N3B	4.36	118.31	111.79
4	E	6005	ANP	C5-C6-N6	4.39	129.43	120.47
3	C	5009	MSL	OE-SD-CG	4.45	111.80	108.37
4	J	6010	ANP	C5-C6-N6	4.47	129.57	120.47
4	C	6003	ANP	C5-C6-N6	4.47	129.57	120.47
4	A	6001	ANP	C5-C6-N6	4.54	129.73	120.47
4	H	6008	ANP	O3A-PB-N3B	4.61	119.39	106.59
4	D	6004	ANP	C5-C6-N6	4.66	129.97	120.47
4	B	6002	ANP	C5'-C4'-C3'	4.66	133.06	115.29
4	D	6004	ANP	O3A-PB-N3B	4.73	119.70	106.59
4	H	6008	ANP	C5'-C4'-C3'	4.73	133.33	115.29
4	H	6008	ANP	O4'-C4'-C5'	4.75	125.43	109.40
4	A	6001	ANP	C5'-C4'-C3'	4.78	133.49	115.29
4	I	6009	ANP	O2B-PB-O1B	4.80	119.84	109.87
4	F	6006	ANP	O1G-PG-N3B	4.86	119.06	111.79
4	G	6007	ANP	C5-C6-N6	4.95	130.56	120.47
4	G	6007	ANP	O1G-PG-N3B	4.97	119.23	111.79
4	I	6009	ANP	O3A-PB-N3B	5.10	120.75	106.59
4	G	6007	ANP	C5'-C4'-C3'	5.27	135.36	115.29
4	E	6005	ANP	C5'-C4'-C3'	5.39	135.84	115.29
4	C	6003	ANP	C5'-C4'-C3'	5.44	136.02	115.29
4	D	6004	ANP	C5'-C4'-C3'	5.54	136.39	115.29
4	I	6009	ANP	C5'-C4'-C3'	5.54	136.41	115.29
4	J	6010	ANP	C5'-C4'-C3'	5.90	137.77	115.29
4	F	6006	ANP	C5'-C4'-C3'	6.14	138.70	115.29
4	H	6008	ANP	C5-C6-N6	7.18	135.11	120.47
4	E	6005	ANP	O1G-PG-N3B	8.63	124.69	111.79
3	C	5007	MSL	OE-SD-CG	9.25	115.49	108.37
3	C	5002	MSL	OE-SD-CG	14.23	119.32	108.37

All (20) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	J	6010	ANP	C4'
4	J	6010	ANP	C1'
4	E	6005	ANP	C4'
4	E	6005	ANP	C1'
4	D	6004	ANP	C4'
4	D	6004	ANP	C1'
4	H	6008	ANP	C4'
4	H	6008	ANP	C1'
4	F	6006	ANP	C4'
4	F	6006	ANP	C1'
4	C	6003	ANP	C4'
4	C	6003	ANP	C1'
4	G	6007	ANP	C4'
4	G	6007	ANP	C1'
4	B	6002	ANP	C4'
4	B	6002	ANP	C1'
4	A	6001	ANP	C4'
4	A	6001	ANP	C1'
4	I	6009	ANP	C4'
4	I	6009	ANP	C1'

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	6002	ANP	O1B-PB-N3B-PG

There are no ring outliers.

20 monomers are involved in 63 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	6001	ANP	7	0
4	B	6002	ANP	3	0
3	C	5001	MSL	2	0
3	C	5002	MSL	6	0
3	C	5003	MSL	5	0
3	C	5004	MSL	2	0
3	C	5005	MSL	7	0
3	C	5006	MSL	2	0
3	C	5007	MSL	6	0
3	C	5008	MSL	2	0
3	C	5009	MSL	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	5010	MSL	2	0
4	C	6003	ANP	4	0
4	D	6004	ANP	6	0
4	E	6005	ANP	6	0
4	F	6006	ANP	4	0
4	G	6007	ANP	4	0
4	H	6008	ANP	3	0
4	I	6009	ANP	3	0
4	J	6010	ANP	3	0

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	353/356 (99%)	-0.77	0 100 100	55, 73, 96, 108	0
1	B	353/356 (99%)	-0.72	0 100 100	55, 73, 96, 108	0
1	C	353/356 (99%)	-0.81	0 100 100	55, 73, 96, 108	0
1	D	353/356 (99%)	-0.75	0 100 100	55, 73, 96, 108	0
1	E	353/356 (99%)	-0.78	1 (0%) 93 90	55, 73, 96, 108	0
1	F	353/356 (99%)	-0.77	0 100 100	55, 73, 96, 108	0
1	G	353/356 (99%)	-0.70	0 100 100	55, 73, 96, 108	0
1	H	353/356 (99%)	-0.74	0 100 100	55, 73, 96, 108	0
1	I	353/356 (99%)	-0.78	0 100 100	55, 73, 96, 108	0
1	J	353/356 (99%)	-0.78	0 100 100	55, 73, 96, 108	0
All	All	3530/3560 (99%)	-0.76	1 (0%) 100 100	55, 73, 96, 108	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	3	CYS	2.1

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 ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	ANP	F	6006	31/31	0.94	0.28	1.17	78,91,100,101	0
4	ANP	E	6005	31/31	0.95	0.25	1.07	79,95,105,106	0
4	ANP	C	6003	31/31	0.95	0.25	0.92	64,76,92,93	0
3	MSL	C	5003	11/11	0.97	0.23	0.89	63,64,66,66	0
3	MSL	C	5008	11/11	0.97	0.23	0.84	63,65,66,67	0
4	ANP	G	6007	31/31	0.95	0.26	0.75	65,86,95,96	0
3	MSL	C	5007	11/11	0.97	0.21	0.64	62,68,77,77	0
4	ANP	D	6004	31/31	0.96	0.23	0.61	83,95,105,106	0
4	ANP	A	6001	31/31	0.95	0.22	0.53	60,76,82,82	0
4	ANP	I	6009	31/31	0.96	0.23	0.52	69,78,84,85	0
3	MSL	C	5006	11/11	0.98	0.23	0.42	73,79,85,85	0
3	MSL	C	5005	11/11	0.96	0.19	0.24	75,78,79,79	0
3	MSL	C	5001	11/11	0.98	0.18	0.19	51,54,57,58	0
3	MSL	C	5002	11/11	0.98	0.20	-0.19	37,41,46,48	0
4	ANP	J	6010	31/31	0.95	0.19	-0.27	47,58,64,67	0
2	MN	A	1003	1/1	0.99	0.22	-0.33	57,57,57,57	0
4	ANP	B	6002	31/31	0.95	0.20	-0.34	42,50,60,65	0
3	MSL	C	5009	11/11	0.99	0.17	-0.36	53,56,64,65	0
4	ANP	H	6008	31/31	0.96	0.20	-0.46	40,48,59,67	0
3	MSL	C	5004	11/11	0.99	0.17	-0.55	71,73,75,77	0
2	MN	H	1072	1/1	0.97	0.19	-0.70	57,57,57,57	0
2	MN	G	1062	1/1	0.98	0.21	-0.78	65,65,65,65	0
3	MSL	C	5010	11/11	0.99	0.16	-0.79	38,42,49,49	0
2	MN	C	1023	1/1	0.96	0.21	-0.84	63,63,63,63	0
2	MN	I	1082	1/1	0.98	0.17	-0.97	67,67,67,67	0
2	MN	C	1022	1/1	0.98	0.17	-1.02	66,66,66,66	0
2	MN	A	1002	1/1	0.98	0.17	-1.08	62,62,62,62	0
2	MN	G	1063	1/1	0.95	0.20	-1.08	63,63,63,63	0
2	MN	D	1033	1/1	0.99	0.18	-1.10	56,56,56,56	0
2	MN	E	1043	1/1	0.89	0.17	-1.20	61,61,61,61	0
2	MN	H	1073	1/1	0.99	0.23	-1.42	48,48,48,48	0
2	MN	E	1042	1/1	0.97	0.15	-1.49	65,65,65,65	0
2	MN	F	1053	1/1	0.87	0.14	-1.59	69,69,69,69	0
2	MN	F	1052	1/1	0.97	0.17	-1.60	70,70,70,70	0
2	MN	D	1032	1/1	0.98	0.16	-1.65	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MN	I	1083	1/1	0.97	0.18	-2.04	62,62,62,62	0
2	MN	B	1012	1/1	0.99	0.17	-2.14	60,60,60,60	0
2	MN	J	1092	1/1	0.99	0.12	-2.41	62,62,62,62	0
2	MN	B	1013	1/1	0.99	0.16	-2.53	56,56,56,56	0
2	MN	J	1093	1/1	0.99	0.21	-5.50	57,57,57,57	0
2	MN	I	1081	1/1	0.98	0.22	-	68,68,68,68	0
2	MN	F	1051	1/1	0.96	0.19	-	69,69,69,69	0
2	MN	C	1021	1/1	0.95	0.17	-	66,66,66,66	0
2	MN	J	1091	1/1	0.91	0.24	-	62,62,62,62	0
2	MN	D	1031	1/1	0.99	0.24	-	65,65,65,65	0
2	MN	G	1061	1/1	0.98	0.17	-	66,66,66,66	0
2	MN	B	1011	1/1	0.95	0.19	-	62,62,62,62	0
2	MN	A	1001	1/1	0.97	0.23	-	68,68,68,68	0
2	MN	H	1071	1/1	0.98	0.24	-	57,57,57,57	0
2	MN	E	1041	1/1	0.96	0.23	-	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.