



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:28 AM GMT

PDB ID : 2D3C  
Title : Crystal Structure of the Maize Glutamine Synthetase complexed with ADP and Phosphinothricin Phosphate  
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 : 3.81 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

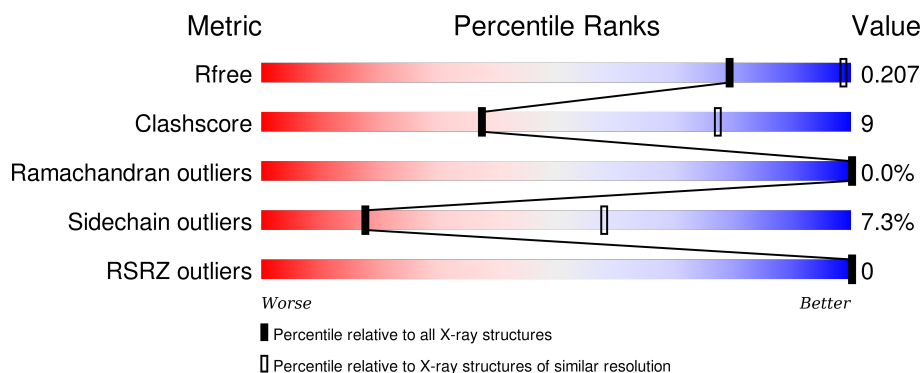
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.81 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))
$R_{free}$	91344	1324 (4.14-3.50)
Clashscore	102246	1028 (4.12-3.52)
Ramachandran outliers	100387	1404 (4.14-3.50)
Sidechain outliers	100360	1399 (4.14-3.50)
RSRZ outliers	91569	1332 (4.14-3.50)

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. 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>79%</div> <div>17%</div> <div>..</div> </div>
1	B	356	<div> <div>76%</div> <div>20%</div> <div>..</div> </div>
1	C	356	<div> <div>78%</div> <div>19%</div> <div>..</div> </div>
1	D	356	<div> <div>77%</div> <div>19%</div> <div>..</div> </div>
1	E	356	<div> <div>78%</div> <div>19%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	356	<div><div></div><div>78%</div><div>19%</div><div></div><div>• •</div></div>
1	G	356	<div><div></div><div>78%</div><div>18%</div><div></div><div>• •</div></div>
1	H	356	<div><div></div><div>79%</div><div>17%</div><div></div><div>• •</div></div>
1	I	356	<div><div></div><div>76%</div><div>19%</div><div></div><div>• •</div></div>
1	J	356	<div><div></div><div>78%</div><div>19%</div><div></div><div>• •</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 28138 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).

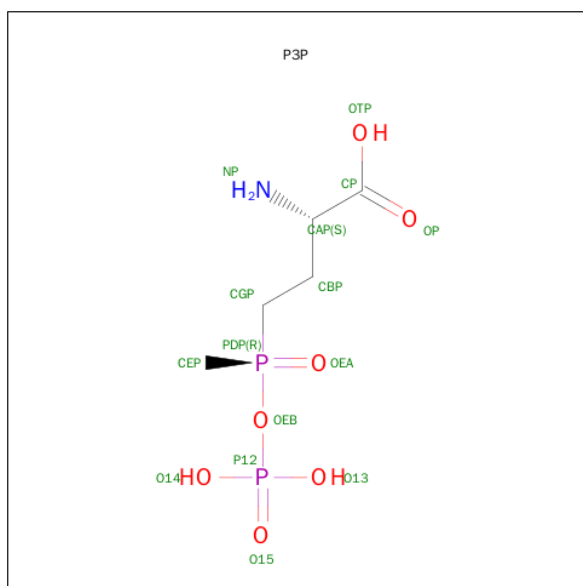
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	3	Total	Mn	0	0
			3	3		
2	J	3	Total	Mn	0	0
			3	3		
2	D	3	Total	Mn	0	0
			3	3		
2	E	3	Total	Mn	0	0
			3	3		

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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-[METHYL(PHOSPHONOOXY)PHOSPHORYL]BUTANOIC ACID (three-letter code: P3P) (formula: C<sub>5</sub>H<sub>13</sub>NO<sub>7</sub>P<sub>2</sub>).



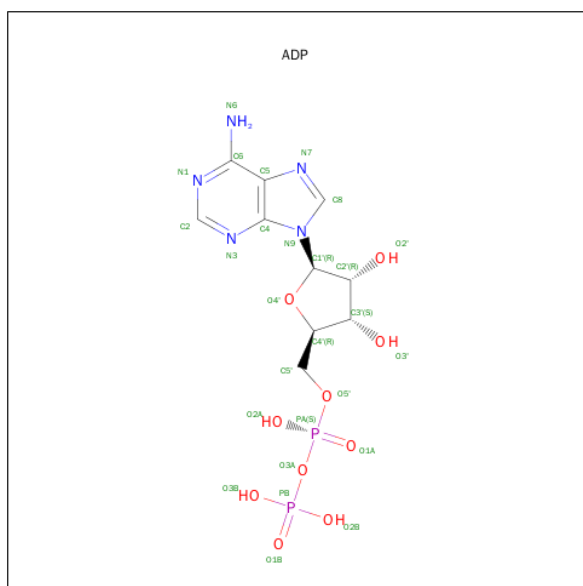
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	B	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	C	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	D	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	E	1	Total	C	N	O	P	0	0
			15	5	1	7	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	F	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	I	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	J	1	Total	C	N	O	P	0	0
			15	5	1	7	2		
3	H	1	Total	C	N	O	P	0	0
			15	5	1	7	2		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

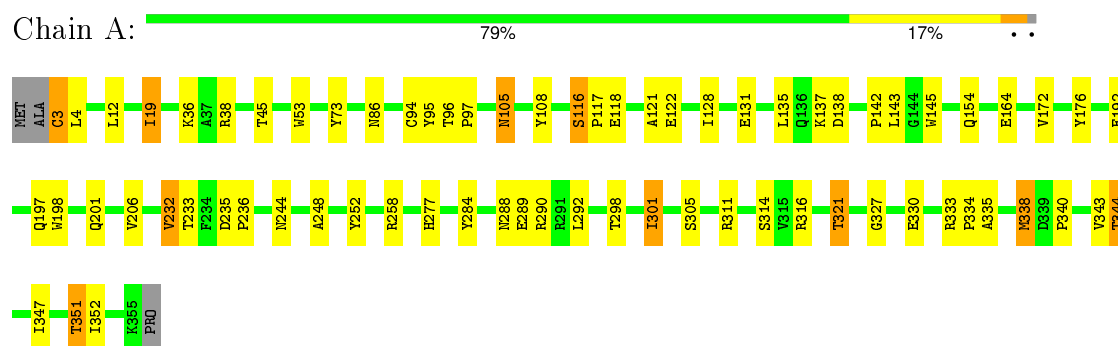
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	25	Total	O	0	0
			25	25		
5	B	26	Total	O	0	0
			26	26		
5	C	11	Total	O	0	0
			11	11		
5	D	30	Total	O	0	0
			30	30		
5	E	30	Total	O	0	0
			30	30		
5	F	31	Total	O	0	0
			31	31		
5	G	22	Total	O	0	0
			22	22		
5	H	21	Total	O	0	0
			21	21		
5	I	27	Total	O	0	0
			27	27		
5	J	15	Total	O	0	0
			15	15		

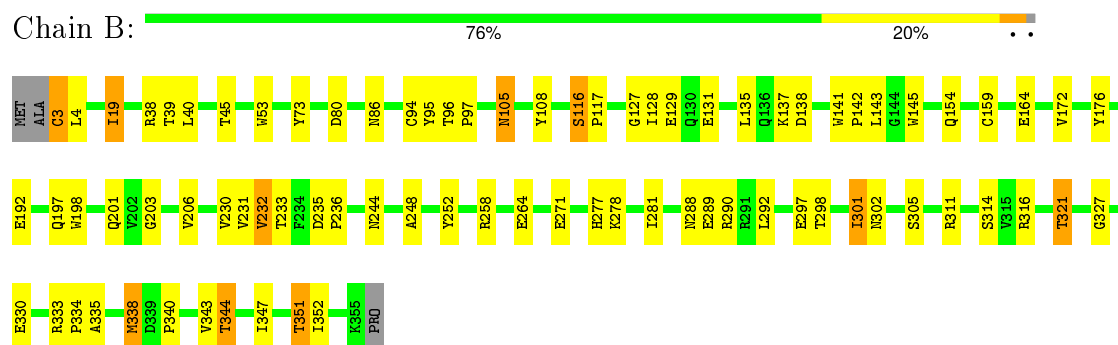
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

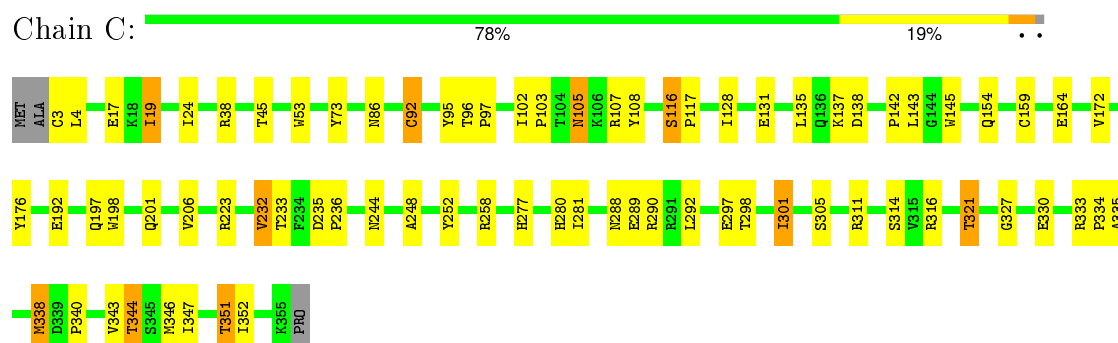
- Molecule 1: glutamine synthetase



- Molecule 1: glutamine synthetase

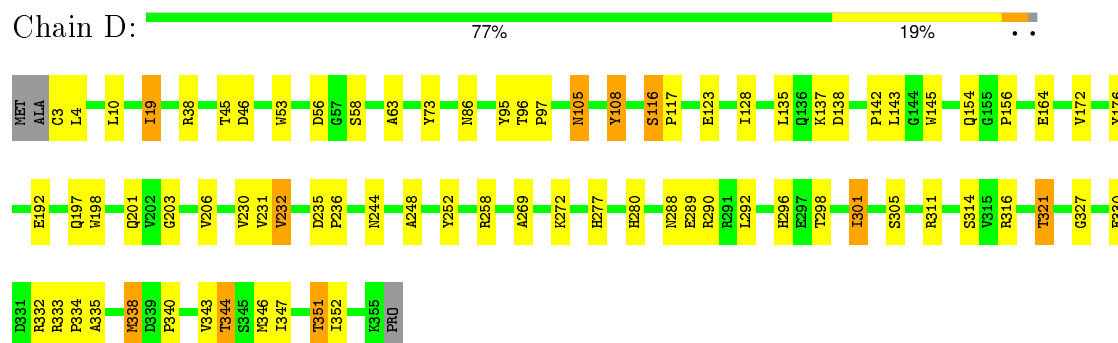


- Molecule 1: glutamine synthetase

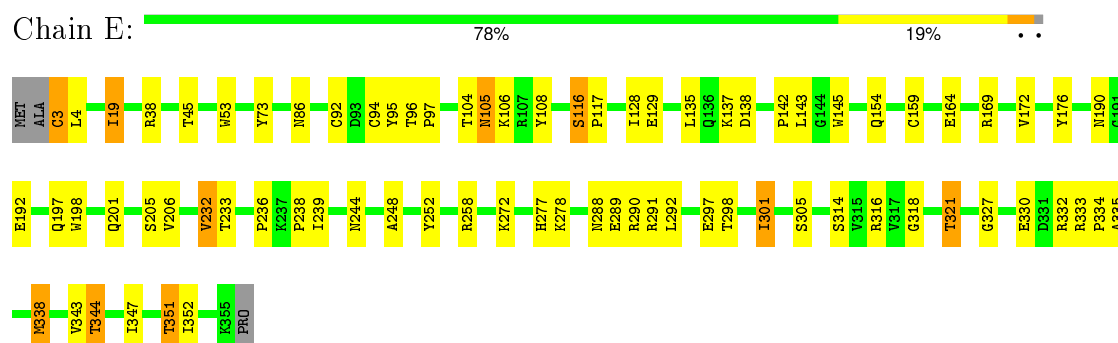


- Molecule 1: glutamine synthetase

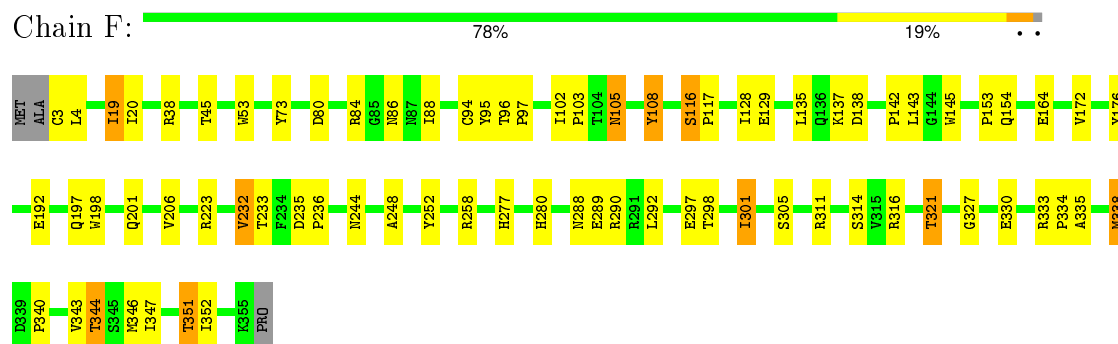




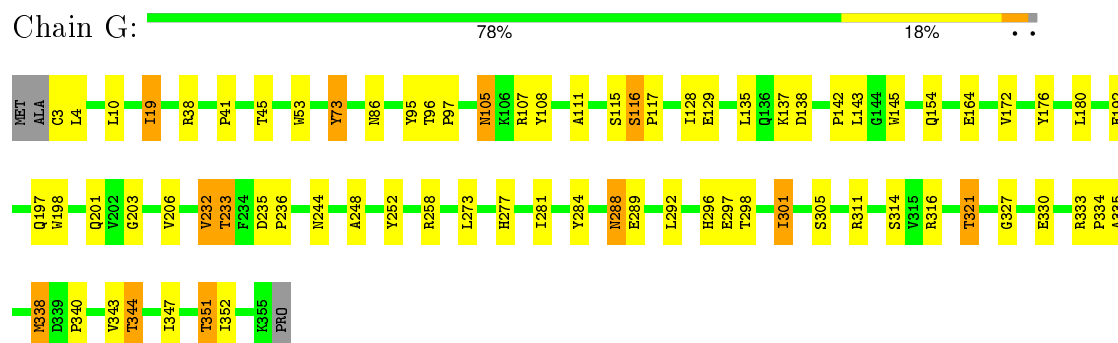
- Molecule 1: glutamine synthetase



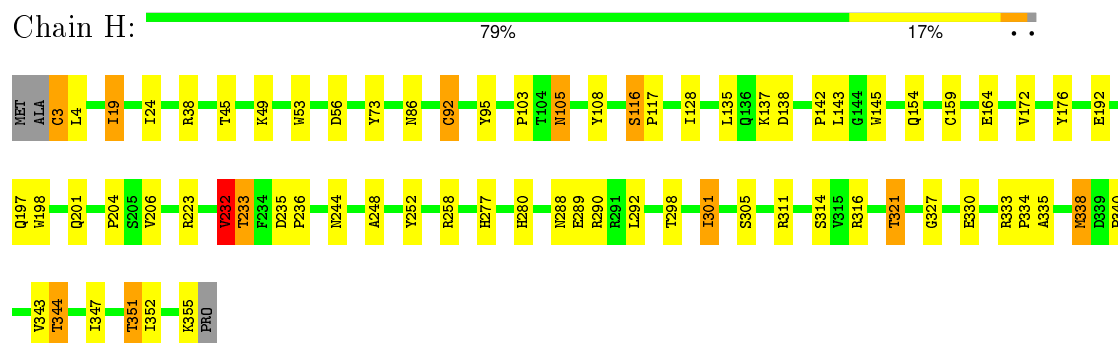
- Molecule 1: glutamine synthetase



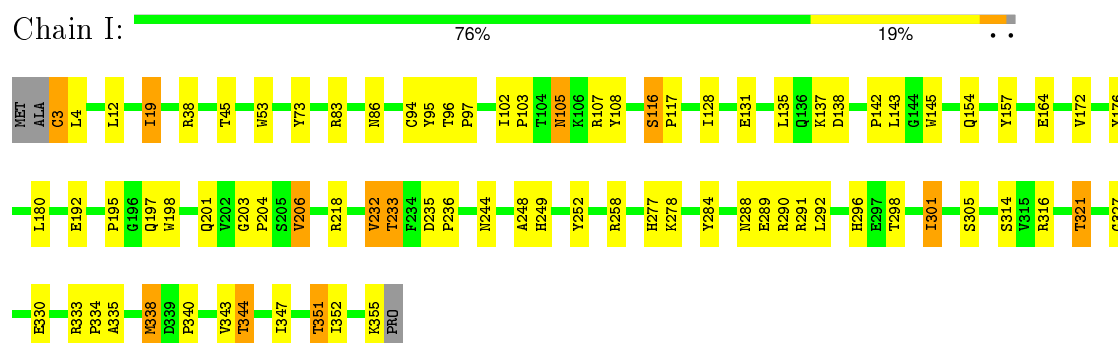
- Molecule 1: glutamine synthetase



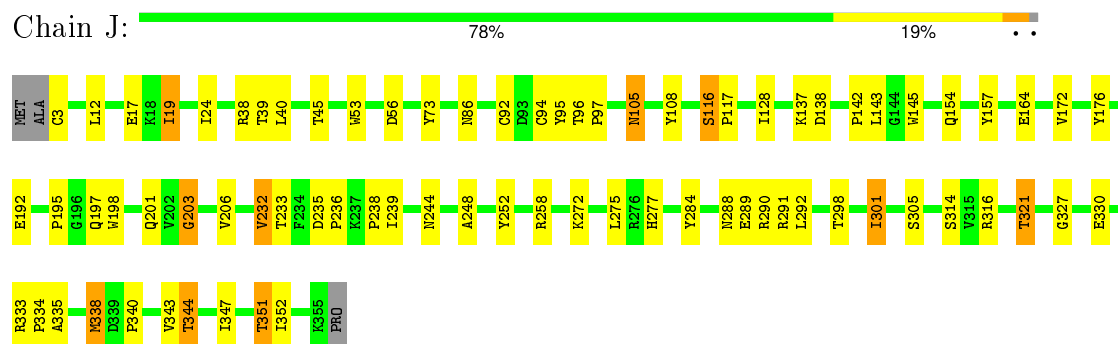
- Molecule 1: glutamine synthetase



- Molecule 1: glutamine synthetase



- Molecule 1: glutamine synthetase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.96Å 191.01Å 118.12Å 90.00° 101.23° 90.00°	Depositor
Resolution (Å)	27.36 – 3.81 27.36 – 3.81	Depositor EDS
% Data completeness (in resolution range)	83.0 (27.36-3.81) 83.1 (27.36-3.81)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.22 (at 3.85Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.185 , 0.229 0.170 , 0.207	Depositor DCC
$R_{free}$ test set	1718 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	86.9	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 56.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 33883 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	28138	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: P3P, MN, ADP

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	0.96	1/2819 (0.0%)	0.81	1/3834 (0.0%)
1	B	0.98	2/2819 (0.1%)	0.82	1/3834 (0.0%)
1	C	0.99	3/2819 (0.1%)	0.81	1/3834 (0.0%)
1	D	0.98	1/2819 (0.0%)	0.84	1/3834 (0.0%)
1	E	0.99	3/2819 (0.1%)	0.84	3/3834 (0.1%)
1	F	1.01	2/2819 (0.1%)	0.83	1/3834 (0.0%)
1	G	0.98	1/2819 (0.0%)	0.83	1/3834 (0.0%)
1	H	0.95	2/2819 (0.1%)	0.81	1/3834 (0.0%)
1	I	0.98	1/2819 (0.0%)	0.81	1/3834 (0.0%)
1	J	0.99	2/2819 (0.1%)	0.83	2/3834 (0.1%)
All	All	0.98	18/28190 (0.1%)	0.82	13/38340 (0.0%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	94	CYS	CB-SG	-9.28	1.66	1.82
1	B	159	CYS	CB-SG	-8.08	1.68	1.82
1	A	94	CYS	CB-SG	-7.07	1.70	1.82
1	C	92	CYS	CB-SG	-6.33	1.71	1.82
1	J	94	CYS	CB-SG	-6.04	1.72	1.82
1	F	94	CYS	CB-SG	-5.57	1.72	1.81
1	J	17	GLU	CG-CD	5.52	1.60	1.51
1	E	94	CYS	CB-SG	-5.39	1.73	1.81
1	C	17	GLU	CG-CD	5.36	1.59	1.51
1	H	159	CYS	CB-SG	-5.30	1.73	1.81
1	C	159	CYS	CB-SG	-5.29	1.73	1.81
1	B	94	CYS	CB-SG	-5.21	1.73	1.81
1	E	159	CYS	CB-SG	-5.20	1.73	1.81
1	H	92	CYS	CB-SG	-5.19	1.73	1.81
1	D	108	TYR	CE2-CZ	5.11	1.45	1.38
1	G	73	TYR	CE2-CZ	5.07	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	92	CYS	CB-SG	-5.02	1.73	1.81
1	F	108	TYR	CE2-CZ	5.01	1.45	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	290	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	D	232	VAL	CB-CA-C	-5.50	100.95	111.40
1	F	232	VAL	CB-CA-C	-5.44	101.06	111.40
1	G	232	VAL	CB-CA-C	-5.39	101.15	111.40
1	E	232	VAL	CB-CA-C	-5.39	101.16	111.40
1	C	232	VAL	CB-CA-C	-5.25	101.43	111.40
1	B	232	VAL	CB-CA-C	-5.17	101.58	111.40
1	J	291	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	J	232	VAL	CB-CA-C	-5.09	101.72	111.40
1	A	232	VAL	CB-CA-C	-5.09	101.74	111.40
1	E	291	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	H	232	VAL	CB-CA-C	-5.03	101.85	111.40
1	I	232	VAL	CB-CA-C	-5.02	101.87	111.40

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	47	0
1	B	2745	0	2653	51	1
1	C	2745	0	2653	46	0
1	D	2745	0	2653	55	0
1	E	2745	0	2653	48	0
1	F	2745	0	2653	52	0
1	G	2745	0	2653	53	0
1	H	2745	0	2653	47	1
1	I	2745	0	2653	56	0
1	J	2745	0	2653	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	A	15	0	10	5	0
3	B	15	0	10	3	0
3	C	15	0	10	4	0
3	D	15	0	10	3	0
3	E	15	0	10	4	0
3	F	15	0	10	4	0
3	G	15	0	10	2	0
3	H	15	0	10	2	0
3	I	15	0	10	4	0
3	J	15	0	10	0	0
4	A	27	0	12	0	0
4	B	27	0	12	2	0
4	C	27	0	12	0	0
4	D	27	0	12	1	0
4	E	27	0	12	0	0
4	F	27	0	12	2	0
4	G	27	0	12	3	0
4	H	27	0	12	0	0
4	I	27	0	12	2	0
4	J	27	0	12	1	0
5	A	25	0	0	7	0
5	B	26	0	0	5	0
5	C	11	0	0	1	0
5	D	30	0	0	11	0
5	E	30	0	0	10	0
5	F	31	0	0	8	0
5	G	22	0	0	7	0
5	H	21	0	0	7	0
5	I	27	0	0	8	0
5	J	15	0	0	3	0
All	All	28138	0	26750	507	1

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 9.

All (507) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:LYS:HA	5:B:6021:HOH:O	1.22	1.29
1:B:344:THR:HG21	5:B:6024:HOH:O	1.44	1.18
1:B:271:GLU:OE1	5:B:6016:HOH:O	1.63	1.14
1:D:123:GLU:HA	5:D:6013:HOH:O	1.54	1.05
1:J:117:PRO:HD2	5:J:6022:HOH:O	1.57	1.03
1:F:154:GLN:HE22	1:F:244:ASN:H	1.08	0.99
1:B:154:GLN:HE22	1:B:244:ASN:H	1.10	0.98
1:E:104:THR:HA	5:E:6025:HOH:O	1.60	0.98
1:A:154:GLN:HE22	1:A:244:ASN:H	1.08	0.97
1:I:154:GLN:HE22	1:I:244:ASN:H	1.09	0.96
1:E:154:GLN:HE22	1:E:244:ASN:H	1.07	0.96
1:H:154:GLN:HE22	1:H:244:ASN:H	1.14	0.95
1:J:154:GLN:HE22	1:J:244:ASN:H	1.14	0.93
1:C:154:GLN:HE22	1:C:244:ASN:H	1.08	0.93
3:A:5001:P3P:O13	3:A:5001:P3P:CEP	2.15	0.92
1:F:223:ARG:NH2	5:F:6030:HOH:O	2.02	0.90
1:D:154:GLN:HE22	1:D:244:ASN:H	1.11	0.90
1:G:154:GLN:HE22	1:G:244:ASN:H	1.10	0.89
1:E:297:GLU:OE2	3:E:5005:P3P:HEP3	1.75	0.87
1:E:106:LYS:HE2	5:E:6025:HOH:O	1.73	0.87
1:E:344:THR:HG21	5:E:6013:HOH:O	1.73	0.86
3:A:5001:P3P:O13	3:A:5001:P3P:HEP2	1.75	0.85
1:G:311:ARG:NH1	3:G:5006:P3P:O14	2.10	0.84
1:D:269:ALA:HA	5:D:6034:HOH:O	1.77	0.83
1:I:83:ARG:HG2	5:I:6030:HOH:O	1.77	0.83
1:E:205:SER:HA	5:E:6020:HOH:O	1.85	0.76
1:C:277:HIS:HE1	1:C:301:ILE:O	1.69	0.75
1:E:278:LYS:HE3	5:E:6030:HOH:O	1.86	0.75
1:G:277:HIS:HE1	1:G:301:ILE:O	1.69	0.75
1:F:277:HIS:HE1	1:F:301:ILE:O	1.70	0.75
1:D:311:ARG:HD3	3:D:5004:P3P:OEA	1.86	0.74
1:J:277:HIS:HE1	1:J:301:ILE:O	1.71	0.74
1:I:277:HIS:HE1	1:I:301:ILE:O	1.72	0.72
1:C:105:ASN:HD22	1:C:105:ASN:C	1.93	0.72
1:A:277:HIS:HE1	1:A:301:ILE:O	1.72	0.72
1:B:277:HIS:HE1	1:B:301:ILE:O	1.72	0.72
1:B:105:ASN:HD22	1:B:105:ASN:C	1.93	0.72
1:D:277:HIS:HE1	1:D:301:ILE:O	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:277:HIS:HE1	1:E:301:ILE:O	1.72	0.71
1:J:105:ASN:HD22	1:J:105:ASN:C	1.94	0.71
1:E:105:ASN:C	1:E:105:ASN:HD22	1.94	0.71
1:F:154:GLN:NE2	1:F:244:ASN:H	1.88	0.71
1:H:277:HIS:HE1	1:H:301:ILE:O	1.74	0.70
1:H:105:ASN:HD22	1:H:105:ASN:C	1.95	0.70
1:I:154:GLN:NE2	1:I:244:ASN:H	1.87	0.70
1:H:49:LYS:HE2	5:H:6025:HOH:O	1.92	0.70
1:A:105:ASN:HD22	1:A:105:ASN:C	1.95	0.70
1:F:20:ILE:O	5:F:6026:HOH:O	2.09	0.69
1:F:105:ASN:HD22	1:F:105:ASN:C	1.95	0.69
1:B:154:GLN:NE2	1:B:244:ASN:H	1.88	0.69
1:B:338:MET:HG3	1:B:343:VAL:HG21	1.74	0.69
1:D:123:GLU:CG	5:D:6013:HOH:O	2.40	0.69
1:A:347:ILE:O	1:A:351:THR:HB	1.93	0.68
1:E:154:GLN:NE2	1:E:244:ASN:H	1.87	0.68
1:F:347:ILE:O	1:F:351:THR:HB	1.94	0.68
1:I:105:ASN:HD22	1:I:105:ASN:C	1.96	0.67
1:B:347:ILE:O	1:B:351:THR:HB	1.95	0.67
1:H:49:LYS:CE	5:H:6025:HOH:O	2.41	0.67
1:A:122:GLU:HA	5:A:6017:HOH:O	1.95	0.67
1:D:296:HIS:HD2	5:D:6023:HOH:O	1.78	0.66
1:G:105:ASN:HD22	1:G:105:ASN:C	1.99	0.66
1:D:347:ILE:O	1:D:351:THR:HB	1.96	0.66
1:A:118:GLU:HB2	5:A:6008:HOH:O	1.95	0.66
1:H:232:VAL:HG23	5:H:6023:HOH:O	1.95	0.66
1:D:105:ASN:HD22	1:D:105:ASN:C	1.99	0.66
1:A:154:GLN:NE2	1:A:244:ASN:H	1.89	0.65
1:F:321:THR:CG2	5:F:6033:HOH:O	2.44	0.65
1:F:321:THR:HG23	5:F:6033:HOH:O	1.96	0.65
1:C:297:GLU:OE2	3:C:5003:P3P:HEP3	1.96	0.65
1:F:129:GLU:OE2	4:F:6007:ADP:O2A	2.14	0.65
1:F:129:GLU:HB3	5:F:6014:HOH:O	1.95	0.65
1:I:347:ILE:O	1:I:351:THR:HB	1.97	0.65
1:C:154:GLN:NE2	1:C:244:ASN:H	1.88	0.64
1:F:338:MET:HG3	1:F:343:VAL:HG21	1.79	0.64
1:G:347:ILE:O	1:G:351:THR:HB	1.98	0.64
1:D:332:ARG:HB2	5:D:6016:HOH:O	1.97	0.64
1:J:338:MET:HG3	1:J:343:VAL:HG21	1.79	0.64
1:D:321:THR:HB	1:D:327:GLY:HA3	1.78	0.64
1:C:347:ILE:O	1:C:351:THR:HB	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:338:MET:HG3	1:D:343:VAL:HG21	1.79	0.64
1:F:277:HIS:CD2	1:F:333:ARG:HH11	2.16	0.64
1:H:321:THR:HB	1:H:327:GLY:HA3	1.79	0.63
1:H:347:ILE:O	1:H:351:THR:HB	1.98	0.63
1:E:338:MET:HG3	1:E:343:VAL:HG21	1.80	0.63
1:G:154:GLN:NE2	1:G:244:ASN:H	1.90	0.63
1:E:169:ARG:HB3	5:E:6028:HOH:O	1.97	0.63
1:I:206:VAL:HG13	5:I:6017:HOH:O	1.98	0.63
3:F:5007:P3P:O13	3:F:5007:P3P:HEP1	1.98	0.63
1:D:154:GLN:NE2	1:D:244:ASN:H	1.91	0.63
1:C:338:MET:HG3	1:C:343:VAL:HG21	1.80	0.63
1:F:297:GLU:OE2	3:F:5007:P3P:HEP3	2.00	0.62
1:C:321:THR:HB	1:C:327:GLY:HA3	1.82	0.62
1:F:153:PRO:HA	5:F:6011:HOH:O	1.98	0.62
1:B:311:ARG:HD3	3:B:5002:P3P:OEA	2.00	0.62
1:G:321:THR:HB	1:G:327:GLY:HA3	1.82	0.62
1:D:311:ARG:NH1	3:D:5004:P3P:O14	2.32	0.61
1:E:347:ILE:O	1:E:351:THR:HB	2.00	0.61
1:J:347:ILE:O	1:J:351:THR:HB	1.99	0.61
1:G:111:ALA:HB3	5:G:6025:HOH:O	1.99	0.61
1:I:338:MET:HG3	1:I:343:VAL:HG21	1.82	0.61
1:A:338:MET:HG3	1:A:343:VAL:HG21	1.83	0.61
1:F:321:THR:HB	1:F:327:GLY:HA3	1.83	0.61
1:G:338:MET:HG3	1:G:343:VAL:HG21	1.83	0.61
1:H:223:ARG:NH2	5:H:6011:HOH:O	2.29	0.61
1:I:321:THR:HB	1:I:327:GLY:HA3	1.82	0.60
1:H:277:HIS:CD2	1:H:333:ARG:HH11	2.20	0.60
1:J:321:THR:HB	1:J:327:GLY:HA3	1.83	0.60
1:I:203:GLY:HA2	4:I:6008:ADP:O3'	2.02	0.60
1:H:338:MET:HG3	1:H:343:VAL:HG21	1.84	0.60
1:C:277:HIS:CD2	1:C:333:ARG:HH11	2.19	0.60
1:A:321:THR:HB	1:A:327:GLY:HA3	1.84	0.60
1:E:321:THR:HB	1:E:327:GLY:HA3	1.83	0.60
1:B:321:THR:HB	1:B:327:GLY:HA3	1.83	0.59
1:B:192:GLU:HB3	1:B:197:GLN:HE21	1.66	0.59
1:C:311:ARG:HD3	3:C:5003:P3P:OEA	2.02	0.59
1:E:351:THR:HG22	1:E:352:ILE:HG13	1.84	0.59
1:I:277:HIS:CD2	1:I:333:ARG:HH11	2.21	0.59
1:A:131:GLU:OE1	3:A:5001:P3P:HBP2	2.03	0.59
1:J:277:HIS:CD2	1:J:333:ARG:HH11	2.19	0.59
1:E:192:GLU:HB3	1:E:197:GLN:HE21	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:154:GLN:NE2	1:H:244:ASN:H	1.92	0.59
1:A:311:ARG:NH1	3:A:5001:P3P:O14	2.36	0.59
1:I:278:LYS:HB2	5:I:6018:HOH:O	2.02	0.58
1:D:192:GLU:HB3	1:D:197:GLN:HE21	1.69	0.58
1:B:277:HIS:CD2	1:B:333:ARG:HH11	2.20	0.58
1:G:277:HIS:CD2	1:G:333:ARG:HH11	2.20	0.58
1:D:156:PRO:HB3	5:D:6018:HOH:O	2.03	0.58
1:I:192:GLU:HB3	1:I:197:GLN:HE21	1.68	0.58
1:G:192:GLU:HB3	1:G:197:GLN:HE21	1.69	0.58
1:I:296:HIS:HD2	5:I:6034:HOH:O	1.85	0.58
1:D:351:THR:HG22	1:D:352:ILE:HG13	1.86	0.58
1:I:351:THR:HG22	1:I:352:ILE:HG13	1.86	0.58
1:E:137:LYS:O	1:E:138:ASP:HB2	2.04	0.57
1:E:277:HIS:CD2	1:E:333:ARG:HH11	2.21	0.57
1:C:192:GLU:HB3	1:C:197:GLN:HE21	1.70	0.57
1:C:351:THR:HG22	1:C:352:ILE:HG13	1.86	0.57
1:A:277:HIS:CD2	1:A:333:ARG:HH11	2.23	0.57
5:D:6030:HOH:O	1:E:190:ASN:HA	2.04	0.56
1:G:41:PRO:HB3	5:G:6027:HOH:O	2.06	0.56
1:E:318:GLY:HA3	5:E:6007:HOH:O	2.04	0.56
1:D:277:HIS:CD2	1:D:333:ARG:HH11	2.24	0.56
1:G:351:THR:HG22	1:G:352:ILE:HG13	1.88	0.56
1:A:192:GLU:HB3	1:A:197:GLN:HE21	1.71	0.56
1:A:351:THR:HG22	1:A:352:ILE:HG13	1.88	0.55
1:J:192:GLU:HB3	1:J:197:GLN:HE21	1.71	0.55
3:I:5008:P3P:O14	4:I:6008:ADP:O3B	2.24	0.55
1:H:311:ARG:HD3	3:H:5010:P3P:OEA	2.05	0.55
1:J:154:GLN:NE2	1:J:244:ASN:H	1.94	0.55
1:F:351:THR:HG22	1:F:352:ILE:HG13	1.89	0.55
1:A:121:ALA:O	5:A:6017:HOH:O	2.17	0.55
1:G:296:HIS:HB2	5:G:6012:HOH:O	2.07	0.55
1:B:297:GLU:OE2	3:B:5002:P3P:HEP3	2.07	0.55
1:A:121:ALA:C	5:A:6017:HOH:O	2.44	0.55
1:H:351:THR:HG22	1:H:352:ILE:HG13	1.89	0.54
1:D:316:ARG:NH1	1:D:330:GLU:OE1	2.38	0.54
1:A:316:ARG:NH1	1:A:330:GLU:OE1	2.38	0.54
1:B:351:THR:HG22	1:B:352:ILE:HG13	1.88	0.54
1:D:123:GLU:HG2	5:D:6013:HOH:O	2.05	0.54
4:G:6006:ADP:O2A	4:G:6006:ADP:O3B	2.25	0.54
1:D:252:TYR:HE1	1:D:351:THR:HG21	1.73	0.54
1:I:131:GLU:OE1	3:I:5008:P3P:HGP1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:GLU:HB3	5:B:6027:HOH:O	2.06	0.54
1:G:73:TYR:CD2	1:G:95:TYR:CE1	2.96	0.54
1:F:129:GLU:CD	4:F:6007:ADP:O2A	2.47	0.53
1:J:137:LYS:O	1:J:138:ASP:HB2	2.08	0.53
1:H:192:GLU:HB3	1:H:197:GLN:HE21	1.72	0.53
1:F:137:LYS:O	1:F:138:ASP:HB2	2.07	0.53
1:D:203:GLY:HA2	4:D:6005:ADP:O3'	2.09	0.53
1:C:333:ARG:N	1:C:334:PRO:CD	2.71	0.53
1:I:252:TYR:HE1	1:I:351:THR:HG21	1.74	0.53
1:F:192:GLU:HB3	1:F:197:GLN:HE21	1.73	0.53
1:I:218:ARG:HB3	5:I:6009:HOH:O	2.08	0.53
1:J:351:THR:HG22	1:J:352:ILE:HG13	1.91	0.52
1:D:56:ASP:OD2	3:E:5005:P3P:HEP1	2.09	0.52
1:E:272:LYS:HE3	5:E:6026:HOH:O	2.10	0.52
1:E:73:TYR:CD2	1:E:95:TYR:CE1	2.98	0.52
1:J:340:PRO:O	1:J:344:THR:HB	2.09	0.52
1:D:252:TYR:CE1	1:D:351:THR:HG21	2.44	0.52
1:F:73:TYR:CD2	1:F:95:TYR:CE1	2.98	0.52
1:H:172:VAL:HG21	1:H:198:TRP:CD2	2.45	0.52
1:B:172:VAL:HG21	1:B:198:TRP:CD2	2.45	0.52
1:A:73:TYR:CD2	1:A:95:TYR:CE1	2.98	0.52
1:F:340:PRO:O	1:F:344:THR:HB	2.10	0.52
1:B:131:GLU:OE1	3:B:5002:P3P:HBP2	2.10	0.51
1:D:192:GLU:OE1	3:D:5004:P3P:HEP2	2.10	0.51
1:A:252:TYR:CE1	1:A:351:THR:HG21	2.45	0.51
1:A:252:TYR:HE1	1:A:351:THR:HG21	1.75	0.51
1:J:252:TYR:HE1	1:J:351:THR:HG21	1.75	0.51
1:I:137:LYS:O	1:I:138:ASP:HB2	2.10	0.51
3:F:5007:P3P:O13	3:F:5007:P3P:CEP	2.58	0.51
1:I:19:ILE:HD11	1:I:86:ASN:HB2	1.93	0.51
1:J:275:LEU:HD21	5:J:6014:HOH:O	2.10	0.51
1:D:272:LYS:HE3	5:D:6034:HOH:O	2.10	0.51
1:A:352:ILE:HA	5:A:6007:HOH:O	2.10	0.51
1:E:292:LEU:HD23	1:E:298:THR:HB	1.93	0.51
1:I:316:ARG:NH1	1:I:330:GLU:OE1	2.42	0.51
1:D:137:LYS:O	1:D:138:ASP:HB2	2.11	0.51
1:I:252:TYR:CE1	1:I:351:THR:HG21	2.46	0.51
1:C:73:TYR:CD2	1:C:95:TYR:CE1	2.98	0.51
1:G:203:GLY:HA2	4:G:6006:ADP:O3'	2.10	0.51
1:D:73:TYR:CD2	1:D:95:TYR:CE1	2.99	0.51
1:F:252:TYR:HE1	1:F:351:THR:HG21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:248:ALA:HB1	1:F:338:MET:HE3	1.92	0.51
1:C:137:LYS:O	1:C:138:ASP:HB2	2.10	0.51
1:F:316:ARG:NH1	1:F:330:GLU:OE1	2.39	0.51
1:D:172:VAL:HG21	1:D:198:TRP:CD2	2.46	0.51
1:E:38:ARG:HB3	1:E:53:TRP:CH2	2.46	0.50
1:H:137:LYS:O	1:H:138:ASP:HB2	2.09	0.50
1:F:172:VAL:HG21	1:F:198:TRP:CD2	2.47	0.50
1:G:137:LYS:O	1:G:138:ASP:HB2	2.11	0.50
1:I:73:TYR:CD2	1:I:95:TYR:CE1	2.99	0.50
1:C:105:ASN:HD21	1:C:108:TYR:H	1.60	0.50
1:E:142:PRO:HB2	1:E:145:TRP:CD1	2.46	0.50
1:D:46:ASP:HB2	5:D:6009:HOH:O	2.11	0.50
1:C:248:ALA:HB1	1:C:338:MET:HE3	1.92	0.50
1:J:252:TYR:CE1	1:J:351:THR:HG21	2.47	0.50
1:D:19:ILE:HD11	1:D:86:ASN:HB2	1.93	0.50
3:A:5001:P3P:HEP1	3:A:5001:P3P:O13	2.07	0.50
1:I:248:ALA:HB1	1:I:338:MET:HE3	1.94	0.50
1:D:333:ARG:N	1:D:334:PRO:CD	2.75	0.50
1:A:292:LEU:HD23	1:A:298:THR:HB	1.94	0.50
1:A:137:LYS:O	1:A:138:ASP:HB2	2.12	0.50
1:G:292:LEU:HD23	1:G:298:THR:HB	1.94	0.49
1:B:292:LEU:HD23	1:B:298:THR:HB	1.94	0.49
1:H:73:TYR:CD2	1:H:95:TYR:CE1	3.00	0.49
1:E:172:VAL:HG21	1:E:198:TRP:CD2	2.46	0.49
1:A:172:VAL:HG21	1:A:198:TRP:CD2	2.46	0.49
1:H:192:GLU:OE1	3:H:5010:P3P:HEP2	2.12	0.49
1:I:305:SER:H	1:I:314:SER:HB2	1.77	0.49
1:J:272:LYS:HE3	5:J:6023:HOH:O	2.12	0.49
1:C:105:ASN:C	1:C:105:ASN:ND2	2.64	0.49
1:C:105:ASN:ND2	1:C:108:TYR:H	2.09	0.49
1:C:223:ARG:NH1	5:C:6007:HOH:O	2.44	0.49
1:G:172:VAL:HG21	1:G:198:TRP:CD2	2.48	0.49
1:D:38:ARG:HB3	1:D:53:TRP:CH2	2.47	0.49
1:E:252:TYR:HE1	1:E:351:THR:HG21	1.77	0.49
1:G:129:GLU:HB3	5:G:6018:HOH:O	2.13	0.49
1:F:252:TYR:CE1	1:F:351:THR:HG21	2.48	0.49
1:C:192:GLU:OE1	3:C:5003:P3P:HEP2	2.11	0.49
1:A:340:PRO:O	1:A:344:THR:HB	2.13	0.49
1:F:292:LEU:HD23	1:F:298:THR:HB	1.94	0.49
1:B:105:ASN:ND2	1:B:105:ASN:C	2.65	0.49
1:B:252:TYR:CE1	1:B:351:THR:HG21	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:236:PRO:HB3	1:F:335:ALA:HB1	1.94	0.49
1:B:301:ILE:H	1:B:301:ILE:HG13	1.39	0.49
1:H:248:ALA:HB1	1:H:338:MET:HE3	1.94	0.49
1:F:129:GLU:CB	5:F:6014:HOH:O	2.59	0.48
1:G:273:LEU:O	5:G:6009:HOH:O	2.19	0.48
1:A:142:PRO:HB2	1:A:145:TRP:CD1	2.48	0.48
1:A:333:ARG:N	1:A:334:PRO:CD	2.76	0.48
1:B:252:TYR:HE1	1:B:351:THR:HG21	1.77	0.48
1:F:301:ILE:HG13	1:F:301:ILE:H	1.47	0.48
1:J:305:SER:H	1:J:314:SER:HB2	1.79	0.48
1:C:292:LEU:HD23	1:C:298:THR:HB	1.95	0.48
1:C:333:ARG:N	1:C:334:PRO:HD3	2.29	0.48
1:D:105:ASN:ND2	1:D:108:TYR:H	2.10	0.48
1:I:296:HIS:CD2	5:I:6034:HOH:O	2.63	0.48
1:I:142:PRO:HB2	1:I:145:TRP:CD1	2.48	0.48
1:G:248:ALA:HB1	1:G:338:MET:HE3	1.96	0.48
1:D:248:ALA:HB1	1:D:338:MET:HE3	1.96	0.48
1:A:248:ALA:HB1	1:A:338:MET:HE3	1.94	0.48
1:I:172:VAL:HG21	1:I:198:TRP:CD2	2.48	0.48
1:H:316:ARG:NH1	1:H:330:GLU:OE1	2.44	0.48
1:E:105:ASN:ND2	1:E:105:ASN:C	2.66	0.48
1:E:252:TYR:CE1	1:E:351:THR:HG21	2.48	0.48
1:J:203:GLY:HA2	4:J:6009:ADP:O3'	2.13	0.48
1:F:333:ARG:N	1:F:334:PRO:CD	2.76	0.48
1:G:340:PRO:O	1:G:344:THR:HB	2.13	0.48
1:C:172:VAL:HG21	1:C:198:TRP:CD2	2.49	0.48
1:J:73:TYR:CD2	1:J:95:TYR:CE1	3.02	0.48
1:H:49:LYS:HE3	5:H:6025:HOH:O	2.10	0.47
1:C:236:PRO:HB3	1:C:335:ALA:HB1	1.95	0.47
1:I:340:PRO:O	1:I:344:THR:HB	2.14	0.47
1:B:19:ILE:HD11	1:B:86:ASN:HB2	1.96	0.47
1:D:105:ASN:HD21	1:D:108:TYR:H	1.60	0.47
1:C:135:LEU:HD23	1:C:142:PRO:HA	1.96	0.47
1:E:129:GLU:HB2	5:E:6022:HOH:O	2.14	0.47
1:I:333:ARG:N	1:I:334:PRO:CD	2.77	0.47
1:C:252:TYR:HE1	1:C:351:THR:HG21	1.79	0.47
1:H:252:TYR:HE1	1:H:351:THR:HG21	1.79	0.47
1:I:236:PRO:HB3	1:I:335:ALA:HB1	1.94	0.47
1:J:142:PRO:HB2	1:J:145:TRP:CD1	2.50	0.47
1:I:301:ILE:H	1:I:301:ILE:HG13	1.40	0.47
1:E:333:ARG:N	1:E:334:PRO:CD	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:292:LEU:HD23	1:I:298:THR:HB	1.96	0.47
1:J:105:ASN:ND2	1:J:105:ASN:C	2.65	0.47
1:F:105:ASN:ND2	1:F:105:ASN:C	2.66	0.47
1:G:252:TYR:HE1	1:G:351:THR:HG21	1.78	0.47
1:G:252:TYR:CE1	1:G:351:THR:HG21	2.49	0.47
1:H:142:PRO:HB2	1:H:145:TRP:CD1	2.49	0.47
1:C:305:SER:H	1:C:314:SER:HB2	1.79	0.47
1:B:105:ASN:ND2	1:B:108:TYR:H	2.12	0.47
1:D:135:LEU:HD23	1:D:142:PRO:HA	1.97	0.47
1:J:172:VAL:HG21	1:J:198:TRP:CD2	2.49	0.47
1:B:271:GLU:CD	5:B:6016:HOH:O	2.36	0.47
1:F:88:ILE:N	5:F:6026:HOH:O	2.48	0.47
1:C:252:TYR:CE1	1:C:351:THR:HG21	2.50	0.47
1:E:248:ALA:HB1	1:E:338:MET:HE3	1.96	0.47
1:G:333:ARG:N	1:G:334:PRO:CD	2.78	0.46
1:B:38:ARG:HB3	1:B:53:TRP:CH2	2.50	0.46
1:H:340:PRO:O	1:H:344:THR:HB	2.15	0.46
1:F:142:PRO:HB2	1:F:145:TRP:CD1	2.51	0.46
1:C:340:PRO:O	1:C:344:THR:HB	2.15	0.46
1:H:38:ARG:HB3	1:H:53:TRP:CH2	2.49	0.46
1:D:292:LEU:HD23	1:D:298:THR:HB	1.96	0.46
1:J:301:ILE:H	1:J:301:ILE:HG13	1.43	0.46
1:G:316:ARG:NH1	1:G:330:GLU:OE1	2.43	0.46
1:A:105:ASN:ND2	1:A:105:ASN:C	2.67	0.46
1:H:252:TYR:CE1	1:H:351:THR:HG21	2.50	0.46
1:A:36:LYS:NZ	5:A:6003:HOH:O	2.48	0.46
3:E:5005:P3P:OEA	3:E:5005:P3P:O14	2.34	0.46
1:B:105:ASN:HD21	1:B:108:TYR:H	1.62	0.46
1:H:333:ARG:N	1:H:334:PRO:CD	2.78	0.46
1:G:105:ASN:ND2	1:G:108:TYR:H	2.12	0.46
1:A:19:ILE:HD11	1:A:86:ASN:HB2	1.98	0.46
1:I:96:THR:HB	1:I:97:PRO:CD	2.45	0.46
1:D:236:PRO:HB3	1:D:335:ALA:HB1	1.97	0.46
1:H:305:SER:H	1:H:314:SER:HB2	1.81	0.46
1:J:38:ARG:HB3	1:J:53:TRP:CH2	2.51	0.46
1:I:291:ARG:NH1	3:I:5008:P3P:OP	2.49	0.46
1:C:316:ARG:NH1	1:C:330:GLU:OE1	2.45	0.46
1:H:4:LEU:HD12	1:H:4:LEU:HA	1.84	0.46
1:G:277:HIS:HD2	1:G:333:ARG:HH11	1.62	0.46
1:B:316:ARG:NH1	1:B:330:GLU:OE1	2.42	0.46
1:A:38:ARG:HB3	1:A:53:TRP:CH2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:SER:HA	1:B:117:PRO:HD3	1.78	0.46
1:I:105:ASN:ND2	1:I:108:TYR:H	2.13	0.46
1:G:135:LEU:HD23	1:G:142:PRO:HA	1.97	0.46
1:A:236:PRO:HB3	1:A:335:ALA:HB1	1.97	0.46
1:G:236:PRO:HB3	1:G:335:ALA:HB1	1.98	0.46
1:B:73:TYR:CD2	1:B:95:TYR:CE1	3.04	0.46
1:B:236:PRO:HB3	1:B:335:ALA:HB1	1.98	0.46
1:G:38:ARG:HB3	1:G:53:TRP:CH2	2.50	0.46
1:C:38:ARG:HB3	1:C:53:TRP:CH2	2.52	0.46
1:H:135:LEU:HD23	1:H:142:PRO:HA	1.99	0.45
1:B:135:LEU:HD23	1:B:142:PRO:HA	1.98	0.45
1:E:236:PRO:HB3	1:E:335:ALA:HB1	1.97	0.45
1:F:277:HIS:HD2	1:F:333:ARG:HH11	1.62	0.45
1:B:333:ARG:N	1:B:334:PRO:CD	2.80	0.45
1:I:249:HIS:HE1	3:I:5008:P3P:OEB	2.00	0.45
1:H:236:PRO:HB3	1:H:335:ALA:HB1	1.99	0.45
1:I:105:ASN:ND2	1:I:105:ASN:C	2.67	0.45
1:H:280:HIS:CG	5:H:6031:HOH:O	2.69	0.45
1:D:96:THR:HB	1:D:97:PRO:CD	2.47	0.45
1:F:19:ILE:HD11	1:F:86:ASN:HB2	1.99	0.45
1:A:333:ARG:N	1:A:334:PRO:HD3	2.32	0.45
1:E:305:SER:H	1:E:314:SER:HB2	1.81	0.45
1:E:96:THR:HB	1:E:97:PRO:CD	2.47	0.45
1:D:4:LEU:HA	1:D:4:LEU:HD12	1.81	0.45
1:A:135:LEU:HD23	1:A:142:PRO:HA	1.98	0.45
1:I:116:SER:HA	1:I:117:PRO:HD3	1.77	0.45
1:B:142:PRO:HB2	1:B:145:TRP:CD1	2.52	0.44
1:B:235:ASP:OD2	1:B:290:ARG:NH2	2.50	0.44
1:I:38:ARG:HB3	1:I:53:TRP:CH2	2.52	0.44
1:F:305:SER:H	1:F:314:SER:HB2	1.82	0.44
1:B:137:LYS:O	1:B:138:ASP:HB2	2.17	0.44
1:J:248:ALA:HB1	1:J:338:MET:HE3	1.99	0.44
1:D:340:PRO:O	1:D:344:THR:HB	2.17	0.44
1:D:280:HIS:NE2	1:D:346:MET:HG2	2.32	0.44
1:J:292:LEU:HD23	1:J:298:THR:HB	1.99	0.44
1:G:105:ASN:HD21	1:G:108:TYR:H	1.64	0.44
1:G:19:ILE:HD11	1:G:86:ASN:HB2	1.99	0.44
1:A:305:SER:H	1:A:314:SER:HB2	1.82	0.44
1:D:333:ARG:N	1:D:334:PRO:HD3	2.32	0.44
1:A:122:GLU:CA	5:A:6017:HOH:O	2.62	0.44
1:G:142:PRO:HB2	1:G:145:TRP:CD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:LEU:HD12	1:C:4:LEU:HA	1.81	0.44
1:A:96:THR:HB	1:A:97:PRO:CD	2.47	0.44
1:I:204:PRO:HD2	5:I:6029:HOH:O	2.17	0.44
1:J:105:ASN:ND2	1:J:108:TYR:H	2.15	0.44
1:H:105:ASN:ND2	1:H:108:TYR:H	2.16	0.44
1:D:116:SER:HA	1:D:117:PRO:HD3	1.77	0.44
1:D:235:ASP:OD2	1:D:290:ARG:NH2	2.50	0.44
1:F:105:ASN:ND2	1:F:108:TYR:H	2.16	0.44
1:C:24:ILE:O	1:C:92:CYS:HB2	2.18	0.44
1:I:355:LYS:HB2	5:I:6016:HOH:O	2.18	0.44
1:H:116:SER:HA	1:H:117:PRO:HD3	1.71	0.44
1:H:292:LEU:HD23	1:H:298:THR:HB	1.98	0.44
1:B:305:SER:H	1:B:314:SER:HB2	1.82	0.44
1:B:248:ALA:HB1	1:B:338:MET:HE3	1.99	0.44
1:I:135:LEU:HD23	1:I:142:PRO:HA	1.99	0.44
1:E:19:ILE:HD11	1:E:86:ASN:HB2	2.00	0.44
1:F:116:SER:HA	1:F:117:PRO:HD3	1.75	0.44
1:A:235:ASP:OD2	1:A:290:ARG:NH2	2.51	0.44
1:D:301:ILE:H	1:D:301:ILE:HG13	1.43	0.44
1:C:19:ILE:HD11	1:C:86:ASN:HB2	2.00	0.44
1:E:116:SER:HA	1:E:117:PRO:HD3	1.76	0.43
1:I:333:ARG:N	1:I:334:PRO:HD3	2.33	0.43
1:E:135:LEU:HD23	1:E:142:PRO:HA	2.00	0.43
1:F:135:LEU:HD23	1:F:142:PRO:HA	2.00	0.43
1:B:340:PRO:O	1:B:344:THR:HB	2.18	0.43
1:I:105:ASN:HD21	1:I:108:TYR:H	1.65	0.43
1:G:305:SER:H	1:G:314:SER:HB2	1.82	0.43
1:D:305:SER:H	1:D:314:SER:HB2	1.83	0.43
1:J:316:ARG:NH1	1:J:330:GLU:OE1	2.45	0.43
1:G:297:GLU:OE2	3:G:5006:P3P:HEP3	2.18	0.43
1:H:105:ASN:HD21	1:H:108:TYR:H	1.65	0.43
1:J:277:HIS:HD2	1:J:333:ARG:HH11	1.62	0.43
1:J:105:ASN:HD21	1:J:108:TYR:H	1.65	0.43
1:I:235:ASP:OD2	1:I:290:ARG:NH2	2.52	0.43
1:J:12:LEU:HD23	1:J:12:LEU:HA	1.88	0.43
1:C:116:SER:HA	1:C:117:PRO:HD3	1.77	0.43
1:B:127:GLY:HA3	4:B:6002:ADP:H1'	1.99	0.43
1:J:238:PRO:O	1:J:239:ILE:HD13	2.19	0.43
1:J:157:TYR:CD1	1:J:195:PRO:HD3	2.54	0.43
1:J:19:ILE:HD11	1:J:86:ASN:HB2	1.99	0.43
1:G:115:SER:CB	5:G:6015:HOH:O	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:116:SER:HA	1:G:117:PRO:HD3	1.77	0.43
1:D:142:PRO:HB2	1:D:145:TRP:CD1	2.53	0.43
1:E:301:ILE:H	1:E:301:ILE:HG13	1.44	0.43
1:H:105:ASN:C	1:H:105:ASN:ND2	2.66	0.43
1:B:96:THR:HB	1:B:97:PRO:CD	2.48	0.43
1:I:157:TYR:CD1	1:I:195:PRO:HD3	2.54	0.43
1:J:236:PRO:HB3	1:J:335:ALA:HB1	2.00	0.43
1:C:277:HIS:HD2	1:C:333:ARG:HH11	1.63	0.42
1:A:105:ASN:ND2	1:A:108:TYR:H	2.16	0.42
1:I:277:HIS:HD2	1:I:333:ARG:HH11	1.67	0.42
1:H:277:HIS:HD2	1:H:333:ARG:HH11	1.64	0.42
1:D:105:ASN:C	1:D:105:ASN:ND2	2.70	0.42
1:F:311:ARG:NH1	3:F:5007:P3P:O13	2.52	0.42
1:A:4:LEU:HA	1:A:4:LEU:HD12	1.85	0.42
1:J:116:SER:HA	1:J:117:PRO:HD3	1.77	0.42
1:J:333:ARG:N	1:J:334:PRO:CD	2.81	0.42
1:E:277:HIS:HD2	1:E:333:ARG:HH11	1.66	0.42
1:G:284:TYR:CD2	1:G:343:VAL:HG22	2.55	0.42
1:E:105:ASN:ND2	1:E:108:TYR:H	2.16	0.42
1:F:235:ASP:OD2	1:F:290:ARG:NH2	2.53	0.42
1:J:24:ILE:O	1:J:92:CYS:HB2	2.19	0.42
1:A:116:SER:HA	1:A:117:PRO:HD3	1.75	0.42
1:A:3:CYS:HB2	1:A:4:LEU:H	1.75	0.42
1:B:230:VAL:CG1	1:B:231:VAL:N	2.82	0.42
1:D:10:LEU:HD23	1:D:10:LEU:HA	1.90	0.42
1:F:333:ARG:N	1:F:334:PRO:HD3	2.35	0.42
1:C:102:ILE:HB	1:C:103:PRO:CD	2.50	0.42
1:H:19:ILE:HD11	1:H:86:ASN:HB2	2.01	0.42
1:C:142:PRO:HB2	1:C:145:TRP:CD1	2.55	0.42
1:H:233:THR:HB	1:H:235:ASP:H	1.85	0.42
1:H:24:ILE:O	1:H:92:CYS:HB2	2.20	0.42
1:E:333:ARG:N	1:E:334:PRO:HD3	2.35	0.42
1:F:280:HIS:NE2	1:F:346:MET:HG2	2.35	0.42
1:C:281:ILE:HA	1:C:281:ILE:HD13	1.88	0.42
1:F:4:LEU:HA	1:F:4:LEU:HD12	1.83	0.42
1:G:96:THR:HB	1:G:97:PRO:CD	2.49	0.42
1:D:58:SER:HA	1:D:63:ALA:O	2.19	0.42
1:B:281:ILE:HA	1:B:281:ILE:HD13	1.89	0.42
1:H:56:ASP:OD1	1:H:56:ASP:C	2.58	0.42
1:H:301:ILE:H	1:H:301:ILE:HG13	1.42	0.41
1:H:3:CYS:HB2	1:H:4:LEU:H	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:355:LYS:HB2	1:I:355:LYS:HE2	1.91	0.41
1:B:203:GLY:HA2	4:B:6002:ADP:O3'	2.20	0.41
1:F:38:ARG:HB3	1:F:53:TRP:CH2	2.55	0.41
1:J:56:ASP:OD1	1:J:56:ASP:C	2.56	0.41
1:G:10:LEU:HD23	1:G:10:LEU:HA	1.91	0.41
1:F:96:THR:HB	1:F:97:PRO:CD	2.49	0.41
1:D:272:LYS:HG3	5:D:6034:HOH:O	2.19	0.41
1:I:180:LEU:HA	1:I:180:LEU:HD23	1.90	0.41
1:G:129:GLU:OE2	4:G:6006:ADP:O2A	2.39	0.41
1:I:105:ASN:ND2	1:I:107:ARG:H	2.18	0.41
1:I:284:TYR:CD2	1:I:343:VAL:HG22	2.56	0.41
1:J:96:THR:HB	1:J:97:PRO:CD	2.51	0.41
1:G:4:LEU:HD12	1:G:4:LEU:HA	1.82	0.41
1:G:115:SER:HB2	5:G:6015:HOH:O	2.19	0.41
1:B:333:ARG:N	1:B:334:PRO:HD3	2.36	0.41
1:H:235:ASP:OD2	1:H:290:ARG:NH2	2.53	0.41
1:F:102:ILE:HB	1:F:103:PRO:CD	2.51	0.41
1:F:84:ARG:HH11	1:F:84:ARG:HD2	1.74	0.41
1:J:235:ASP:OD2	1:J:290:ARG:NH2	2.54	0.41
1:E:105:ASN:HD21	1:E:108:TYR:H	1.68	0.41
1:A:105:ASN:HD21	1:A:108:TYR:H	1.68	0.41
1:F:105:ASN:HD21	1:F:108:TYR:H	1.68	0.41
1:C:131:GLU:OE1	3:C:5003:P3P:HBP2	2.21	0.41
1:A:284:TYR:CD2	1:A:343:VAL:HG22	2.55	0.41
1:I:233:THR:HB	1:I:235:ASP:H	1.86	0.41
1:A:12:LEU:HD23	1:A:12:LEU:HA	1.91	0.41
1:I:3:CYS:HB2	1:I:4:LEU:H	1.80	0.41
1:G:288:ASN:HA	1:G:288:ASN:HD22	1.68	0.41
1:I:12:LEU:HD23	1:I:12:LEU:HA	1.92	0.41
1:C:235:ASP:OD2	1:C:290:ARG:NH2	2.53	0.41
1:E:3:CYS:HB2	1:E:4:LEU:H	1.80	0.41
1:E:316:ARG:NH1	1:E:330:GLU:OE1	2.44	0.41
1:G:284:TYR:CE2	1:G:343:VAL:HG22	2.56	0.41
1:C:280:HIS:NE2	1:C:346:MET:HG2	2.36	0.41
1:C:277:HIS:CE1	1:C:301:ILE:O	2.60	0.40
1:C:105:ASN:ND2	1:C:107:ARG:H	2.19	0.40
1:A:301:ILE:HG13	1:A:301:ILE:H	1.41	0.40
1:B:129:GLU:O	1:B:248:ALA:HA	2.21	0.40
1:G:105:ASN:C	1:G:105:ASN:ND2	2.70	0.40
1:E:238:PRO:O	1:E:239:ILE:HD13	2.21	0.40
1:J:284:TYR:CD2	1:J:343:VAL:HG22	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:180:LEU:HD23	1:G:180:LEU:HA	1.89	0.40
1:G:233:THR:HB	1:G:235:ASP:H	1.86	0.40
1:E:332:ARG:NH2	3:E:5005:P3P:O14	2.54	0.40
1:E:129:GLU:O	5:E:6022:HOH:O	2.22	0.40
1:D:230:VAL:CG1	1:D:231:VAL:N	2.84	0.40
1:B:80:ASP:C	1:B:80:ASP:OD1	2.59	0.40
1:G:333:ARG:N	1:G:334:PRO:HD3	2.37	0.40
1:D:314:SER:HB3	1:D:333:ARG:HD3	2.03	0.40
1:G:105:ASN:HD22	1:G:107:ARG:H	1.69	0.40
1:C:96:THR:HB	1:C:97:PRO:CD	2.51	0.40
1:H:103:PRO:HA	5:H:6027:HOH:O	2.20	0.40
1:B:39:THR:O	1:B:40:LEU:HD23	2.20	0.40
1:G:281:ILE:HA	1:G:281:ILE:HD13	1.83	0.40
1:F:80:ASP:C	1:F:80:ASP:OD1	2.60	0.40
1:I:102:ILE:HB	1:I:103:PRO:CD	2.52	0.40
1:B:141:TRP:HA	1:B:142:PRO:HD3	1.95	0.40
1:B:3:CYS:HB2	1:B:4:LEU:H	1.79	0.40
1:J:39:THR:O	1:J:40:LEU:HD23	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ASN:O	1:H:355:LYS:CB[2_655]	2.16	0.04

## 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%)	334 (95%)	17 (5%)	0	100	100
1	B	351/356 (99%)	333 (95%)	18 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	351/356 (99%)	332 (95%)	19 (5%)	0	100	100
1	D	351/356 (99%)	333 (95%)	18 (5%)	0	100	100
1	E	351/356 (99%)	333 (95%)	18 (5%)	0	100	100
1	F	351/356 (99%)	334 (95%)	17 (5%)	0	100	100
1	G	351/356 (99%)	334 (95%)	17 (5%)	0	100	100
1	H	351/356 (99%)	332 (95%)	19 (5%)	0	100	100
1	I	351/356 (99%)	333 (95%)	18 (5%)	0	100	100
1	J	351/356 (99%)	336 (96%)	14 (4%)	1 (0%)	46	83
All	All	3510/3560 (99%)	3334 (95%)	175 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	203	GLY

### 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%)	267 (93%)	21 (7%)	17	58
1	B	288/290 (99%)	267 (93%)	21 (7%)	17	58
1	C	288/290 (99%)	267 (93%)	21 (7%)	17	58
1	D	288/290 (99%)	268 (93%)	20 (7%)	19	60
1	E	288/290 (99%)	267 (93%)	21 (7%)	17	58
1	F	288/290 (99%)	267 (93%)	21 (7%)	17	58
1	G	288/290 (99%)	267 (93%)	21 (7%)	17	58
1	H	288/290 (99%)	266 (92%)	22 (8%)	16	56
1	I	288/290 (99%)	267 (93%)	21 (7%)	17	58
1	J	288/290 (99%)	267 (93%)	21 (7%)	17	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2880/2900 (99%)	2670 (93%)	210 (7%)	17 58

All (210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	CYS
1	A	19	ILE
1	A	45	THR
1	A	105	ASN
1	A	116	SER
1	A	128	ILE
1	A	143	LEU
1	A	164	GLU
1	A	176	TYR
1	A	201	GLN
1	A	206	VAL
1	A	232	VAL
1	A	233	THR
1	A	258	ARG
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	351	THR
1	B	3	CYS
1	B	19	ILE
1	B	45	THR
1	B	105	ASN
1	B	116	SER
1	B	128	ILE
1	B	143	LEU
1	B	164	GLU
1	B	176	TYR
1	B	201	GLN
1	B	206	VAL
1	B	232	VAL
1	B	233	THR
1	B	258	ARG
1	B	288	ASN
1	B	289	GLU

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Mol	Chain	Res	Type
1	B	301	ILE
1	B	321	THR
1	B	338	MET
1	B	344	THR
1	B	351	THR
1	C	3	CYS
1	C	19	ILE
1	C	45	THR
1	C	105	ASN
1	C	116	SER
1	C	128	ILE
1	C	143	LEU
1	C	164	GLU
1	C	176	TYR
1	C	201	GLN
1	C	206	VAL
1	C	232	VAL
1	C	233	THR
1	C	258	ARG
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	351	THR
1	D	3	CYS
1	D	19	ILE
1	D	45	THR
1	D	105	ASN
1	D	116	SER
1	D	128	ILE
1	D	143	LEU
1	D	164	GLU
1	D	176	TYR
1	D	201	GLN
1	D	206	VAL
1	D	232	VAL
1	D	258	ARG
1	D	288	ASN
1	D	289	GLU
1	D	301	ILE

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Mol	Chain	Res	Type
1	D	321	THR
1	D	338	MET
1	D	344	THR
1	D	351	THR
1	E	3	CYS
1	E	19	ILE
1	E	45	THR
1	E	105	ASN
1	E	116	SER
1	E	128	ILE
1	E	143	LEU
1	E	164	GLU
1	E	176	TYR
1	E	201	GLN
1	E	206	VAL
1	E	232	VAL
1	E	233	THR
1	E	258	ARG
1	E	288	ASN
1	E	289	GLU
1	E	301	ILE
1	E	321	THR
1	E	338	MET
1	E	344	THR
1	E	351	THR
1	F	3	CYS
1	F	19	ILE
1	F	45	THR
1	F	105	ASN
1	F	116	SER
1	F	128	ILE
1	F	143	LEU
1	F	164	GLU
1	F	176	TYR
1	F	201	GLN
1	F	206	VAL
1	F	232	VAL
1	F	233	THR
1	F	258	ARG
1	F	288	ASN
1	F	289	GLU
1	F	301	ILE

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Mol	Chain	Res	Type
1	F	321	THR
1	F	338	MET
1	F	344	THR
1	F	351	THR
1	G	3	CYS
1	G	19	ILE
1	G	45	THR
1	G	105	ASN
1	G	116	SER
1	G	128	ILE
1	G	143	LEU
1	G	164	GLU
1	G	176	TYR
1	G	201	GLN
1	G	206	VAL
1	G	232	VAL
1	G	233	THR
1	G	258	ARG
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	351	THR
1	H	3	CYS
1	H	19	ILE
1	H	45	THR
1	H	105	ASN
1	H	116	SER
1	H	128	ILE
1	H	143	LEU
1	H	164	GLU
1	H	176	TYR
1	H	201	GLN
1	H	204	PRO
1	H	206	VAL
1	H	232	VAL
1	H	233	THR
1	H	258	ARG
1	H	288	ASN
1	H	289	GLU

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Mol	Chain	Res	Type
1	H	301	ILE
1	H	321	THR
1	H	338	MET
1	H	344	THR
1	H	351	THR
1	I	3	CYS
1	I	19	ILE
1	I	45	THR
1	I	105	ASN
1	I	116	SER
1	I	128	ILE
1	I	143	LEU
1	I	164	GLU
1	I	176	TYR
1	I	201	GLN
1	I	206	VAL
1	I	232	VAL
1	I	233	THR
1	I	258	ARG
1	I	288	ASN
1	I	289	GLU
1	I	301	ILE
1	I	321	THR
1	I	338	MET
1	I	344	THR
1	I	351	THR
1	J	3	CYS
1	J	19	ILE
1	J	45	THR
1	J	105	ASN
1	J	116	SER
1	J	128	ILE
1	J	143	LEU
1	J	164	GLU
1	J	176	TYR
1	J	201	GLN
1	J	206	VAL
1	J	232	VAL
1	J	233	THR
1	J	258	ARG
1	J	288	ASN
1	J	289	GLU

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Mol	Chain	Res	Type
1	J	301	ILE
1	J	321	THR
1	J	338	MET
1	J	344	THR
1	J	351	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) 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	277	HIS
1	A	288	ASN
1	A	296	HIS
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	277	HIS
1	B	288	ASN
1	B	296	HIS
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
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

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

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Mol	Chain	Res	Type
1	I	154	GLN
1	I	190	ASN
1	I	197	GLN
1	I	201	GLN
1	I	244	ASN
1	I	277	HIS
1	I	288	ASN
1	I	296	HIS
1	I	324	ASN
1	J	105	ASN
1	J	136	GLN
1	J	154	GLN
1	J	190	ASN
1	J	197	GLN
1	J	201	GLN
1	J	251	ASN
1	J	277	HIS
1	J	288	ASN
1	J	296	HIS
1	J	324	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 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
3	P3P	A	5001	2	7,14,14	4.91	2 (28%)	7,21,21	1.28	1 (14%)
4	ADP	A	6001	2	22,29,29	1.23	3 (13%)	27,45,45	3.29	9 (33%)
3	P3P	B	5002	1,2	7,14,14	3.21	3 (42%)	7,21,21	2.40	3 (42%)
4	ADP	B	6002	2	22,29,29	1.28	2 (9%)	27,45,45	3.78	8 (29%)
3	P3P	C	5003	2	7,14,14	4.12	2 (28%)	7,21,21	2.38	4 (57%)
4	ADP	C	6003	2	22,29,29	1.26	2 (9%)	27,45,45	2.90	10 (37%)
3	P3P	D	5004	2	7,14,14	4.30	2 (28%)	7,21,21	1.83	2 (28%)
4	ADP	D	6005	2	22,29,29	1.10	2 (9%)	27,45,45	2.85	8 (29%)
3	P3P	E	5005	2	7,14,14	2.77	3 (42%)	7,21,21	1.83	2 (28%)
4	ADP	E	6004	2	22,29,29	1.26	1 (4%)	27,45,45	2.63	11 (40%)
3	P3P	F	5007	2	7,14,14	3.18	2 (28%)	7,21,21	2.40	3 (42%)
4	ADP	F	6007	2	22,29,29	0.88	1 (4%)	27,45,45	2.89	7 (25%)
3	P3P	G	5006	2	7,14,14	4.06	2 (28%)	7,21,21	1.77	3 (42%)
4	ADP	G	6006	2	22,29,29	1.01	1 (4%)	27,45,45	2.38	7 (25%)
3	P3P	H	5010	2	7,14,14	5.22	2 (28%)	7,21,21	1.26	1 (14%)
4	ADP	H	6010	2	22,29,29	1.00	0	27,45,45	3.18	11 (40%)
3	P3P	I	5008	2	7,14,14	4.12	2 (28%)	7,21,21	1.56	1 (14%)
4	ADP	I	6008	2	22,29,29	1.16	1 (4%)	27,45,45	2.81	9 (33%)
3	P3P	J	5009	2	7,14,14	3.55	2 (28%)	7,21,21	1.74	2 (28%)
4	ADP	J	6009	2	22,29,29	0.95	0	27,45,45	2.37	4 (14%)

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
3	P3P	A	5001	2	-	0/8/16/16	0/0/0/0
4	ADP	A	6001	2	-	0/12/32/32	0/3/3/3
3	P3P	B	5002	1,2	-	0/8/16/16	0/0/0/0
4	ADP	B	6002	2	-	0/12/32/32	0/3/3/3
3	P3P	C	5003	2	-	0/8/16/16	0/0/0/0
4	ADP	C	6003	2	-	0/12/32/32	0/3/3/3
3	P3P	D	5004	2	-	0/8/16/16	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	D	6005	2	-	0/12/32/32	0/3/3/3
3	P3P	E	5005	2	-	0/8/16/16	0/0/0/0
4	ADP	E	6004	2	-	0/12/32/32	0/3/3/3
3	P3P	F	5007	2	-	0/8/16/16	0/0/0/0
4	ADP	F	6007	2	-	0/12/32/32	0/3/3/3
3	P3P	G	5006	2	-	0/8/16/16	0/0/0/0
4	ADP	G	6006	2	-	0/12/32/32	0/3/3/3
3	P3P	H	5010	2	-	0/8/16/16	0/0/0/0
4	ADP	H	6010	2	-	0/12/32/32	0/3/3/3
3	P3P	I	5008	2	-	0/8/16/16	0/0/0/0
4	ADP	I	6008	2	-	0/12/32/32	0/3/3/3
3	P3P	J	5009	2	-	0/8/16/16	0/0/0/0
4	ADP	J	6009	2	-	0/12/32/32	0/3/3/3

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	5010	P3P	PDP-CGP	-13.18	1.67	1.79
3	A	5001	P3P	PDP-CGP	-11.38	1.69	1.79
3	I	5008	P3P	PDP-CGP	-10.02	1.70	1.79
3	G	5006	P3P	PDP-CGP	-9.84	1.70	1.79
3	D	5004	P3P	PDP-CGP	-9.67	1.70	1.79
3	C	5003	P3P	PDP-CGP	-9.63	1.70	1.79
3	J	5009	P3P	PDP-CGP	-8.47	1.71	1.79
3	B	5002	P3P	PDP-CGP	-7.34	1.73	1.79
3	F	5007	P3P	PDP-CGP	-6.96	1.73	1.79
3	E	5005	P3P	PDP-CGP	-4.19	1.75	1.79
4	D	6005	ADP	C2'-C3'	-2.38	1.46	1.53
4	A	6001	ADP	C2'-C3'	-2.23	1.47	1.53
4	F	6007	ADP	O4'-C1'	2.01	1.43	1.41
4	D	6005	ADP	C2-N3	2.07	1.35	1.32
4	A	6001	ADP	O4'-C1'	2.18	1.44	1.41
3	B	5002	P3P	P12-O15	2.59	1.59	1.51
3	E	5005	P3P	P12-O13	2.73	1.64	1.54
4	B	6002	ADP	C4-N3	2.84	1.39	1.35
3	B	5002	P3P	PDP-OEA	2.96	1.55	1.50
4	A	6001	ADP	C4-N3	3.17	1.40	1.35
4	C	6003	ADP	O4'-C1'	3.20	1.45	1.41
4	G	6006	ADP	O4'-C1'	3.35	1.45	1.41
4	C	6003	ADP	C2-N3	3.41	1.38	1.32
4	E	6004	ADP	O4'-C1'	3.44	1.45	1.41
4	B	6002	ADP	O4'-C1'	3.48	1.45	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	5009	P3P	PDP-OEA	3.92	1.57	1.50
3	G	5006	P3P	PDP-OEA	4.01	1.57	1.50
3	H	5010	P3P	PDP-OEA	4.04	1.57	1.50
4	I	6008	ADP	O4'-C1'	4.12	1.46	1.41
3	I	5008	P3P	PDP-OEA	4.27	1.58	1.50
3	F	5007	P3P	PDP-OEA	4.53	1.58	1.50
3	C	5003	P3P	PDP-OEA	5.01	1.59	1.50
3	E	5005	P3P	PDP-OEA	5.19	1.60	1.50
3	D	5004	P3P	PDP-OEA	5.80	1.61	1.50
3	A	5001	P3P	PDP-OEA	6.07	1.61	1.50

All (106) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	6002	ADP	N3-C2-N1	-16.48	116.28	128.89
4	A	6001	ADP	N3-C2-N1	-13.45	118.60	128.89
4	F	6007	ADP	N3-C2-N1	-11.48	120.11	128.89
4	H	6010	ADP	N3-C2-N1	-11.37	120.19	128.89
4	I	6008	ADP	N3-C2-N1	-11.12	120.38	128.89
4	D	6005	ADP	N3-C2-N1	-10.29	121.02	128.89
4	G	6006	ADP	N3-C2-N1	-10.15	121.12	128.89
4	C	6003	ADP	N3-C2-N1	-9.77	121.41	128.89
4	E	6004	ADP	N3-C2-N1	-9.21	121.84	128.89
4	J	6009	ADP	N3-C2-N1	-8.27	122.56	128.89
4	B	6002	ADP	C2'-C1'-N9	-6.04	105.07	114.29
4	D	6005	ADP	C4'-O4'-C1'	-5.18	104.03	109.72
4	C	6003	ADP	O3'-C3'-C2'	-4.90	95.90	111.83
4	H	6010	ADP	C2'-C1'-N9	-4.86	106.86	114.29
4	D	6005	ADP	C1'-N9-C4	-4.67	119.90	126.94
4	H	6010	ADP	C1'-N9-C4	-4.39	120.32	126.94
4	F	6007	ADP	C4'-O4'-C1'	-4.15	105.16	109.72
4	I	6008	ADP	C1'-N9-C4	-4.02	120.87	126.94
4	H	6010	ADP	O3A-PA-O5'	-3.94	92.49	102.94
4	A	6001	ADP	O3'-C3'-C2'	-3.62	100.06	111.83
4	B	6002	ADP	C4'-O4'-C1'	-3.58	105.78	109.72
4	D	6005	ADP	C4-C5-N7	-3.52	106.24	109.48
4	D	6005	ADP	O3'-C3'-C2'	-3.51	100.42	111.83
4	J	6009	ADP	C4-C5-N7	-3.48	106.28	109.48
4	C	6003	ADP	C2'-C1'-N9	-3.44	109.04	114.29
4	A	6001	ADP	O2'-C2'-C3'	-3.40	100.76	111.83
4	C	6003	ADP	O3A-PA-O5'	-3.35	94.04	102.94
4	F	6007	ADP	C1'-N9-C4	-3.19	122.13	126.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	6002	ADP	PA-O3A-PB	-3.09	122.31	132.67
3	B	5002	P3P	O14-P12-O15	-3.07	100.71	110.58
4	A	6001	ADP	O5'-PA-O1A	-3.04	97.83	109.62
4	C	6003	ADP	C4-C5-N7	-2.98	106.74	109.48
4	I	6008	ADP	C4'-O4'-C1'	-2.97	106.45	109.72
4	A	6001	ADP	O3A-PA-O5'	-2.92	95.19	102.94
4	H	6010	ADP	O3'-C3'-C2'	-2.90	102.40	111.83
4	D	6005	ADP	O3A-PA-O5'	-2.79	95.53	102.94
4	C	6003	ADP	PA-O3A-PB	-2.72	123.53	132.67
4	E	6004	ADP	O3'-C3'-C4'	-2.70	102.94	111.05
4	A	6001	ADP	C4'-O4'-C1'	-2.64	106.82	109.72
4	E	6004	ADP	O3'-C3'-C2'	-2.61	103.33	111.83
4	H	6010	ADP	O2B-PB-O1B	-2.58	102.29	110.58
4	C	6003	ADP	O3'-C3'-C4'	-2.44	103.74	111.05
4	H	6010	ADP	PA-O3A-PB	-2.42	124.56	132.67
3	C	5003	P3P	O13-P12-O15	-2.40	102.86	110.58
4	G	6006	ADP	C1'-N9-C4	-2.32	123.45	126.94
4	H	6010	ADP	C4-C5-N7	-2.29	107.37	109.48
4	G	6006	ADP	O3'-C3'-C2'	-2.25	104.51	111.83
4	B	6002	ADP	O3'-C3'-C2'	-2.23	104.57	111.83
4	I	6008	ADP	O4'-C4'-C3'	-2.20	100.72	105.15
4	E	6004	ADP	C1'-N9-C4	-2.13	123.73	126.94
4	E	6004	ADP	O5'-C5'-C4'	-2.12	101.31	109.12
4	G	6006	ADP	PA-O3A-PB	-2.09	125.67	132.67
3	F	5007	P3P	O14-P12-OEB	-2.07	95.72	105.09
4	E	6004	ADP	O2'-C2'-C3'	-2.05	105.15	111.83
4	A	6001	ADP	C2'-C3'-C4'	2.01	106.74	102.61
4	C	6003	ADP	O3B-PB-O2B	2.01	115.04	107.38
4	I	6008	ADP	O3B-PB-O1B	2.02	117.07	110.58
3	J	5009	P3P	CEP-PDP-CGP	2.03	111.19	107.53
4	F	6007	ADP	O3B-PB-O2B	2.04	115.16	107.38
4	E	6004	ADP	N6-C6-N1	2.06	123.62	119.20
3	G	5006	P3P	O13-P12-OEB	2.09	114.59	105.09
4	B	6002	ADP	O3B-PB-O1B	2.20	117.66	110.58
4	G	6006	ADP	O4'-C1'-N9	2.29	112.89	108.10
4	E	6004	ADP	C2'-C3'-C4'	2.33	107.39	102.61
4	F	6007	ADP	O2B-PB-O1B	2.37	118.20	110.58
3	C	5003	P3P	O13-P12-OEB	2.42	116.05	105.09
3	G	5006	P3P	O13-P12-O15	2.45	118.46	110.58
3	H	5010	P3P	O13-P12-OEB	2.45	116.20	105.09
3	E	5005	P3P	CEP-PDP-CGP	2.48	112.01	107.53
4	D	6005	ADP	O4'-C1'-N9	2.52	113.37	108.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	6008	ADP	O2B-PB-O1B	2.54	118.76	110.58
4	D	6005	ADP	O3B-PB-O2B	2.57	117.19	107.38
4	I	6008	ADP	O5'-C5'-C4'	2.59	118.67	109.12
3	C	5003	P3P	O14-P12-O15	2.69	119.24	110.58
3	D	5004	P3P	O14-P12-O13	2.71	117.71	107.38
3	F	5007	P3P	O14-P12-O13	2.72	117.75	107.38
4	H	6010	ADP	O3B-PB-O2B	2.74	117.82	107.38
4	H	6010	ADP	C2'-C3'-C4'	2.74	108.25	102.61
4	G	6006	ADP	C2'-C1'-N9	2.75	118.50	114.29
3	G	5006	P3P	CEP-PDP-CGP	2.76	112.51	107.53
4	G	6006	ADP	O3B-PB-O1B	2.88	119.83	110.58
4	A	6001	ADP	O2B-PB-O1B	2.91	119.93	110.58
4	J	6009	ADP	O3B-PB-O1B	2.92	119.96	110.58
3	A	5001	P3P	O14-P12-O13	2.92	118.51	107.38
3	I	5008	P3P	O14-P12-O13	3.05	118.99	107.38
4	B	6002	ADP	N6-C6-N1	3.11	125.87	119.20
3	J	5009	P3P	O14-P12-O13	3.15	119.38	107.38
4	I	6008	ADP	O4'-C1'-N9	3.18	114.75	108.10
3	B	5002	P3P	CEP-PDP-CGP	3.24	113.38	107.53
3	D	5004	P3P	O14-P12-O15	3.27	121.10	110.58
4	F	6007	ADP	C2'-C1'-N9	3.38	119.45	114.29
4	C	6003	ADP	C2'-C3'-C4'	3.49	109.79	102.61
4	I	6008	ADP	C2'-C1'-N9	3.63	119.84	114.29
4	H	6010	ADP	O3B-PB-O1B	3.70	122.49	110.58
4	E	6004	ADP	O4'-C1'-N9	3.73	115.91	108.10
4	E	6004	ADP	C2'-C1'-N9	3.77	120.05	114.29
3	C	5003	P3P	O14-P12-O13	3.77	121.74	107.38
3	E	5005	P3P	O14-P12-O13	3.97	122.49	107.38
3	B	5002	P3P	O13-P12-O15	4.11	123.80	110.58
4	E	6004	ADP	O3B-PB-O1B	4.24	124.24	110.58
4	B	6002	ADP	O4'-C1'-N9	4.61	117.75	108.10
4	C	6003	ADP	O4'-C1'-N9	4.72	117.98	108.10
3	F	5007	P3P	CEP-PDP-CGP	4.97	116.51	107.53
4	F	6007	ADP	O4'-C1'-N9	5.00	118.57	108.10
4	A	6001	ADP	O4'-C1'-N9	5.19	118.97	108.10
4	J	6009	ADP	O4'-C1'-N9	5.84	120.33	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

15 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	5001	P3P	5	0
3	B	5002	P3P	3	0
4	B	6002	ADP	2	0
3	C	5003	P3P	4	0
3	D	5004	P3P	3	0
4	D	6005	ADP	1	0
3	E	5005	P3P	4	0
3	F	5007	P3P	4	0
4	F	6007	ADP	2	0
3	G	5006	P3P	2	0
4	G	6006	ADP	3	0
3	H	5010	P3P	2	0
3	I	5008	P3P	4	0
4	I	6008	ADP	2	0
4	J	6009	ADP	1	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, 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	353/356 (99%)	-0.73	0 100 100	49, 66, 89, 100	0
1	B	353/356 (99%)	-0.69	0 100 100	49, 66, 89, 100	0
1	C	353/356 (99%)	-0.74	0 100 100	49, 66, 89, 100	0
1	D	353/356 (99%)	-0.70	0 100 100	49, 67, 89, 100	0
1	E	353/356 (99%)	-0.73	0 100 100	49, 67, 89, 100	0
1	F	353/356 (99%)	-0.70	0 100 100	49, 67, 89, 100	0
1	G	353/356 (99%)	-0.70	0 100 100	49, 67, 89, 100	0
1	H	353/356 (99%)	-0.70	0 100 100	49, 66, 89, 100	0
1	I	353/356 (99%)	-0.73	0 100 100	49, 66, 89, 100	0
1	J	353/356 (99%)	-0.71	0 100 100	49, 66, 89, 100	0
All	All	3530/3560 (99%)	-0.71	0 100 100	49, 67, 89, 100	0

There are no RSRZ outliers to report.

### 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. 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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	ADP	A	6001	27/27	0.93	0.25	1.62	55,76,90,90	0
4	ADP	C	6003	27/27	0.90	0.26	1.41	45,68,81,83	0
2	MN	C	1021	1/1	0.93	0.27	1.36	88,88,88,88	0
4	ADP	E	6004	27/27	0.92	0.25	0.87	81,87,94,95	0
3	P3P	C	5003	15/15	0.97	0.21	0.76	48,53,58,59	0
4	ADP	D	6005	27/27	0.95	0.22	0.49	67,73,90,90	0
3	P3P	J	5009	15/15	0.97	0.21	0.17	46,48,56,58	0
3	P3P	F	5007	15/15	0.98	0.20	0.04	66,68,73,77	0
3	P3P	D	5004	15/15	0.98	0.19	0.02	64,67,75,76	0
4	ADP	G	6006	27/27	0.96	0.20	0.00	55,68,76,79	0
3	P3P	A	5001	15/15	0.97	0.18	-0.02	50,54,64,65	0
4	ADP	J	6009	27/27	0.93	0.22	-0.02	44,54,60,62	0
4	ADP	F	6007	27/27	0.94	0.21	-0.04	76,85,92,92	0
3	P3P	G	5006	15/15	0.98	0.18	-0.07	61,67,80,80	0
4	ADP	I	6008	27/27	0.94	0.19	-0.11	62,71,74,75	0
3	P3P	I	5008	15/15	0.96	0.19	-0.18	41,49,59,59	0
3	P3P	B	5002	15/15	0.96	0.18	-0.19	30,32,40,41	0
3	P3P	E	5005	15/15	0.97	0.19	-0.27	65,73,78,81	0
2	MN	F	1053	1/1	0.99	0.17	-0.46	63,63,63,63	0
4	ADP	B	6002	27/27	0.96	0.17	-0.46	37,46,53,54	0
3	P3P	H	5010	15/15	0.97	0.17	-0.50	30,35,41,41	0
4	ADP	H	6010	27/27	0.95	0.16	-0.57	29,31,40,43	0
2	MN	B	1013	1/1	0.95	0.18	-0.58	54,54,54,54	0
2	MN	D	1032	1/1	0.97	0.20	-0.75	83,83,83,83	0
2	MN	A	1002	1/1	0.98	0.20	-0.79	62,62,62,62	0
2	MN	D	1033	1/1	0.99	0.14	-0.92	51,51,51,51	0
2	MN	G	1062	1/1	0.99	0.18	-1.12	69,69,69,69	0
2	MN	C	1023	1/1	0.98	0.14	-1.27	56,56,56,56	0
2	MN	I	1082	1/1	0.99	0.15	-1.35	67,67,67,67	0
2	MN	D	1031	1/1	0.95	0.14	-1.48	57,57,57,57	0
2	MN	J	1092	1/1	1.00	0.20	-1.49	61,61,61,61	0
2	MN	F	1052	1/1	0.99	0.16	-1.55	54,54,54,54	0
2	MN	C	1022	1/1	0.99	0.14	-1.60	51,51,51,51	0
2	MN	E	1043	1/1	0.94	0.14	-1.66	71,71,71,71	0
2	MN	J	1093	1/1	0.99	0.15	-1.77	41,41,41,41	0
2	MN	G	1063	1/1	0.95	0.14	-1.79	51,51,51,51	0
2	MN	H	1073	1/1	0.99	0.11	-1.97	28,28,28,28	0
2	MN	A	1003	1/1	0.96	0.12	-2.02	40,40,40,40	0
2	MN	I	1083	1/1	0.97	0.12	-2.03	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MN	E	1042	1/1	0.99	0.19	-2.16	73,73,73,73	0
2	MN	B	1012	1/1	0.97	0.13	-2.48	32,32,32,32	0
2	MN	H	1072	1/1	1.00	0.15	-3.33	49,49,49,49	0
2	MN	F	1051	1/1	0.98	0.25	-	86,86,86,86	0
2	MN	E	1041	1/1	0.90	0.16	-	68,68,68,68	0
2	MN	G	1061	1/1	0.99	0.17	-	58,58,58,58	0
2	MN	H	1071	1/1	0.97	0.17	-	52,52,52,52	0
2	MN	B	1011	1/1	0.96	0.20	-	61,61,61,61	0
2	MN	J	1091	1/1	0.99	0.22	-	52,52,52,52	0
2	MN	A	1001	1/1	0.94	0.24	-	52,52,52,52	0
2	MN	I	1081	1/1	0.99	0.15	-	53,53,53,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.