



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 6, 2024 – 03:37 AM EST

PDB ID : 1Z7N
Title : ATP Phosphoribosyl transferase (HisZG ATP-PRTase) from *Lactococcus lactis* with bound PRPP substrate
Authors : Champagne, K.S.; Sissler, M.; Larrabee, Y.; Doublet, S.; Francklyn, C.S.
Deposited on : 2005-03-25
Resolution : 3.25 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

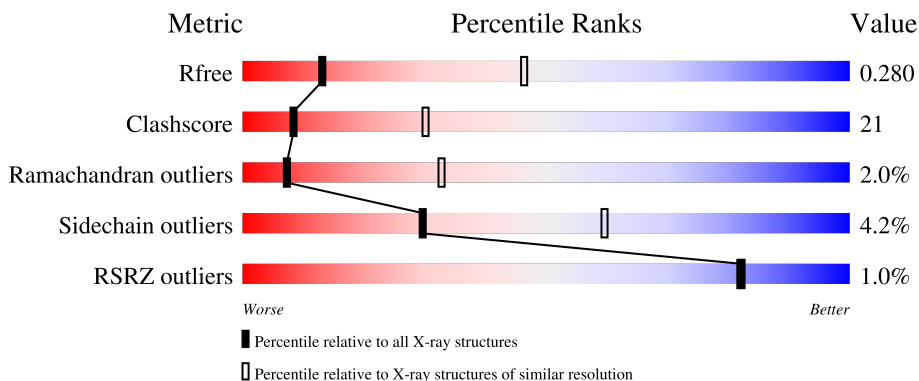
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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

Mol	Chain	Length	Quality of chain
1	A	344	
1	B	344	
1	C	344	
1	D	344	
2	E	208	

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Mol	Chain	Length	Quality of chain
2	F	208	<p>%</p> <p>57% 38%</p>
2	G	208	<p>%</p> <p>53% 41%</p>
2	H	208	<p>%</p> <p>55% 39%</p>

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
4	PO4	G	1001	-	-	X	X

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 16750 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 ATP phosphoribosyltransferase regulatory subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	2547	1636	415	485	11	21	0	0
1	B	318	2584	1657	424	492	11	12	0	0
1	C	304	2472	1591	399	471	11	10	0	0
1	D	312	2541	1633	416	481	11	5	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	cloning artifact	UNP Q02147
A	-14	ARG	-	cloning artifact	UNP Q02147
A	-13	GLY	-	cloning artifact	UNP Q02147
A	-12	SER	-	cloning artifact	UNP Q02147
A	-11	HIS	-	expression tag	UNP Q02147
A	-10	HIS	-	expression tag	UNP Q02147
A	-9	HIS	-	expression tag	UNP Q02147
A	-8	HIS	-	expression tag	UNP Q02147
A	-7	HIS	-	expression tag	UNP Q02147
A	-6	HIS	-	expression tag	UNP Q02147
A	-5	GLY	-	cloning artifact	UNP Q02147
A	-4	SER	-	cloning artifact	UNP Q02147
A	-3	ILE	-	cloning artifact	UNP Q02147
A	-2	GLU	-	cloning artifact	UNP Q02147
A	-1	GLY	-	cloning artifact	UNP Q02147
A	0	ARG	-	cloning artifact	UNP Q02147
B	-15	MET	-	cloning artifact	UNP Q02147
B	-14	ARG	-	cloning artifact	UNP Q02147
B	-13	GLY	-	cloning artifact	UNP Q02147
B	-12	SER	-	cloning artifact	UNP Q02147
B	-11	HIS	-	expression tag	UNP Q02147

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	HIS	-	expression tag	UNP Q02147
B	-9	HIS	-	expression tag	UNP Q02147
B	-8	HIS	-	expression tag	UNP Q02147
B	-7	HIS	-	expression tag	UNP Q02147
B	-6	HIS	-	expression tag	UNP Q02147
B	-5	GLY	-	cloning artifact	UNP Q02147
B	-4	SER	-	cloning artifact	UNP Q02147
B	-3	ILE	-	cloning artifact	UNP Q02147
B	-2	GLU	-	cloning artifact	UNP Q02147
B	-1	GLY	-	cloning artifact	UNP Q02147
B	0	ARG	-	cloning artifact	UNP Q02147
C	-15	MET	-	cloning artifact	UNP Q02147
C	-14	ARG	-	cloning artifact	UNP Q02147
C	-13	GLY	-	cloning artifact	UNP Q02147
C	-12	SER	-	cloning artifact	UNP Q02147
C	-11	HIS	-	expression tag	UNP Q02147
C	-10	HIS	-	expression tag	UNP Q02147
C	-9	HIS	-	expression tag	UNP Q02147
C	-8	HIS	-	expression tag	UNP Q02147
C	-7	HIS	-	expression tag	UNP Q02147
C	-6	HIS	-	expression tag	UNP Q02147
C	-5	GLY	-	cloning artifact	UNP Q02147
C	-4	SER	-	cloning artifact	UNP Q02147
C	-3	ILE	-	cloning artifact	UNP Q02147
C	-2	GLU	-	cloning artifact	UNP Q02147
C	-1	GLY	-	cloning artifact	UNP Q02147
C	0	ARG	-	cloning artifact	UNP Q02147
D	-15	MET	-	cloning artifact	UNP Q02147
D	-14	ARG	-	cloning artifact	UNP Q02147
D	-13	GLY	-	cloning artifact	UNP Q02147
D	-12	SER	-	cloning artifact	UNP Q02147
D	-11	HIS	-	expression tag	UNP Q02147
D	-10	HIS	-	expression tag	UNP Q02147
D	-9	HIS	-	expression tag	UNP Q02147
D	-8	HIS	-	expression tag	UNP Q02147
D	-7	HIS	-	expression tag	UNP Q02147
D	-6	HIS	-	expression tag	UNP Q02147
D	-5	GLY	-	cloning artifact	UNP Q02147
D	-4	SER	-	cloning artifact	UNP Q02147
D	-3	ILE	-	cloning artifact	UNP Q02147
D	-2	GLU	-	cloning artifact	UNP Q02147
D	-1	GLY	-	cloning artifact	UNP Q02147

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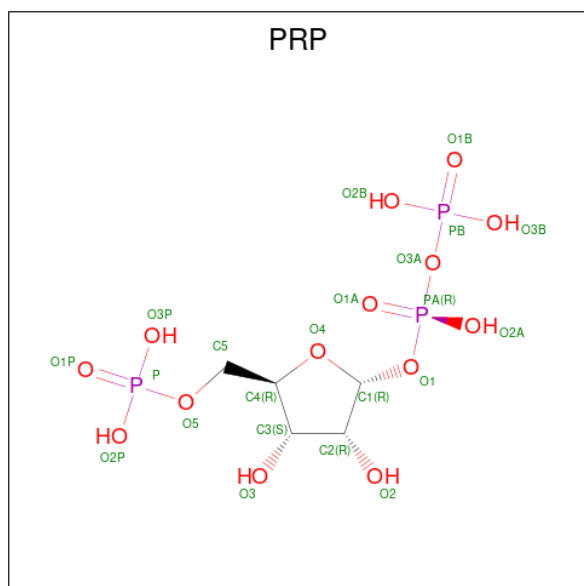
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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	ARG	-	cloning artifact	UNP Q02147

- Molecule 2 is a protein called ATP phosphoribosyltransferase.

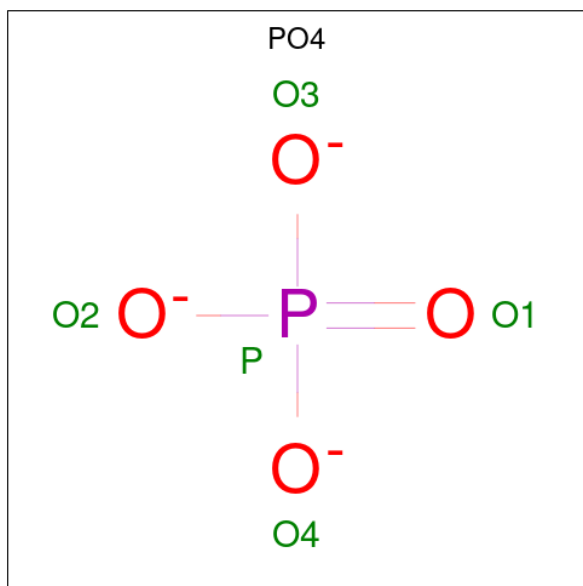
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	203	Total	C	N	O	S	9	0	0
			1630	1048	266	312	4			
2	F	205	Total	C	N	O	S	0	0	0
			1643	1055	269	315	4			
2	G	203	Total	C	N	O	S	4	0	0
			1632	1048	267	313	4			
2	H	200	Total	C	N	O	S	0	0	0
			1603	1030	261	308	4			

- Molecule 3 is 1-O-pyrophosphono-5-O-phosphono-alpha-D-ribofuranose (three-letter code: PRP) (formula: $C_5H_{13}O_{14}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	1	Total	C	O	P	0	0
			22	5	14	3		
3	F	1	Total	C	O	P	0	0
			22	5	14	3		
3	G	1	Total	C	O	P	0	0
			22	5	14	3		
3	H	1	Total	C	O	P	0	0
			22	5	14	3		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).

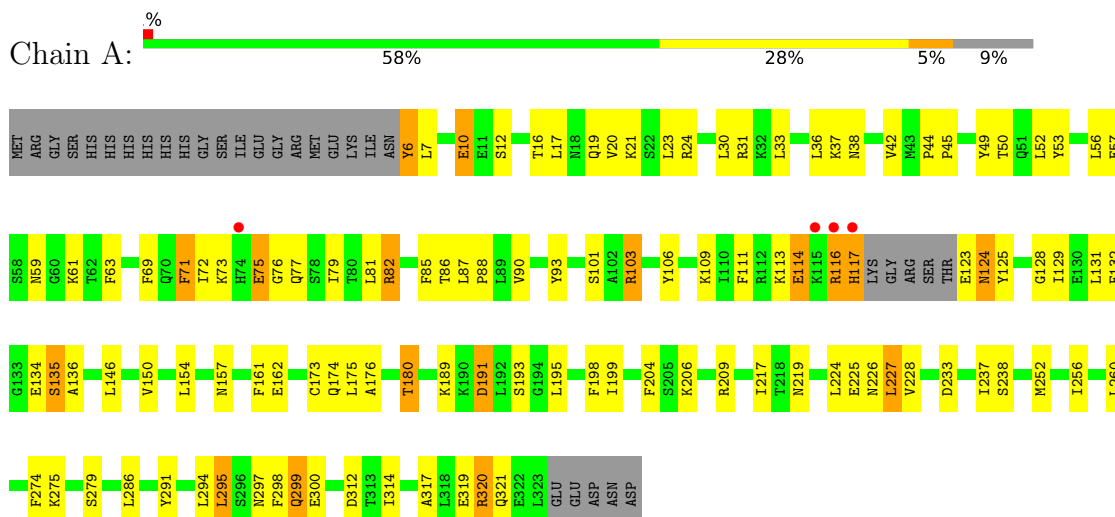


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	F	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		

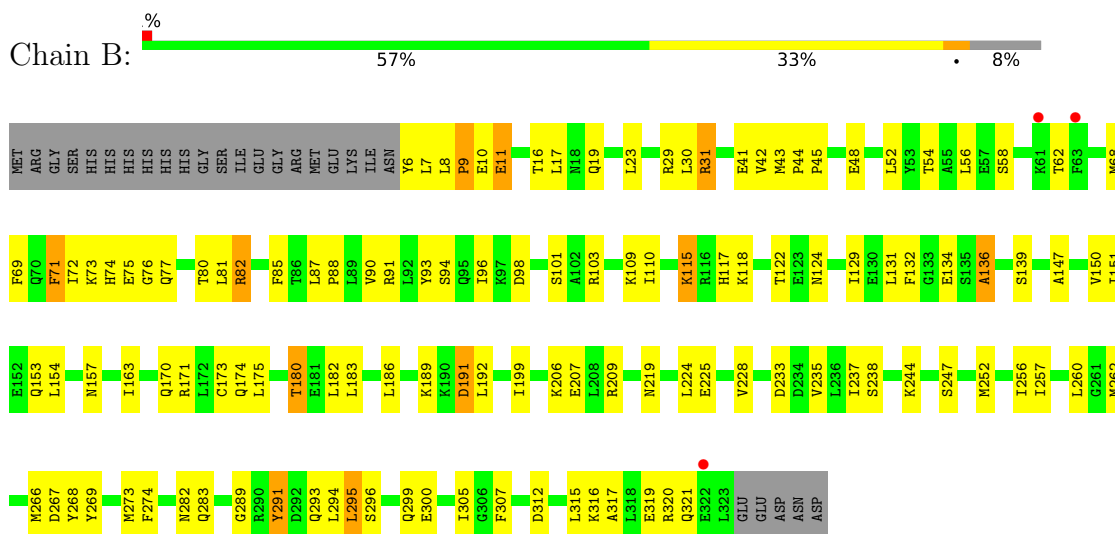
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: ATP phosphoribosyltransferase regulatory subunit

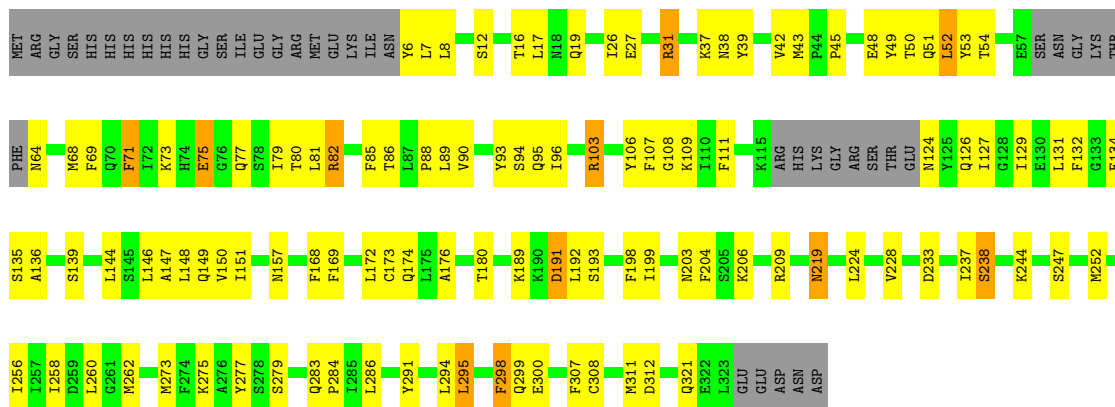


- Molecule 1: ATP phosphoribosyltransferase regulatory subunit

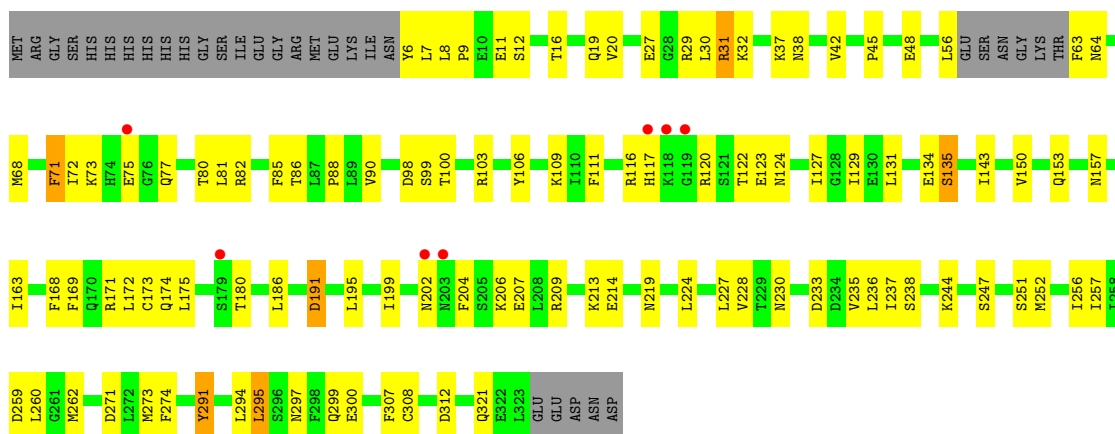


- Molecule 1: ATP phosphoribosyltransferase regulatory subunit

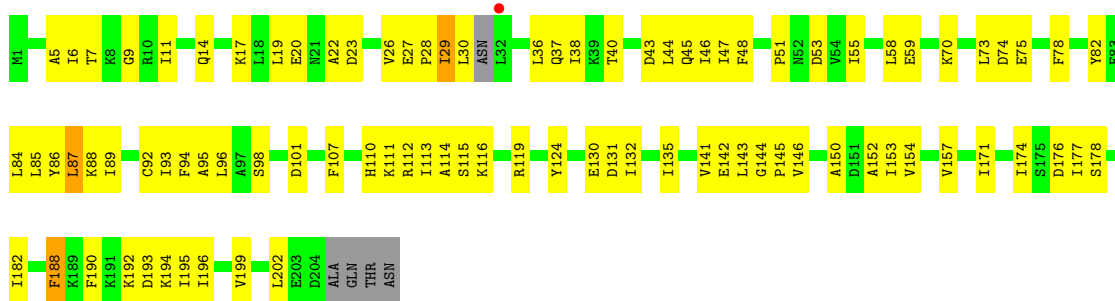




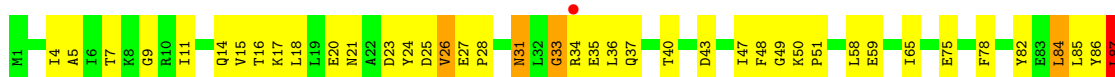
• Molecule 1: ATP phosphoribosyltransferase regulatory subunit

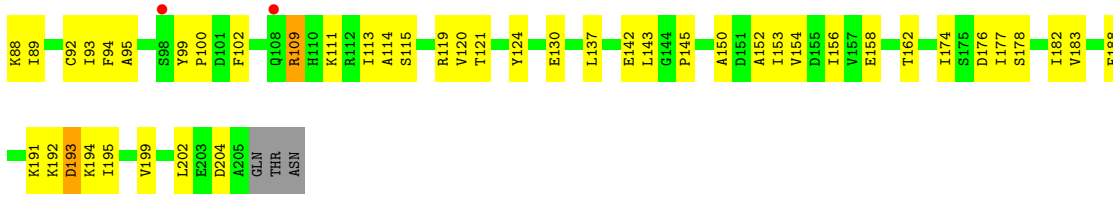


• Molecule 2: ATP phosphoribosyltransferase

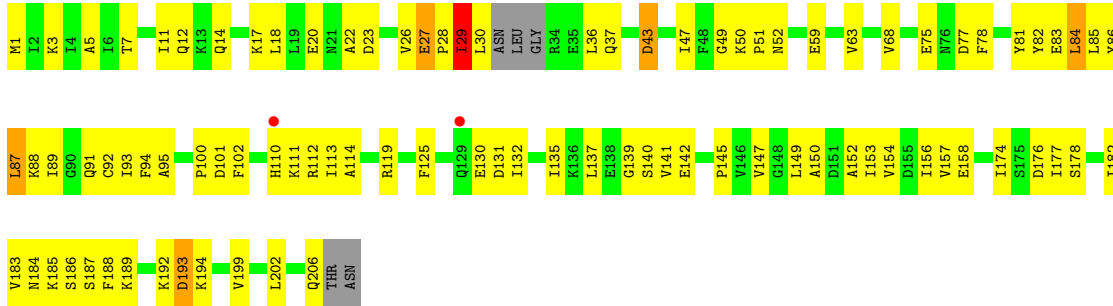


• Molecule 2: ATP phosphoribosyltransferase

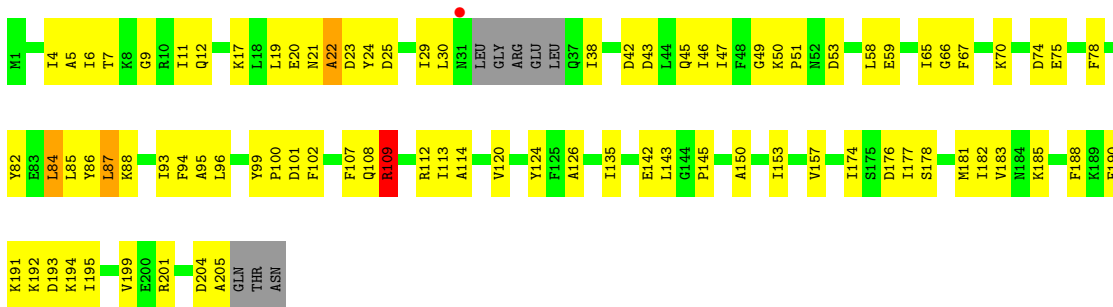




- Molecule 2: ATP phosphoribosyltransferase



- Molecule 2: ATP phosphoribosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	151.68Å 222.94Å 86.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.00 – 3.25 28.71 – 3.26	Depositor EDS
% Data completeness (in resolution range)	85.7 (29.00-3.25) 86.0 (28.71-3.26)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 3.24Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.247 , 0.301 0.229 , 0.280	Depositor DCC
R_{free} test set	1981 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	61.3	Xtrriage
Anisotropy	0.073	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	16750	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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: PRP, PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.53	1/2589 (0.0%)	0.67	3/3475 (0.1%)
1	B	0.47	0/2627	0.63	0/3526
1	C	0.47	0/2511	0.66	0/3370
1	D	0.43	0/2583	0.60	0/3466
2	E	0.57	1/1652 (0.1%)	0.73	5/2220 (0.2%)
2	F	0.43	0/1666	0.63	1/2241 (0.0%)
2	G	0.44	0/1654	0.66	1/2223 (0.0%)
2	H	0.46	0/1625	0.68	1/2185 (0.0%)
All	All	0.48	2/16907 (0.0%)	0.65	11/22706 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	E	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	29	ILE	C-N	-13.02	1.04	1.34
1	A	114	GLU	C-N	-5.85	1.20	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	GLU	C-N-CA	-7.37	103.27	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	29	ILE	CA-C-N	-7.03	101.73	117.20
2	E	188	PHE	CB-CG-CD1	6.77	125.54	120.80
2	E	188	PHE	CB-CG-CD2	-6.28	116.41	120.80
2	G	29	ILE	N-CA-C	-6.03	94.72	111.00
2	F	33	GLY	N-CA-C	5.67	127.27	113.10
1	A	114	GLU	CA-C-N	-5.50	105.10	117.20
1	A	116	ARG	C-N-CA	5.44	135.30	121.70
2	H	22	ALA	N-CA-C	-5.42	96.36	111.00
2	E	188	PHE	CB-CA-C	5.12	120.65	110.40
2	E	29	ILE	C-N-CA	-5.04	109.09	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	GLU	Mainchain
2	E	26	VAL	Mainchain
2	E	29	ILE	Mainchain

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	2547	0	2573	112	0
1	B	2584	0	2616	110	0
1	C	2472	0	2504	117	0
1	D	2541	0	2575	100	0
2	E	1630	0	1679	86	0
2	F	1643	0	1692	83	0
2	G	1632	0	1679	80	0
2	H	1603	0	1647	79	0
3	E	22	0	8	0	0
3	F	22	0	8	1	0
3	G	22	0	8	1	0
3	H	22	0	8	0	0
4	F	5	0	0	0	0
4	G	5	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	16750	0	16997	704	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (704) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:ARG:O	1:A:117:HIS:CD2	1.76	1.37
2:E:27:GLU:O	2:E:30:LEU:HG	1.24	1.28
1:A:116:ARG:C	1:A:117:HIS:CD2	2.08	1.25
1:A:116:ARG:O	1:A:117:HIS:CG	1.91	1.22
2:H:19:LEU:O	2:H:22:ALA:O	1.63	1.15
2:E:36:LEU:HD13	2:F:143:LEU:HG	1.29	1.13
1:D:73:LYS:HE3	1:D:75:GLU:HB3	1.39	1.04
1:C:173:CYS:HB3	1:C:180:THR:HG22	1.40	1.00
1:B:73:LYS:HE3	1:B:75:GLU:HB3	1.44	0.99
2:G:111:LYS:HE2	2:G:130:GLU:OE2	1.65	0.97
1:A:299:GLN:HG2	1:A:300:GLU:H	1.26	0.96
1:B:115:LYS:HG3	2:G:77:ASP:OD2	1.66	0.95
1:C:73:LYS:HE3	1:C:75:GLU:HB3	1.47	0.95
2:E:27:GLU:O	2:E:30:LEU:CG	2.14	0.95
1:C:299:GLN:HG2	1:C:300:GLU:H	1.32	0.94
1:A:116:ARG:HB3	1:A:117:HIS:CD2	2.04	0.93
2:H:87:LEU:HD23	2:H:87:LEU:H	1.32	0.93
1:A:73:LYS:HE3	1:A:75:GLU:HB3	1.50	0.92
2:E:86:TYR:HE1	2:E:178:SER:HG	0.98	0.92
2:G:59:GLU:HG3	2:G:78:PHE:CE1	2.06	0.91
1:D:173:CYS:HB3	1:D:180:THR:HG22	1.52	0.89
1:A:73:LYS:HE2	1:A:77:GLN:HB2	1.55	0.88
1:C:12:SER:HB2	1:D:45:PRO:HB2	1.55	0.88
2:H:86:TYR:HE1	2:H:178:SER:HG	1.17	0.87
1:A:116:ARG:HB3	1:A:117:HIS:NE2	1.89	0.87
2:E:36:LEU:CD1	2:F:143:LEU:HG	2.03	0.87
1:A:73:LYS:HG2	1:A:77:GLN:H	1.40	0.86
2:F:93:ILE:HG22	2:F:176:ASP:HA	1.57	0.85
2:E:36:LEU:HD13	2:F:143:LEU:CG	2.07	0.85
2:E:87:LEU:HD23	2:E:87:LEU:H	1.41	0.84
1:A:109:LYS:HD3	1:A:123:GLU:HG2	1.59	0.83
1:D:299:GLN:HG2	1:D:300:GLU:H	1.42	0.82
2:E:59:GLU:HG3	2:E:78:PHE:CE1	2.15	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:193:ASP:OD2	2:G:194:LYS:HG3	1.80	0.82
2:G:27:GLU:H	2:G:28:PRO:CD	1.92	0.81
1:B:199:ILE:HG21	1:B:209:ARG:HG3	1.62	0.81
2:F:86:TYR:HE1	2:F:178:SER:HG	1.26	0.80
2:F:195:ILE:O	2:F:199:VAL:HG23	1.82	0.80
1:A:90:VAL:HG13	1:A:295:LEU:HD22	1.64	0.80
1:C:73:LYS:HE2	1:C:77:GLN:HB2	1.62	0.80
2:H:193:ASP:OD2	2:H:194:LYS:HG3	1.82	0.80
2:E:111:LYS:HE2	2:E:130:GLU:OE2	1.82	0.80
2:F:59:GLU:HG3	2:F:78:PHE:CE1	2.17	0.80
2:F:111:LYS:HE2	2:F:130:GLU:OE2	1.82	0.80
2:G:86:TYR:HE1	2:G:178:SER:HG	1.29	0.79
1:C:199:ILE:HD13	1:C:209:ARG:HG3	1.64	0.79
1:D:202:ASN:HB2	1:D:204:PHE:HE1	1.47	0.78
1:C:45:PRO:HG3	1:D:8:LEU:HD11	1.64	0.78
1:A:299:GLN:HG2	1:A:300:GLU:N	1.99	0.78
1:C:81:LEU:HD11	1:D:81:LEU:HD21	1.64	0.78
1:C:193:SER:OG	2:H:86:TYR:HB3	1.85	0.77
1:C:199:ILE:HG21	1:C:209:ARG:HG3	1.67	0.77
2:E:113:ILE:HG23	2:E:153:ILE:HA	1.66	0.77
1:B:16:THR:HG23	1:B:19:GLN:H	1.51	0.75
1:C:131:LEU:HD21	1:C:134:GLU:HB3	1.68	0.75
1:A:173:CYS:HB3	1:A:180:THR:HG22	1.69	0.74
1:A:73:LYS:HE2	1:A:77:GLN:CB	2.18	0.74
2:F:193:ASP:OD2	2:F:194:LYS:HG3	1.87	0.74
2:G:86:TYR:HE1	2:G:178:SER:OG	1.70	0.74
1:B:48:GLU:HG2	1:B:52:LEU:HD22	1.70	0.74
1:D:56:LEU:HD21	1:D:63:PHE:CE1	2.23	0.73
2:E:195:ILE:O	2:E:199:VAL:HG23	1.89	0.73
1:A:199:ILE:HG21	1:A:209:ARG:HG3	1.69	0.73
2:F:18:LEU:HD23	2:F:202:LEU:HD22	1.70	0.73
2:H:86:TYR:CE2	2:H:88:LYS:HG2	2.24	0.72
1:B:73:LYS:HE2	1:B:77:GLN:HB2	1.71	0.72
2:E:86:TYR:HE1	2:E:178:SER:OG	1.71	0.72
2:F:16:THR:CG2	2:F:28:PRO:HG3	2.20	0.72
1:A:116:ARG:C	1:A:117:HIS:HD2	1.90	0.72
2:F:16:THR:HG22	2:F:28:PRO:HG3	1.72	0.72
1:A:299:GLN:CG	1:A:300:GLU:H	2.02	0.71
2:H:193:ASP:CG	2:H:194:LYS:H	1.93	0.71
2:G:87:LEU:HD23	2:G:87:LEU:H	1.55	0.71
1:A:116:ARG:CB	1:A:117:HIS:CD2	2.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:LEU:HD23	1:D:7:LEU:H	1.54	0.70
2:F:109:ARG:HG2	2:F:109:ARG:HH11	1.57	0.70
2:F:87:LEU:HD23	2:F:87:LEU:H	1.57	0.70
1:C:49:TYR:CE2	1:D:9:PRO:HB3	2.26	0.70
1:B:189:LYS:HE2	2:G:81:TYR:CE1	2.28	0.69
2:E:95:ALA:HA	2:E:174:ILE:HG12	1.74	0.69
2:E:193:ASP:OD2	2:E:194:LYS:HG3	1.92	0.69
2:G:189:LYS:NZ	4:G:1001:PO4:O2	2.22	0.69
1:B:30:LEU:HD21	1:B:150:VAL:HG13	1.75	0.68
1:A:73:LYS:HE2	1:A:77:GLN:CG	2.24	0.68
1:A:116:ARG:O	1:A:117:HIS:NE2	2.25	0.68
1:A:131:LEU:HD21	1:A:134:GLU:HB3	1.76	0.68
1:B:96:ILE:HG22	1:B:98:ASP:H	1.59	0.68
2:F:114:ALA:HB1	2:F:137:LEU:HD12	1.74	0.68
2:H:195:ILE:O	2:H:199:VAL:HG23	1.94	0.68
2:H:59:GLU:HG3	2:H:78:PHE:CE1	2.30	0.67
1:C:7:LEU:HG	2:G:131:ASP:HB2	1.77	0.67
1:D:8:LEU:HG	1:D:9:PRO:HD2	1.76	0.67
1:C:90:VAL:HG13	1:C:295:LEU:HD22	1.76	0.67
2:E:36:LEU:HB3	2:F:143:LEU:HD21	1.76	0.67
1:D:16:THR:HG23	1:D:19:GLN:H	1.60	0.66
1:D:73:LYS:HE2	1:D:77:GLN:HB2	1.77	0.66
1:C:173:CYS:CB	1:C:180:THR:HG22	2.22	0.66
2:E:36:LEU:CB	2:F:143:LEU:HD21	2.24	0.66
2:H:38:ILE:HD11	2:H:46:ILE:HB	1.77	0.66
1:B:293:GLN:O	1:B:296:SER:HB2	1.96	0.66
1:B:147:ALA:O	1:B:151:ILE:HG13	1.95	0.66
1:D:131:LEU:HD21	1:D:134:GLU:HB3	1.78	0.66
1:C:73:LYS:HE2	1:C:77:GLN:CB	2.25	0.66
2:E:30:LEU:HD22	2:E:38:ILE:HG12	1.78	0.66
1:B:30:LEU:CD2	1:B:150:VAL:HG13	2.26	0.66
1:C:45:PRO:HB2	1:D:12:SER:HB2	1.78	0.66
1:A:224:LEU:HD22	1:A:260:LEU:HD12	1.76	0.66
1:A:20:VAL:HG22	1:B:43:MET:HG3	1.78	0.65
2:F:25:ASP:O	2:F:27:GLU:HG2	1.96	0.65
2:G:113:ILE:HG21	2:G:154:VAL:HG23	1.79	0.65
2:H:96:LEU:HD12	2:H:153:ILE:O	1.96	0.65
1:A:320:ARG:O	1:A:320:ARG:HG2	1.95	0.65
1:C:73:LYS:HE2	1:C:77:GLN:CG	2.26	0.65
1:C:71:PHE:HE2	1:D:71:PHE:HE2	1.44	0.64
1:C:81:LEU:HB3	1:C:111:PHE:CD1	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:ILE:CD1	1:A:146:LEU:HD13	2.27	0.64
2:G:18:LEU:HD23	2:G:202:LEU:HD22	1.79	0.64
1:B:117:HIS:O	1:B:118:LYS:CG	2.46	0.64
2:G:93:ILE:HG13	2:G:157:VAL:O	1.98	0.64
2:H:30:LEU:HD11	2:H:38:ILE:HG23	1.78	0.64
2:F:84:LEU:HD12	2:F:183:VAL:HG21	1.78	0.64
1:C:71:PHE:HD2	1:D:71:PHE:HD2	1.45	0.64
1:D:202:ASN:HB2	1:D:204:PHE:CE1	2.31	0.63
2:F:86:TYR:HE1	2:F:178:SER:OG	1.81	0.63
2:G:95:ALA:HA	2:G:174:ILE:HG12	1.79	0.63
1:B:163:ILE:HG22	1:B:274:PHE:HB3	1.79	0.63
2:E:38:ILE:HD11	2:E:46:ILE:HB	1.79	0.63
1:D:291:TYR:CD1	1:D:294:LEU:HD12	2.34	0.63
1:D:109:LYS:HE2	1:D:123:GLU:HB3	1.80	0.62
2:F:58:LEU:C	2:F:58:LEU:HD23	2.20	0.62
1:B:206:LYS:HD3	1:B:206:LYS:C	2.20	0.62
1:C:45:PRO:O	1:C:82:ARG:HG3	2.00	0.62
1:A:71:PHE:CE1	1:A:79:ILE:HD11	2.34	0.62
1:A:116:ARG:C	1:A:117:HIS:CG	2.49	0.62
1:B:72:ILE:HG13	1:D:71:PHE:HA	1.82	0.62
1:A:131:LEU:C	1:A:131:LEU:HD23	2.20	0.61
1:C:42:VAL:HG11	1:C:89:LEU:HD22	1.81	0.61
1:D:199:ILE:HD13	1:D:209:ARG:HG3	1.80	0.61
1:B:29:ARG:HD2	1:B:153:GLN:OE1	2.01	0.61
2:F:37:GLN:HE21	2:F:47:ILE:HD11	1.65	0.61
2:G:85:LEU:HG	2:G:86:TYR:N	2.16	0.61
2:E:28:PRO:C	2:E:30:LEU:N	2.54	0.61
2:F:193:ASP:CG	2:F:194:LYS:H	2.03	0.61
2:H:94:PHE:CD1	2:H:177:ILE:HD11	2.36	0.61
1:D:202:ASN:O	1:D:204:PHE:HD1	1.84	0.61
2:H:58:LEU:HD13	2:H:182:ILE:HG13	1.82	0.60
2:H:84:LEU:HD12	2:H:183:VAL:HG21	1.82	0.60
1:A:16:THR:HG23	1:A:19:GLN:H	1.66	0.60
2:F:109:ARG:HG2	2:F:109:ARG:NH1	2.16	0.60
2:G:27:GLU:N	2:G:28:PRO:CD	2.61	0.60
1:C:224:LEU:HD22	1:C:260:LEU:HD12	1.82	0.60
1:C:129:ILE:HD11	1:C:307:PHE:CE2	2.36	0.60
1:A:71:PHE:CE2	1:B:71:PHE:CE2	2.90	0.60
1:B:173:CYS:HB3	1:B:180:THR:HG22	1.84	0.60
2:G:142:GLU:O	2:G:145:PRO:HD2	2.02	0.60
1:C:81:LEU:CD1	1:D:81:LEU:HD21	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:145:PRO:HA	2:F:150:ALA:O	2.01	0.60
2:G:113:ILE:HG23	2:G:153:ILE:HA	1.84	0.60
1:D:206:LYS:HD3	1:D:206:LYS:C	2.21	0.60
2:G:86:TYR:HE1	2:G:178:SER:CB	2.14	0.60
1:A:154:LEU:HD13	1:A:314:ILE:HD13	1.84	0.60
2:F:188:PHE:CE2	2:F:192:LYS:HE2	2.37	0.60
1:A:71:PHE:CD1	1:A:79:ILE:HD11	2.37	0.59
1:B:131:LEU:HD21	1:B:134:GLU:HB3	1.84	0.59
2:F:191:LYS:O	2:F:195:ILE:HG12	2.01	0.59
2:H:85:LEU:HG	2:H:86:TYR:N	2.17	0.59
2:G:84:LEU:HD12	2:G:183:VAL:HG21	1.83	0.59
2:H:188:PHE:O	2:H:192:LYS:HB2	2.01	0.59
1:A:73:LYS:CE	1:A:77:GLN:HB2	2.28	0.59
1:B:6:TYR:HB2	1:B:7:LEU:HD12	1.84	0.59
2:G:185:LYS:O	2:G:189:LYS:HG2	2.02	0.59
2:H:38:ILE:HD12	2:H:38:ILE:C	2.23	0.59
1:B:73:LYS:HE2	1:B:77:GLN:CB	2.32	0.59
2:E:143:LEU:HG	2:F:36:LEU:HD13	1.84	0.59
1:B:150:VAL:O	1:B:154:LEU:HG	2.03	0.59
2:H:188:PHE:CE2	2:H:192:LYS:HE2	2.37	0.59
1:C:71:PHE:CE2	1:D:71:PHE:HE2	2.21	0.59
2:F:87:LEU:O	2:F:89:ILE:HG12	2.02	0.59
1:C:204:PHE:O	1:C:209:ARG:NH2	2.36	0.58
1:D:124:ASN:HA	1:D:312:ASP:OD2	2.02	0.58
1:D:90:VAL:HG13	1:D:295:LEU:HD22	1.83	0.58
2:E:38:ILE:HD12	2:E:38:ILE:C	2.24	0.58
2:F:75:GLU:OE1	2:F:120:VAL:HG23	2.02	0.58
2:E:94:PHE:CD1	2:E:177:ILE:HD11	2.38	0.58
2:G:125:PHE:CD1	2:G:132:ILE:HD13	2.38	0.58
2:H:93:ILE:O	2:H:93:ILE:HD12	2.03	0.58
2:E:7:THR:OG1	2:E:11:ILE:HB	2.03	0.58
2:H:65:ILE:HD13	2:H:181:MET:HE3	1.84	0.58
1:A:49:TYR:CD2	1:B:9:PRO:HG3	2.38	0.58
2:H:93:ILE:HG22	2:H:176:ASP:HA	1.86	0.58
2:G:113:ILE:HD12	2:G:113:ILE:N	2.19	0.58
2:H:17:LYS:HE3	2:H:21:ASN:HD21	1.68	0.58
2:E:111:LYS:HE2	2:E:130:GLU:CD	2.25	0.58
2:G:29:ILE:HB	2:G:30:LEU:HD12	1.86	0.57
2:F:7:THR:HA	2:F:49:GLY:O	2.03	0.57
2:G:36:LEU:HD23	2:H:143:LEU:HG	1.85	0.57
1:C:49:TYR:CZ	1:D:9:PRO:HB3	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:LYS:HD3	1:C:206:LYS:C	2.24	0.57
1:C:275:LYS:HD3	1:C:277:TYR:CE1	2.39	0.57
1:D:199:ILE:HG21	1:D:209:ARG:HG3	1.86	0.57
2:E:188:PHE:O	2:E:192:LYS:HB2	2.05	0.57
1:C:37:LYS:O	1:C:38:ASN:HB2	2.05	0.57
1:C:219:ASN:HB3	1:C:258:ILE:O	2.05	0.57
1:B:237:ILE:HG13	1:B:238:SER:N	2.19	0.57
1:B:73:LYS:HE2	1:B:77:GLN:CG	2.35	0.57
1:B:129:ILE:HD11	1:B:307:PHE:CE2	2.40	0.57
1:C:12:SER:HB2	1:D:45:PRO:CB	2.31	0.57
1:C:71:PHE:HD2	1:D:71:PHE:CD2	2.22	0.57
1:C:283:GLN:HB3	1:C:284:PRO:HD2	1.86	0.57
2:H:86:TYR:HE1	2:H:178:SER:OG	1.85	0.57
1:B:175:LEU:HD11	1:B:233:ASP:OD1	2.05	0.57
2:E:14:GLN:HE21	2:E:89:ILE:HD12	1.70	0.57
2:H:7:THR:OG1	2:H:11:ILE:HB	2.04	0.57
2:H:38:ILE:HD12	2:H:38:ILE:O	2.05	0.57
1:C:71:PHE:HE2	1:D:71:PHE:CE2	2.23	0.57
1:D:56:LEU:HD11	1:D:63:PHE:CG	2.39	0.56
1:C:124:ASN:HA	1:C:312:ASP:OD2	2.06	0.56
1:C:71:PHE:CE2	1:D:71:PHE:CE2	2.93	0.56
1:C:71:PHE:CD2	1:D:71:PHE:HD2	2.22	0.56
1:D:116:ARG:HG3	1:D:117:HIS:CD2	2.40	0.56
2:F:95:ALA:HA	2:F:174:ILE:HG12	1.88	0.56
2:F:113:ILE:HG23	2:F:153:ILE:HA	1.88	0.56
2:G:87:LEU:HA	2:G:206:GLN:NE2	2.20	0.56
1:D:27:GLU:HG2	1:D:127:ILE:HD11	1.88	0.56
2:H:86:TYR:CZ	2:H:88:LYS:HG2	2.40	0.56
1:B:58:SER:HB3	1:B:266:MET:HA	1.85	0.56
2:F:7:THR:OG1	2:F:11:ILE:HB	2.06	0.56
1:B:11:GLU:C	1:B:122:THR:HG21	2.26	0.56
1:A:175:LEU:HD11	1:A:233:ASP:OD1	2.06	0.56
1:C:71:PHE:CD2	1:D:71:PHE:CD2	2.94	0.56
2:H:145:PRO:HA	2:H:150:ALA:O	2.06	0.56
1:A:217:ILE:HB	2:E:196:ILE:HD11	1.88	0.56
1:C:192:LEU:HD12	2:H:84:LEU:HA	1.88	0.56
1:D:29:ARG:HD2	1:D:153:GLN:OE1	2.07	0.56
2:H:86:TYR:HE1	2:H:178:SER:CB	2.18	0.56
2:H:193:ASP:CG	2:H:194:LYS:N	2.60	0.56
1:A:20:VAL:CG2	1:B:43:MET:HG3	2.36	0.55
2:H:58:LEU:CD1	2:H:182:ILE:HG13	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLU:O	1:A:321:GLN:N	2.40	0.55
1:B:224:LEU:O	1:B:228:VAL:HG23	2.07	0.55
1:C:71:PHE:CE1	1:C:79:ILE:HD11	2.41	0.55
2:F:31:ASN:OD1	2:F:35:GLU:HG2	2.07	0.55
1:B:117:HIS:O	1:B:118:LYS:HG3	2.06	0.55
1:D:224:LEU:HD22	1:D:260:LEU:HD12	1.88	0.55
1:A:233:ASP:O	1:A:237:ILE:HG23	2.07	0.55
1:B:16:THR:HG22	1:B:19:GLN:HG3	1.89	0.55
1:C:299:GLN:HG2	1:C:300:GLU:N	2.13	0.55
2:G:189:LYS:HZ1	4:G:1001:PO4:P	2.30	0.55
2:F:86:TYR:HE1	2:F:178:SER:CB	2.19	0.55
1:B:85:PHE:O	1:B:88:PRO:HG2	2.07	0.54
1:C:16:THR:HG23	1:C:19:GLN:H	1.71	0.54
1:D:244:LYS:O	1:D:247:SER:HB3	2.07	0.54
2:F:58:LEU:CD1	2:F:182:ILE:HG13	2.37	0.54
1:C:69:PHE:O	1:C:80:THR:HG23	2.07	0.54
1:B:23:LEU:HB2	1:B:315:LEU:HD11	1.89	0.54
2:H:124:TYR:CG	2:H:174:ILE:HD12	2.43	0.54
1:A:45:PRO:O	1:A:82:ARG:HG3	2.07	0.54
1:A:86:THR:O	1:A:90:VAL:HG23	2.07	0.54
2:H:86:TYR:O	2:H:86:TYR:CG	2.58	0.54
1:A:12:SER:HB2	1:B:45:PRO:HB2	1.88	0.54
1:D:37:LYS:O	1:D:38:ASN:HB2	2.08	0.54
2:G:7:THR:OG1	2:G:11:ILE:HB	2.08	0.54
2:H:113:ILE:HD12	2:H:113:ILE:N	2.22	0.54
1:A:129:ILE:HD13	1:A:146:LEU:HD13	1.88	0.54
1:B:16:THR:CG2	1:B:19:GLN:HG3	2.38	0.54
1:D:169:PHE:O	1:D:172:LEU:HB3	2.08	0.54
1:D:168:PHE:CE2	1:D:260:LEU:HB3	2.43	0.53
1:D:299:GLN:HG2	1:D:300:GLU:N	2.17	0.53
2:E:86:TYR:HE1	2:E:178:SER:CB	2.20	0.53
2:F:124:TYR:CG	2:F:174:ILE:HD12	2.44	0.53
2:E:116:LYS:HG2	2:E:116:LYS:O	2.08	0.53
2:E:58:LEU:HD13	2:E:182:ILE:HG13	1.91	0.53
1:A:319:GLU:C	1:A:321:GLN:H	2.10	0.53
1:B:16:THR:HG22	1:B:19:GLN:CG	2.39	0.53
2:G:147:VAL:HG23	2:G:149:LEU:H	1.73	0.53
2:G:7:THR:HG22	2:G:51:PRO:HA	1.90	0.53
2:G:37:GLN:HB3	2:G:47:ILE:HG12	1.89	0.53
1:C:94:SER:C	1:C:96:ILE:H	2.12	0.53
1:C:275:LYS:HA	1:C:286:LEU:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:143:LEU:HD21	2:F:36:LEU:HB2	1.91	0.53
2:E:193:ASP:CG	2:E:194:LYS:H	2.11	0.53
2:G:188:PHE:O	2:G:192:LYS:HB2	2.09	0.53
2:E:143:LEU:O	2:E:144:GLY:C	2.46	0.53
1:A:71:PHE:HE2	1:B:71:PHE:CE2	2.25	0.53
1:C:79:ILE:HD13	1:D:11:GLU:HG3	1.90	0.53
1:D:68:MET:HB2	1:D:80:THR:HG21	1.92	0.53
1:B:299:GLN:HG2	1:B:300:GLU:H	1.73	0.52
2:H:112:ARG:C	2:H:113:ILE:HD12	2.29	0.52
1:A:116:ARG:O	1:A:117:HIS:CE1	2.62	0.52
2:E:114:ALA:HA	2:E:135:ILE:O	2.10	0.52
1:D:116:ARG:HG3	1:D:117:HIS:HD2	1.74	0.52
1:B:90:VAL:HG13	1:B:295:LEU:HD22	1.92	0.52
1:C:81:LEU:HD21	1:D:81:LEU:HD11	1.91	0.52
1:A:124:ASN:HA	1:A:312:ASP:OD2	2.09	0.52
1:B:71:PHE:HA	1:D:72:ILE:HG13	1.92	0.52
1:C:157:ASN:OD1	1:C:321:GLN:NE2	2.43	0.52
1:C:233:ASP:O	1:C:237:ILE:HG23	2.10	0.52
1:D:85:PHE:O	1:D:88:PRO:HG2	2.10	0.52
1:B:224:LEU:HD22	1:B:260:LEU:HD12	1.91	0.52
1:C:16:THR:O	1:C:19:GLN:N	2.41	0.52
2:H:5:ALA:HA	2:H:47:ILE:O	2.10	0.52
2:H:17:LYS:O	2:H:20:GLU:HB3	2.10	0.52
1:B:157:ASN:OD1	1:B:321:GLN:NE2	2.43	0.52
1:B:206:LYS:HA	1:B:209:ARG:NH1	2.24	0.51
1:C:169:PHE:O	1:C:172:LEU:HB3	2.10	0.51
2:F:50:LYS:HB3	2:F:51:PRO:HD2	1.92	0.51
2:G:93:ILE:HG22	2:G:176:ASP:HA	1.92	0.51
1:D:56:LEU:HD11	1:D:63:PHE:CD1	2.45	0.51
2:E:87:LEU:HD12	2:E:89:ILE:HD12	1.93	0.51
1:C:43:MET:SD	1:D:20:VAL:HG13	2.51	0.51
1:C:192:LEU:HD12	2:H:84:LEU:CA	2.41	0.51
1:C:39:TYR:CD2	1:C:103:ARG:HB3	2.44	0.51
2:F:27:GLU:N	2:F:28:PRO:CD	2.74	0.51
2:F:86:TYR:CG	2:F:86:TYR:O	2.63	0.51
2:G:50:LYS:HB3	2:G:51:PRO:HD2	1.93	0.51
2:H:86:TYR:HE1	2:H:178:SER:HB3	1.76	0.51
2:H:108:GLN:O	2:H:109:ARG:HB3	2.10	0.51
1:B:69:PHE:O	1:B:80:THR:HG23	2.10	0.51
2:F:37:GLN:NE2	2:F:47:ILE:HD11	2.25	0.51
2:E:113:ILE:HD13	2:E:132:ILE:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:15:VAL:O	2:F:16:THR:C	2.50	0.50
2:E:22:ALA:O	2:E:23:ASP:HB2	2.11	0.50
1:D:81:LEU:HB3	1:D:111:PHE:HD1	1.76	0.50
2:H:66:GLY:O	2:H:182:ILE:HG12	2.11	0.50
1:A:157:ASN:OD1	1:A:321:GLN:NE2	2.44	0.50
1:D:206:LYS:HD3	1:D:206:LYS:O	2.12	0.50
1:B:48:GLU:CG	1:B:52:LEU:HD22	2.41	0.50
1:C:73:LYS:HG2	1:C:77:GLN:H	1.76	0.50
2:G:86:TYR:CE1	2:G:178:SER:OG	2.53	0.50
1:A:93:TYR:CD2	1:A:295:LEU:HD11	2.47	0.50
1:B:109:LYS:HA	1:B:124:ASN:O	2.11	0.50
1:B:262:MET:SD	1:B:273:MET:HG3	2.52	0.50
1:A:206:LYS:HD3	1:A:206:LYS:C	2.32	0.50
1:B:170:GLN:O	1:B:173:CYS:HB2	2.12	0.50
2:F:114:ALA:HB1	2:F:137:LEU:CD1	2.41	0.50
1:A:81:LEU:HB3	1:A:111:PHE:CD1	2.47	0.49
1:A:146:LEU:O	1:A:150:VAL:HG23	2.12	0.49
1:D:206:LYS:HA	1:D:209:ARG:NH1	2.27	0.49
1:C:31:ARG:HG3	1:C:31:ARG:HH11	1.77	0.49
1:C:93:TYR:HD2	1:C:295:LEU:HD11	1.77	0.49
1:C:131:LEU:C	1:C:131:LEU:HD23	2.32	0.49
2:E:36:LEU:HB2	2:F:143:LEU:HD21	1.94	0.49
1:A:30:LEU:HD21	1:A:150:VAL:HG13	1.93	0.49
1:D:157:ASN:OD1	1:D:321:GLN:NE2	2.45	0.49
2:E:14:GLN:NE2	2:E:89:ILE:HD12	2.27	0.49
2:F:16:THR:HG21	2:F:28:PRO:HG3	1.95	0.49
1:B:7:LEU:HD21	2:H:126:ALA:HA	1.95	0.49
1:C:27:GLU:HG2	1:C:127:ILE:HD11	1.94	0.49
1:D:31:ARG:HH11	1:D:31:ARG:HG3	1.78	0.49
2:E:112:ARG:O	2:E:150:ALA:HB1	2.13	0.49
1:C:85:PHE:O	1:C:88:PRO:HG2	2.13	0.49
2:F:4:ILE:HA	2:F:65:ILE:O	2.12	0.49
2:G:7:THR:HA	2:G:49:GLY:O	2.12	0.49
1:B:207:GLU:H	1:B:207:GLU:CD	2.15	0.49
1:C:81:LEU:HB3	1:C:111:PHE:HD1	1.73	0.49
1:D:131:LEU:C	1:D:131:LEU:HD23	2.33	0.49
2:G:75:GLU:OE2	2:G:119:ARG:HB2	2.13	0.49
2:H:85:LEU:CG	2:H:86:TYR:N	2.76	0.49
1:D:30:LEU:HD21	1:D:150:VAL:HG13	1.95	0.48
1:D:171:ARG:HG2	1:D:235:VAL:HB	1.94	0.48
2:E:92:CYS:O	2:E:93:ILE:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:93:ILE:HA	2:F:177:ILE:HG12	1.94	0.48
1:B:16:THR:O	1:B:17:LEU:C	2.51	0.48
1:B:68:MET:HB2	1:B:80:THR:HG21	1.94	0.48
2:G:29:ILE:C	2:G:30:LEU:HD12	2.34	0.48
1:A:193:SER:OG	2:E:86:TYR:HB3	2.13	0.48
2:F:25:ASP:HB3	2:F:40:THR:HB	1.95	0.48
2:G:27:GLU:H	2:G:28:PRO:HD2	1.76	0.48
1:B:206:LYS:HD3	1:B:206:LYS:O	2.12	0.48
2:G:27:GLU:H	2:G:28:PRO:HD3	1.75	0.48
1:B:72:ILE:HG22	1:B:76:GLY:HA2	1.95	0.48
2:F:27:GLU:HA	2:F:27:GLU:OE2	2.12	0.48
2:G:112:ARG:HG3	2:G:150:ALA:HA	1.96	0.48
2:H:114:ALA:HA	2:H:135:ILE:O	2.14	0.48
1:A:85:PHE:O	1:A:88:PRO:HG2	2.14	0.48
1:A:116:ARG:CA	1:A:117:HIS:CD2	2.93	0.48
1:A:217:ILE:HB	2:E:196:ILE:CD1	2.44	0.48
1:A:317:ALA:O	1:A:321:GLN:HB2	2.14	0.48
1:B:171:ARG:HG2	1:B:235:VAL:HB	1.96	0.48
1:D:86:THR:O	1:D:90:VAL:HG23	2.13	0.48
2:G:30:LEU:HD12	2:G:30:LEU:N	2.28	0.48
1:A:72:ILE:HG22	1:A:73:LYS:N	2.29	0.48
1:D:214:GLU:HG2	1:D:227:LEU:HD11	1.96	0.48
2:E:112:ARG:HG3	2:E:150:ALA:HA	1.95	0.48
1:A:134:GLU:HG3	1:A:135:SER:N	2.29	0.48
1:A:319:GLU:C	1:A:321:GLN:N	2.67	0.48
1:C:148:LEU:HD11	1:C:256:ILE:HD11	1.96	0.48
2:F:75:GLU:CD	2:F:119:ARG:HB2	2.34	0.48
2:G:92:CYS:O	2:G:93:ILE:HG23	2.14	0.48
1:A:23:LEU:HD11	1:A:125:TYR:CE2	2.49	0.48
1:D:186:LEU:CD2	1:D:191:ASP:HB3	2.44	0.48
2:E:93:ILE:HG13	2:E:157:VAL:O	2.14	0.48
2:G:5:ALA:HA	2:G:47:ILE:O	2.14	0.47
1:A:10:GLU:O	1:A:10:GLU:HG3	2.13	0.47
1:A:73:LYS:HG3	1:A:76:GLY:H	1.79	0.47
1:C:7:LEU:C	1:C:8:LEU:HD12	2.35	0.47
1:C:244:LYS:O	1:C:247:SER:HB3	2.13	0.47
1:B:117:HIS:O	1:B:118:LYS:HG2	2.14	0.47
1:D:209:ARG:HG2	1:D:213:LYS:HE2	1.96	0.47
2:F:93:ILE:O	2:F:156:ILE:HA	2.13	0.47
2:G:7:THR:CG2	2:G:68:VAL:HG12	2.44	0.47
2:H:70:LYS:HE3	2:H:74:ASP:OD1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:7:THR:HA	2:H:49:GLY:O	2.15	0.47
1:A:131:LEU:HD21	1:A:134:GLU:CB	2.42	0.47
1:C:86:THR:O	1:C:90:VAL:HG23	2.14	0.47
1:C:93:TYR:CD2	1:C:295:LEU:HD11	2.49	0.47
1:C:173:CYS:O	1:C:176:ALA:N	2.43	0.47
2:F:113:ILE:N	2:F:113:ILE:HD12	2.30	0.47
1:A:103:ARG:HG2	1:A:103:ARG:HH11	1.78	0.47
1:C:68:MET:HB2	1:C:80:THR:CG2	2.44	0.47
1:C:108:GLY:O	1:C:126:GLN:N	2.45	0.47
1:C:134:GLU:HG3	1:C:135:SER:N	2.29	0.47
2:E:87:LEU:HD12	2:E:89:ILE:CD1	2.45	0.47
2:G:14:GLN:NE2	2:G:89:ILE:HB	2.29	0.47
1:A:279:SER:HA	2:E:190:PHE:CE1	2.49	0.47
1:C:71:PHE:HE1	1:C:79:ILE:HD11	1.78	0.47
1:D:81:LEU:O	1:D:82:ARG:C	2.53	0.47
1:D:262:MET:SD	1:D:273:MET:HG3	2.55	0.47
2:G:18:LEU:CD2	2:G:202:LEU:HD22	2.44	0.47
2:H:99:TYR:O	2:H:102:PHE:HB2	2.14	0.47
1:B:73:LYS:HG2	1:B:77:GLN:H	1.79	0.47
1:C:262:MET:SD	1:C:273:MET:HG3	2.55	0.47
2:E:17:LYS:O	2:E:20:GLU:HB3	2.15	0.47
2:E:55:ILE:HD11	2:E:73:LEU:HD23	1.96	0.47
2:F:82:TYR:O	2:F:182:ILE:HA	2.14	0.47
2:H:113:ILE:HG23	2:H:153:ILE:HA	1.96	0.47
1:A:275:LYS:HA	1:A:286:LEU:O	2.15	0.47
1:C:16:THR:O	1:C:17:LEU:C	2.54	0.47
1:C:299:GLN:CG	1:C:300:GLU:H	2.10	0.47
2:E:70:LYS:HE3	2:E:74:ASP:OD1	2.15	0.47
2:E:82:TYR:O	2:E:182:ILE:HA	2.15	0.47
2:F:4:ILE:HG12	2:F:65:ILE:HB	1.96	0.47
2:F:84:LEU:CD1	2:F:183:VAL:HG21	2.45	0.47
2:H:142:GLU:O	2:H:145:PRO:HD2	2.15	0.47
1:B:71:PHE:HA	1:D:72:ILE:CG1	2.46	0.46
1:B:72:ILE:CG1	1:D:71:PHE:HA	2.45	0.46
1:D:68:MET:HB2	1:D:80:THR:CG2	2.45	0.46
2:E:113:ILE:HG21	2:E:154:VAL:HG23	1.97	0.46
2:F:94:PHE:CD1	2:F:177:ILE:HD11	2.50	0.46
2:H:85:LEU:HG	2:H:86:TYR:H	1.80	0.46
1:B:124:ASN:HA	1:B:312:ASP:OD2	2.15	0.46
1:D:7:LEU:H	1:D:7:LEU:CD2	2.27	0.46
1:C:8:LEU:HB3	1:C:12:SER:OG	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:115:SER:HA	2:E:141:VAL:HG11	1.95	0.46
2:E:143:LEU:HD21	2:F:36:LEU:CB	2.44	0.46
1:C:48:GLU:HG2	1:C:52:LEU:HD22	1.95	0.46
2:E:111:LYS:CE	2:E:130:GLU:OE2	2.59	0.46
2:F:7:THR:HG22	2:F:51:PRO:HA	1.98	0.46
2:F:121:THR:HG23	2:F:154:VAL:HG21	1.98	0.46
1:C:45:PRO:CB	1:D:12:SER:HB2	2.44	0.46
2:E:95:ALA:CA	2:E:174:ILE:HG12	2.45	0.46
2:G:112:ARG:C	2:G:113:ILE:HD12	2.36	0.46
2:G:193:ASP:CG	2:G:194:LYS:H	2.18	0.46
1:A:226:ASN:O	1:A:228:VAL:N	2.48	0.46
1:B:54:THR:C	1:B:56:LEU:H	2.19	0.46
2:G:85:LEU:CG	2:G:86:TYR:N	2.79	0.46
2:E:47:ILE:HG22	2:E:48:PHE:N	2.30	0.46
2:H:38:ILE:C	2:H:38:ILE:CD1	2.84	0.46
1:B:58:SER:HA	1:B:267:ASP:HB3	1.98	0.46
1:C:16:THR:HG22	1:C:19:GLN:HG3	1.97	0.46
2:F:85:LEU:HG	2:F:86:TYR:N	2.30	0.46
1:C:199:ILE:HG21	1:C:209:ARG:CG	2.43	0.46
2:G:184:ASN:O	2:G:187:SER:HB2	2.15	0.46
1:A:73:LYS:HG2	1:A:77:GLN:N	2.20	0.46
1:C:279:SER:HA	2:H:190:PHE:CE1	2.51	0.46
1:D:45:PRO:HG2	1:D:48:GLU:OE1	2.16	0.46
1:A:16:THR:HG22	1:A:19:GLN:OE1	2.16	0.45
1:A:24:ARG:HE	1:B:41:GLU:CD	2.20	0.45
1:A:73:LYS:HE2	1:A:77:GLN:HG2	1.99	0.45
1:B:58:SER:HA	1:B:267:ASP:CB	2.46	0.45
2:G:94:PHE:CE2	2:G:156:ILE:HG23	2.51	0.45
2:H:7:THR:O	2:H:12:GLN:HB2	2.16	0.45
1:C:37:LYS:NZ	1:C:149:GLN:HE22	2.14	0.45
2:G:95:ALA:CA	2:G:174:ILE:HG12	2.46	0.45
1:A:16:THR:O	1:A:17:LEU:C	2.55	0.45
1:A:81:LEU:O	1:A:82:ARG:C	2.54	0.45
2:H:100:PRO:C	2:H:102:PHE:H	2.19	0.45
1:C:206:LYS:HD3	1:C:206:LYS:O	2.17	0.45
2:E:5:ALA:HA	2:E:47:ILE:O	2.16	0.45
2:E:53:ASP:OD1	2:F:137:LEU:HA	2.17	0.45
2:H:75:GLU:OE1	2:H:120:VAL:HG23	2.16	0.45
1:B:189:LYS:C	1:B:191:ASP:N	2.67	0.45
1:C:49:TYR:O	1:C:50:THR:C	2.55	0.45
1:C:94:SER:O	1:C:96:ILE:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:LEU:O	1:A:225:GLU:C	2.55	0.45
1:C:52:LEU:C	1:C:54:THR:H	2.19	0.45
1:C:131:LEU:HD23	1:C:131:LEU:O	2.17	0.45
1:D:56:LEU:HD21	1:D:63:PHE:CZ	2.51	0.45
2:G:17:LYS:O	2:G:20:GLU:N	2.49	0.45
1:A:176:ALA:HA	1:A:204:PHE:CZ	2.51	0.45
1:B:283:GLN:OE1	1:B:283:GLN:HA	2.17	0.45
2:H:23:ASP:O	2:H:201:ARG:NH2	2.50	0.45
1:B:131:LEU:HD23	1:B:131:LEU:C	2.37	0.45
1:D:48:GLU:OE2	1:D:48:GLU:HA	2.17	0.45
1:D:175:LEU:HD11	1:D:233:ASP:OD1	2.17	0.45
2:E:37:GLN:HE21	2:E:45:GLN:NE2	2.15	0.45
2:E:93:ILE:HG22	2:E:176:ASP:HA	1.98	0.45
1:C:311:MET:O	1:C:312:ASP:C	2.55	0.45
1:D:237:ILE:HG13	1:D:238:SER:N	2.32	0.45
2:H:4:ILE:O	2:H:46:ILE:HA	2.17	0.45
1:B:81:LEU:O	1:B:82:ARG:C	2.55	0.44
1:C:291:TYR:CD1	1:C:294:LEU:HD12	2.52	0.44
2:F:92:CYS:O	2:F:93:ILE:HG23	2.18	0.44
2:G:125:PHE:CD1	2:G:132:ILE:CD1	2.99	0.44
1:A:69:PHE:CZ	1:A:113:LYS:HG2	2.52	0.44
1:B:317:ALA:O	1:B:321:GLN:HB2	2.17	0.44
2:E:92:CYS:O	2:E:93:ILE:CG2	2.65	0.44
1:A:162:GLU:O	1:A:274:PHE:HB2	2.17	0.44
2:H:191:LYS:O	2:H:195:ILE:HG12	2.18	0.44
1:B:256:ILE:HG22	1:B:257:ILE:N	2.33	0.44
1:D:207:GLU:HG2	1:D:230:ASN:O	2.18	0.44
1:A:49:TYR:CZ	1:B:9:PRO:HA	2.52	0.44
1:C:49:TYR:O	1:C:51:GLN:N	2.51	0.44
2:E:85:LEU:HG	2:E:86:TYR:N	2.33	0.44
1:A:71:PHE:CD2	1:B:71:PHE:CD2	3.06	0.44
2:F:47:ILE:HG22	2:F:48:PHE:N	2.33	0.44
1:A:57:GLU:HB3	1:A:63:PHE:CE1	2.53	0.44
1:A:300:GLU:OE1	1:A:300:GLU:HA	2.17	0.44
1:B:319:GLU:C	1:B:321:GLN:N	2.71	0.44
2:E:142:GLU:O	2:E:145:PRO:HD2	2.17	0.44
2:H:7:THR:HG22	2:H:51:PRO:HA	1.99	0.44
1:A:71:PHE:CE2	1:B:71:PHE:HE2	2.33	0.44
1:D:247:SER:O	1:D:251:SER:HB3	2.18	0.44
2:E:124:TYR:CG	2:E:174:ILE:HD12	2.53	0.44
2:F:86:TYR:HE1	2:F:178:SER:HB3	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:ARG:O	1:B:320:ARG:HG2	2.18	0.43
2:E:14:GLN:O	2:E:17:LYS:HB3	2.18	0.43
1:A:237:ILE:HG13	1:A:238:SER:N	2.32	0.43
1:C:168:PHE:CE2	1:C:260:LEU:HB3	2.54	0.43
1:C:198:PHE:CE2	1:C:204:PHE:HE1	2.36	0.43
1:C:228:VAL:HG12	1:C:237:ILE:HG22	2.00	0.43
1:D:32:LYS:HE3	1:D:32:LYS:HB2	1.89	0.43
1:D:106:TYR:O	1:D:127:ILE:HA	2.17	0.43
2:E:86:TYR:O	2:E:86:TYR:CG	2.69	0.43
2:E:112:ARG:H	2:E:112:ARG:HG2	1.69	0.43
2:F:14:GLN:NE2	2:F:89:ILE:HB	2.33	0.43
2:H:29:ILE:HG12	2:H:29:ILE:O	2.18	0.43
1:A:52:LEU:HD23	1:A:53:TYR:CD2	2.53	0.43
1:B:93:TYR:HD2	1:B:295:LEU:HD11	1.82	0.43
1:B:93:TYR:CD2	1:B:295:LEU:HD11	2.53	0.43
1:C:106:TYR:OH	1:C:308:CYS:HB2	2.18	0.43
2:G:7:THR:O	2:G:12:GLN:HB2	2.18	0.43
1:A:56:LEU:HD22	1:A:297:ASN:CG	2.39	0.43
2:E:30:LEU:HD22	2:E:38:ILE:HG21	2.01	0.43
1:A:226:ASN:O	1:A:227:LEU:C	2.57	0.43
1:B:48:GLU:OE2	1:B:91:ARG:NH1	2.40	0.43
1:D:16:THR:HG22	1:D:19:GLN:CG	2.49	0.43
1:D:224:LEU:O	1:D:228:VAL:HG23	2.18	0.43
2:F:58:LEU:HD13	2:F:182:ILE:CD1	2.47	0.43
2:G:1:MET:HB2	2:G:43:ASP:O	2.18	0.43
2:G:87:LEU:O	2:G:89:ILE:HG13	2.17	0.43
2:G:158:GLU:HB3	3:G:4009:PRP:O2P	2.18	0.43
2:H:58:LEU:C	2:H:58:LEU:HD23	2.39	0.43
1:B:16:THR:HG22	1:B:19:GLN:OE1	2.19	0.43
1:B:58:SER:C	1:B:267:ASP:HB2	2.39	0.43
1:C:81:LEU:O	1:C:82:ARG:C	2.56	0.43
2:G:36:LEU:HD12	2:G:36:LEU:N	2.33	0.43
2:G:86:TYR:HE1	2:G:178:SER:HB3	1.82	0.43
2:H:6:ILE:HG22	2:H:7:THR:N	2.33	0.43
1:C:68:MET:HB2	1:C:80:THR:HG21	2.01	0.43
1:A:37:LYS:O	1:A:38:ASN:HB2	2.18	0.43
1:A:117:HIS:CD2	1:A:117:HIS:N	2.77	0.43
1:B:101:SER:HA	1:B:132:PHE:O	2.19	0.43
1:B:192:LEU:HD12	2:G:199:VAL:HG11	2.00	0.43
1:B:316:LYS:HB2	1:B:316:LYS:HE3	1.77	0.43
2:E:36:LEU:HD13	2:F:143:LEU:CD1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:114:ALA:HB1	2:G:137:LEU:HD12	2.00	0.43
1:A:206:LYS:HA	1:A:209:ARG:NH1	2.33	0.43
2:H:6:ILE:HG21	2:H:12:GLN:HA	2.01	0.43
1:D:163:ILE:O	1:D:163:ILE:HG13	2.19	0.43
2:F:18:LEU:CD2	2:F:202:LEU:HD22	2.44	0.43
2:G:100:PRO:C	2:G:102:PHE:H	2.23	0.43
1:D:8:LEU:HB3	2:E:131:ASP:OD2	2.18	0.42
1:D:214:GLU:HG2	1:D:227:LEU:CD1	2.49	0.42
1:D:256:ILE:HG22	1:D:257:ILE:N	2.34	0.42
2:E:143:LEU:O	2:E:146:VAL:N	2.52	0.42
1:A:59:ASN:C	1:A:61:LYS:H	2.22	0.42
1:C:7:LEU:N	1:C:7:LEU:HD12	2.33	0.42
1:C:189:LYS:C	1:C:191:ASP:N	2.73	0.42
2:G:59:GLU:HG3	2:G:78:PHE:CZ	2.51	0.42
1:C:275:LYS:HD3	1:C:277:TYR:OH	2.19	0.42
2:E:86:TYR:CE2	2:E:88:LYS:HG2	2.54	0.42
2:G:114:ALA:HA	2:G:135:ILE:O	2.19	0.42
2:H:24:TYR:HA	2:H:42:ASP:OD2	2.20	0.42
1:A:71:PHE:HE1	1:A:79:ILE:HD11	1.83	0.42
1:A:217:ILE:HD12	1:A:217:ILE:C	2.39	0.42
1:B:56:LEU:HD11	1:B:87:LEU:HD11	2.02	0.42
1:B:73:LYS:HG2	1:B:77:GLN:N	2.34	0.42
1:C:144:LEU:HD23	1:C:144:LEU:HA	1.64	0.42
2:E:6:ILE:HG22	2:E:7:THR:N	2.34	0.42
2:E:113:ILE:HG23	2:E:153:ILE:CA	2.45	0.42
1:B:16:THR:O	1:B:19:GLN:N	2.53	0.42
1:B:44:PRO:HG2	1:B:85:PHE:CD2	2.54	0.42
1:C:27:GLU:OE2	1:C:107:PHE:HB3	2.19	0.42
2:E:98:SER:HB2	2:E:152:ALA:CB	2.49	0.42
2:F:58:LEU:HD23	2:F:58:LEU:O	2.18	0.42
1:A:49:TYR:O	1:A:50:THR:C	2.58	0.42
1:A:195:LEU:O	1:A:198:PHE:HB3	2.20	0.42
1:C:275:LYS:HD3	1:C:277:TYR:HE1	1.83	0.42
1:D:16:THR:HG22	1:D:19:GLN:HG3	2.00	0.42
1:C:134:GLU:HB3	1:C:139:SER:OG	2.19	0.42
1:D:129:ILE:HD11	1:D:307:PHE:CE2	2.55	0.42
1:D:186:LEU:HD13	1:D:195:LEU:HA	2.02	0.42
2:E:96:LEU:O	2:E:171:ILE:HG12	2.20	0.42
2:E:141:VAL:O	2:E:141:VAL:HG12	2.20	0.42
1:A:93:TYR:HD2	1:A:295:LEU:HD11	1.82	0.42
1:A:294:LEU:HA	1:A:297:ASN:ND2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:HIS:C	1:B:76:GLY:N	2.71	0.42
2:G:29:ILE:HG22	2:G:30:LEU:H	1.84	0.42
2:H:85:LEU:CG	2:H:86:TYR:H	2.31	0.42
1:A:6:TYR:HB3	1:A:7:LEU:H	1.59	0.42
1:A:24:ARG:HG3	1:B:41:GLU:OE2	2.19	0.42
1:B:269:TYR:CE1	1:B:291:TYR:HD2	2.37	0.42
1:D:98:ASP:O	1:D:100:THR:N	2.48	0.42
2:G:94:PHE:CD1	2:G:177:ILE:HD11	2.55	0.42
2:F:5:ALA:HA	2:F:47:ILE:O	2.20	0.41
2:G:51:PRO:HG2	2:G:52:ASN:H	1.84	0.41
2:G:81:TYR:CD1	2:G:81:TYR:C	2.94	0.41
1:A:71:PHE:CE1	1:A:79:ILE:CD1	3.02	0.41
1:B:30:LEU:HD22	1:B:150:VAL:HG13	2.02	0.41
1:C:52:LEU:HD23	1:C:53:TYR:CD2	2.55	0.41
2:F:20:GLU:O	2:F:23:ASP:N	2.41	0.41
2:F:99:TYR:O	2:F:102:PHE:HB2	2.20	0.41
2:F:113:ILE:HA	2:F:152:ALA:O	2.19	0.41
2:H:82:TYR:CE2	2:H:185:LYS:HE2	2.55	0.41
2:H:95:ALA:HA	2:H:174:ILE:HG12	2.02	0.41
1:A:33:LEU:O	1:A:36:LEU:HB3	2.19	0.41
1:A:298:PHE:HB2	1:A:299:GLN:H	1.48	0.41
1:B:110:ILE:HG13	1:B:124:ASN:HB2	2.02	0.41
1:B:182:LEU:O	1:B:183:LEU:C	2.57	0.41
1:C:146:LEU:O	1:C:150:VAL:HG23	2.19	0.41
2:E:177:ILE:HG22	2:E:178:SER:N	2.35	0.41
2:G:22:ALA:O	2:G:23:ASP:HB2	2.20	0.41
2:G:86:TYR:CE1	2:G:178:SER:HB3	2.55	0.41
2:E:7:THR:HG22	2:E:51:PRO:HA	2.01	0.41
2:G:17:LYS:O	2:G:20:GLU:HB3	2.20	0.41
2:G:113:ILE:HA	2:G:152:ALA:O	2.20	0.41
2:H:87:LEU:HD23	2:H:87:LEU:N	2.16	0.41
1:B:8:LEU:H	1:B:8:LEU:HG	1.73	0.41
1:B:191:ASP:HA	2:G:83:GLU:O	2.20	0.41
1:D:120:ARG:HG2	1:D:120:ARG:HH11	1.83	0.41
1:D:274:PHE:N	1:D:274:PHE:CD2	2.88	0.41
2:E:87:LEU:H	2:E:87:LEU:CD2	2.15	0.41
2:H:85:LEU:HD12	2:H:86:TYR:H	1.86	0.41
1:B:68:MET:HB2	1:B:80:THR:CG2	2.51	0.41
1:C:82:ARG:NH2	1:C:109:LYS:O	2.44	0.41
1:C:199:ILE:HD13	1:C:209:ARG:CG	2.42	0.41
1:C:298:PHE:CD1	1:C:298:PHE:N	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:19:LEU:HD23	2:E:202:LEU:HD21	2.01	0.41
2:F:58:LEU:HD13	2:F:182:ILE:HG13	2.02	0.41
2:F:158:GLU:HB3	3:F:4008:PRP:O3P	2.21	0.41
2:H:30:LEU:HD11	2:H:38:ILE:CG2	2.47	0.41
2:H:112:ARG:HG3	2:H:150:ALA:HA	2.02	0.41
1:A:20:VAL:O	1:A:21:LYS:C	2.58	0.41
1:B:136:ALA:O	1:B:139:SER:HB2	2.21	0.41
1:D:134:GLU:HG3	1:D:135:SER:N	2.36	0.41
1:A:101:SER:HA	1:A:132:PHE:O	2.20	0.41
1:A:116:ARG:O	1:A:117:HIS:ND1	2.45	0.41
1:A:161:PHE:HD2	1:A:256:ILE:HD12	1.86	0.41
1:B:244:LYS:O	1:B:247:SER:HB3	2.21	0.41
1:B:268:TYR:CE1	1:B:294:LEU:HD11	2.56	0.41
1:C:6:TYR:HB3	1:C:7:LEU:H	1.69	0.41
1:C:90:VAL:HG22	1:C:132:PHE:CZ	2.56	0.41
1:C:147:ALA:O	1:C:151:ILE:HG13	2.20	0.41
1:C:237:ILE:HG13	1:C:238:SER:N	2.36	0.41
2:E:40:THR:OG1	2:E:44:LEU:HB2	2.21	0.41
2:F:188:PHE:O	2:F:192:LYS:HB2	2.20	0.41
2:H:38:ILE:O	2:H:45:GLN:HA	2.20	0.41
2:H:67:PHE:CE2	2:H:181:MET:HG3	2.55	0.41
2:H:204:ASP:O	2:H:205:ALA:HB2	2.21	0.41
1:A:44:PRO:HB2	1:A:82:ARG:HD3	2.02	0.41
1:B:87:LEU:HD23	1:B:87:LEU:HA	1.81	0.41
1:C:73:LYS:CE	1:C:77:GLN:HB2	2.40	0.41
1:C:131:LEU:HD21	1:C:134:GLU:CB	2.46	0.41
1:D:30:LEU:CD2	1:D:150:VAL:HG13	2.51	0.41
1:D:175:LEU:HD12	1:D:236:LEU:HD11	2.03	0.41
2:F:24:TYR:C	2:F:26:VAL:H	2.25	0.41
2:G:139:GLY:O	2:G:141:VAL:N	2.54	0.41
2:H:50:LYS:O	2:H:53:ASP:HB2	2.20	0.41
1:B:31:ARG:HH11	1:B:31:ARG:HG3	1.85	0.40
1:B:73:LYS:HE3	1:B:75:GLU:CB	2.33	0.40
2:E:58:LEU:CD1	2:E:182:ILE:HG13	2.50	0.40
2:H:93:ILE:HG13	2:H:157:VAL:O	2.20	0.40
1:A:87:LEU:N	1:A:88:PRO:HD2	2.36	0.40
1:B:94:SER:C	1:B:96:ILE:H	2.25	0.40
1:B:186:LEU:HA	1:B:186:LEU:HD23	1.88	0.40
1:B:282:ASN:HA	2:G:186:SER:HB2	2.03	0.40
1:D:259:ASP:OD1	1:D:262:MET:N	2.54	0.40
1:A:189:LYS:C	1:A:191:ASP:N	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:ILE:O	1:C:27:GLU:C	2.60	0.40
1:D:168:PHE:CZ	1:D:260:LEU:HD22	2.57	0.40
2:F:142:GLU:HG2	2:F:162:THR:HG22	2.03	0.40
2:G:3:LYS:HB2	2:G:63:VAL:HA	2.04	0.40
1:A:16:THR:O	1:A:19:GLN:N	2.55	0.40
1:D:143:ILE:HD13	1:D:143:ILE:HA	1.97	0.40
2:E:75:GLU:CD	2:E:119:ARG:HB2	2.42	0.40
2:E:86:TYR:CZ	2:E:88:LYS:HG2	2.57	0.40
2:F:17:LYS:O	2:F:20:GLU:HB3	2.22	0.40
2:F:17:LYS:HE3	2:F:21:ASN:HD21	1.87	0.40
1:A:106:TYR:CZ	1:A:128:GLY:HA3	2.57	0.40
1:B:289:GLY:O	1:B:305:ILE:HG13	2.22	0.40
2:F:100:PRO:C	2:F:102:PHE:H	2.24	0.40
2:G:82:TYR:O	2:G:182:ILE:HA	2.21	0.40
2:H:86:TYR:CE1	2:H:178:SER:HB3	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	309/344 (90%)	272 (88%)	32 (10%)	5 (2%)	9	37
1	B	316/344 (92%)	275 (87%)	37 (12%)	4 (1%)	12	41
1	C	298/344 (87%)	265 (89%)	29 (10%)	4 (1%)	12	41
1	D	308/344 (90%)	285 (92%)	20 (6%)	3 (1%)	15	47
2	E	199/208 (96%)	165 (83%)	31 (16%)	3 (2%)	10	39
2	F	203/208 (98%)	170 (84%)	25 (12%)	8 (4%)	3	18
2	G	199/208 (96%)	167 (84%)	24 (12%)	8 (4%)	3	17
2	H	196/208 (94%)	162 (83%)	29 (15%)	5 (3%)	5	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2028/2208 (92%)	1761 (87%)	227 (11%)	40 (2%)	7	33

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	84	LEU
2	G	84	LEU
2	G	140	SER
1	A	191	ASP
1	B	115	LYS
1	B	136	ALA
1	B	191	ASP
1	C	95	GLN
1	C	136	ALA
1	C	191	ASP
1	D	191	ASP
2	E	84	LEU
2	F	9	GLY
2	F	88	LYS
2	G	88	LYS
2	H	9	GLY
2	H	25	ASP
2	H	84	LEU
1	A	227	LEU
1	A	320	ARG
2	F	26	VAL
2	F	33	GLY
2	F	34	ARG
2	F	87	LEU
2	F	193	ASP
2	G	101	ASP
1	A	136	ALA
1	A	299	GLN
2	H	101	ASP
1	C	203	ASN
1	D	99	SER
2	E	101	ASP
2	G	29	ILE
2	G	91	GLN
2	H	109	ARG
1	D	271	ASP
2	G	193	ASP

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Mol	Chain	Res	Type
1	B	9	PRO
2	E	9	GLY
2	G	27	GLU

5.3.2 Protein sidechains [i](#)

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	284/311 (91%)	267 (94%)	17 (6%)	19	49
1	B	288/311 (93%)	273 (95%)	15 (5%)	23	53
1	C	276/311 (89%)	263 (95%)	13 (5%)	26	57
1	D	283/311 (91%)	268 (95%)	15 (5%)	22	53
2	E	182/186 (98%)	178 (98%)	4 (2%)	52	74
2	F	183/186 (98%)	177 (97%)	6 (3%)	38	65
2	G	182/186 (98%)	178 (98%)	4 (2%)	52	74
2	H	179/186 (96%)	175 (98%)	4 (2%)	52	74
All	All	1857/1988 (93%)	1779 (96%)	78 (4%)	30	59

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	TYR
1	A	10	GLU
1	A	31	ARG
1	A	42	VAL
1	A	71	PHE
1	A	75	GLU
1	A	82	ARG
1	A	103	ARG
1	A	117	HIS
1	A	124	ASN
1	A	135	SER
1	A	174	GLN

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Mol	Chain	Res	Type
1	A	180	THR
1	A	219	ASN
1	A	252	MET
1	A	291	TYR
1	A	295	LEU
1	B	10	GLU
1	B	11	GLU
1	B	31	ARG
1	B	42	VAL
1	B	62	THR
1	B	71	PHE
1	B	82	ARG
1	B	103	ARG
1	B	174	GLN
1	B	180	THR
1	B	219	ASN
1	B	225	GLU
1	B	252	MET
1	B	291	TYR
1	B	295	LEU
1	C	31	ARG
1	C	52	LEU
1	C	64	ASN
1	C	71	PHE
1	C	75	GLU
1	C	82	ARG
1	C	103	ARG
1	C	174	GLN
1	C	219	ASN
1	C	238	SER
1	C	252	MET
1	C	295	LEU
1	C	298	PHE
1	D	6	TYR
1	D	31	ARG
1	D	42	VAL
1	D	64	ASN
1	D	71	PHE
1	D	103	ARG
1	D	122	THR
1	D	135	SER
1	D	174	GLN

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Mol	Chain	Res	Type
1	D	219	ASN
1	D	252	MET
1	D	291	TYR
1	D	295	LEU
1	D	297	ASN
1	D	308	CYS
2	E	43	ASP
2	E	87	LEU
2	E	107	PHE
2	E	110	HIS
2	F	31	ASN
2	F	43	ASP
2	F	87	LEU
2	F	109	ARG
2	F	115	SER
2	F	204	ASP
2	G	26	VAL
2	G	43	ASP
2	G	87	LEU
2	G	110	HIS
2	H	43	ASP
2	H	87	LEU
2	H	107	PHE
2	H	109	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	117	HIS
1	A	124	ASN
1	A	149	GLN
1	A	297	ASN
1	A	310	HIS
1	B	65	GLN
1	B	70	GLN
1	B	124	ASN
1	C	70	GLN
1	C	124	ASN
1	C	149	GLN
1	D	70	GLN
1	D	117	HIS

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Mol	Chain	Res	Type
1	D	124	ASN
1	D	297	ASN
1	D	310	HIS
2	E	14	GLN
2	E	21	ASN
2	E	45	GLN
2	F	14	GLN
2	F	21	ASN
2	F	31	ASN
2	F	37	GLN
2	F	45	GLN
2	F	104	ASN
2	F	106	ASN
2	F	161	ASN
2	G	14	GLN
2	G	21	ASN
2	G	161	ASN
2	G	206	GLN
2	H	14	GLN
2	H	21	ASN
2	H	37	GLN
2	H	161	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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	PO4	G	1001	-	4,4,4	1.53	0	6,6,6	0.42	0
3	PRP	F	4008	-	19,22,22	0.98	1 (5%)	33,35,35	1.00	2 (6%)
3	PRP	G	4009	-	19,22,22	0.99	1 (5%)	33,35,35	1.01	1 (3%)
4	PO4	F	1002	-	4,4,4	1.54	0	6,6,6	0.42	0
3	PRP	H	4010	-	19,22,22	1.02	1 (5%)	33,35,35	0.99	1 (3%)
3	PRP	E	4007	-	19,22,22	1.23	2 (10%)	33,35,35	1.07	1 (3%)

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	PRP	H	4010	-	-	1/16/33/33	0/1/1/1
3	PRP	E	4007	-	-	4/16/33/33	0/1/1/1
3	PRP	G	4009	-	-	6/16/33/33	0/1/1/1
3	PRP	F	4008	-	-	3/16/33/33	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	4007	PRP	O4-C4	3.22	1.52	1.45
3	E	4007	PRP	C1-C2	2.72	1.56	1.52
3	H	4010	PRP	O4-C4	2.62	1.50	1.45
3	F	4008	PRP	O4-C4	2.54	1.50	1.45
3	G	4009	PRP	O4-C4	2.48	1.50	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	4009	PRP	P-O5-C5	2.43	124.98	118.30
3	E	4007	PRP	P-O5-C5	2.39	124.87	118.30
3	H	4010	PRP	P-O5-C5	2.18	124.30	118.30
3	F	4008	PRP	O3P-P-O5	-2.09	101.18	106.73
3	F	4008	PRP	P-O5-C5	2.06	123.97	118.30

There are no chirality outliers.

All (14) torsion outliers are listed below:

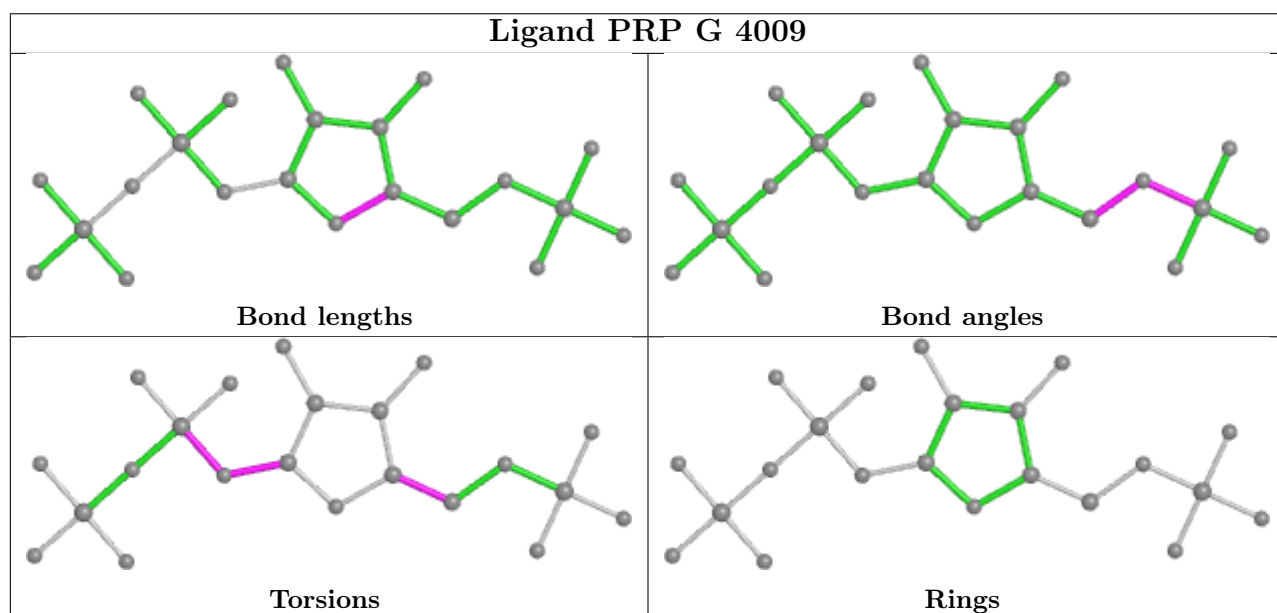
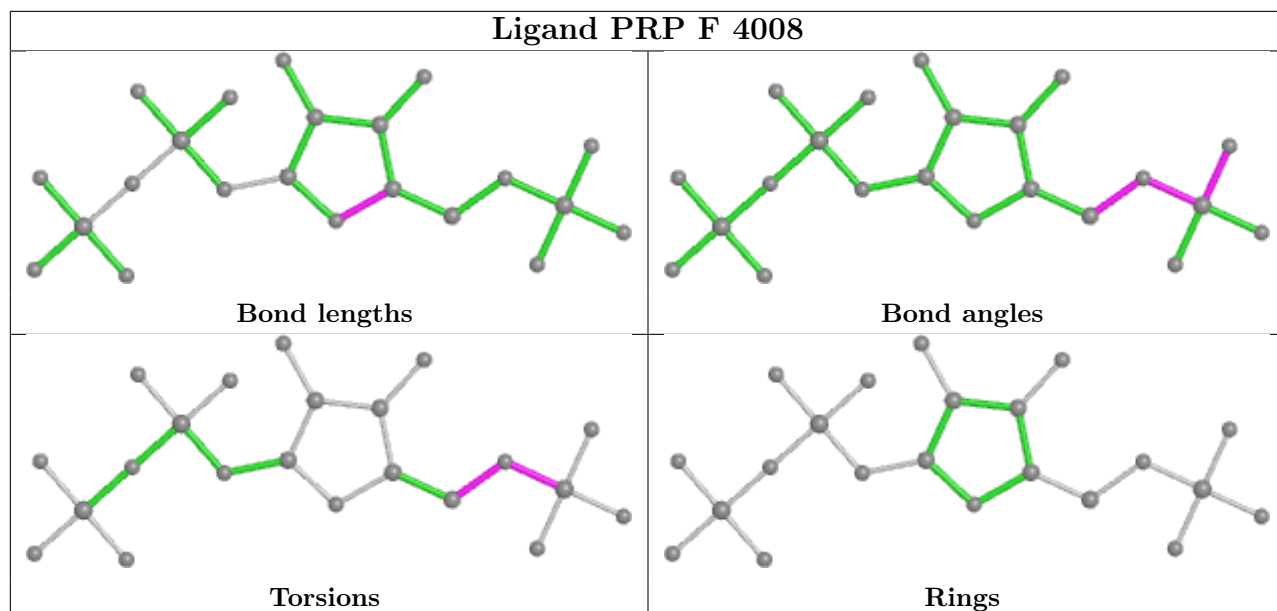
Mol	Chain	Res	Type	Atoms
3	E	4007	PRP	PA-O3A-PB-O2B
3	F	4008	PRP	C5-O5-P-O1P
3	E	4007	PRP	C3-C4-C5-O5
3	E	4007	PRP	O4-C4-C5-O5
3	G	4009	PRP	C3-C4-C5-O5
3	G	4009	PRP	C1-O1-PA-O2A
3	G	4009	PRP	C1-O1-PA-O3A
3	F	4008	PRP	C5-O5-P-O3P
3	G	4009	PRP	C1-O1-PA-O1A
3	G	4009	PRP	O4-C4-C5-O5
3	E	4007	PRP	PA-O3A-PB-O3B
3	F	4008	PRP	C4-C5-O5-P
3	G	4009	PRP	C2-C1-O1-PA
3	H	4010	PRP	C2-C1-O1-PA

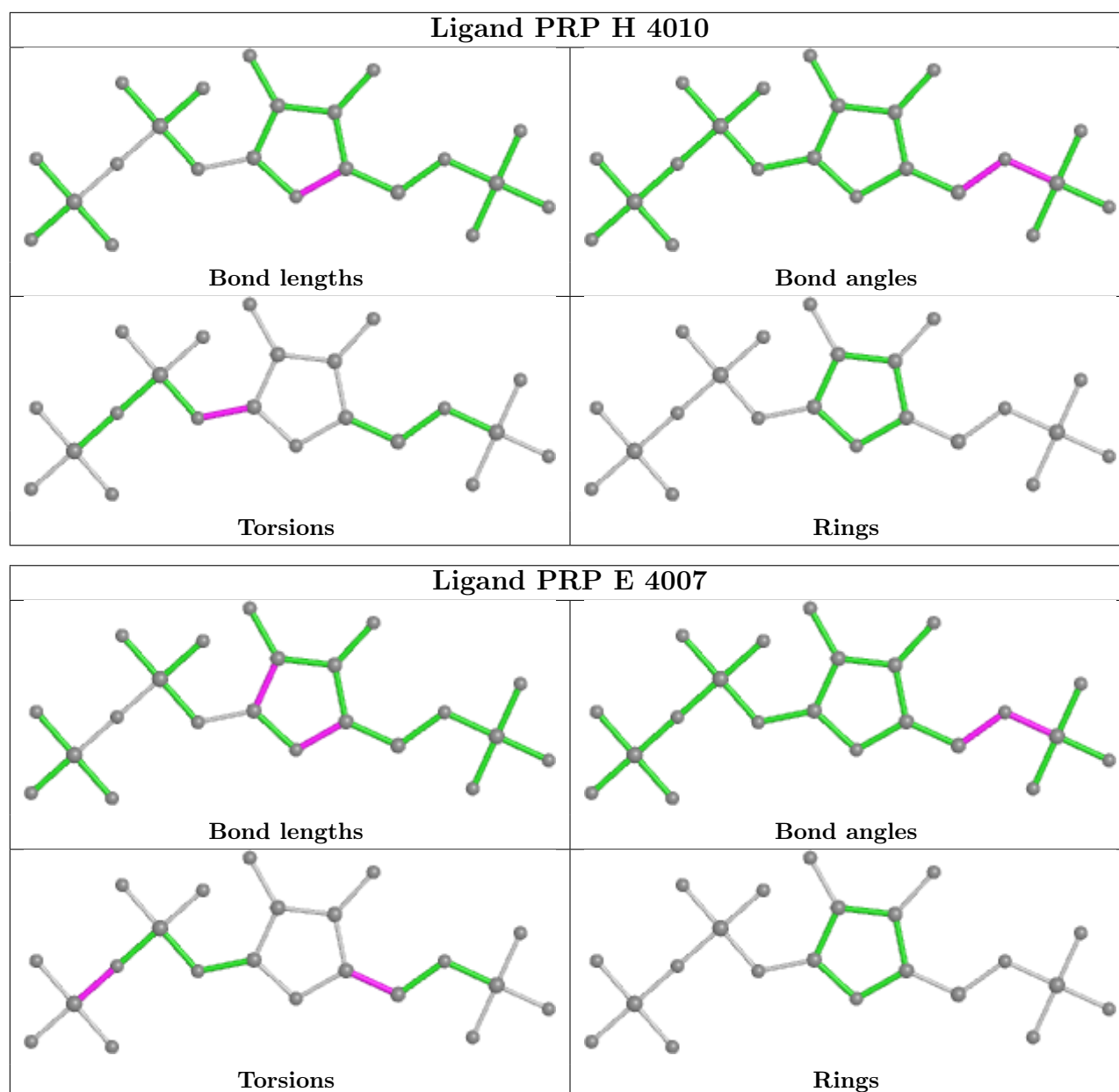
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1001	PO4	2	0
3	F	4008	PRP	1	0
3	G	4009	PRP	1	0

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





5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	E	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	29:ILE	C	30:LEU	N	1.04

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	311/344 (90%)	-0.44	4 (1%) 77 75	14, 43, 117, 169	2 (0%)
1	B	316/344 (91%)	-0.35	3 (0%) 84 84	17, 55, 119, 176	0
1	C	304/344 (88%)	-0.36	0 100 100	17, 50, 109, 182	3 (0%)
1	D	312/344 (90%)	-0.22	7 (2%) 62 59	22, 70, 126, 166	1 (0%)
2	E	202/208 (97%)	-0.41	1 (0%) 91 90	25, 61, 120, 166	0
2	F	205/208 (98%)	-0.25	3 (1%) 73 71	26, 71, 126, 162	0
2	G	202/208 (97%)	-0.33	2 (0%) 82 82	25, 62, 119, 164	0
2	H	200/208 (96%)	-0.32	1 (0%) 91 90	27, 65, 129, 168	0
All	All	2052/2208 (92%)	-0.34	21 (1%) 82 82	14, 59, 123, 182	6 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	31	ASN	3.5
2	F	108	GLN	3.5
1	B	61	LYS	3.4
1	A	117	HIS	3.2
2	F	98	SER	3.0
1	D	203	ASN	2.9
1	D	118	LYS	2.9
1	D	119	GLY	2.7
1	A	74	HIS	2.6
1	A	116	ARG	2.5
2	F	34	ARG	2.5
1	D	179	SER	2.5
1	A	115	LYS	2.3
1	D	117	HIS	2.3
2	G	110	HIS	2.2
2	G	129	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	32	LEU	2.1
1	D	75	GLU	2.0
1	D	202	ASN	2.0
1	B	63	PHE	2.0
1	B	322	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

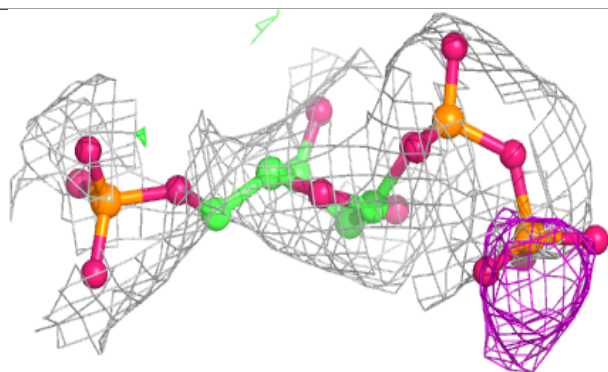
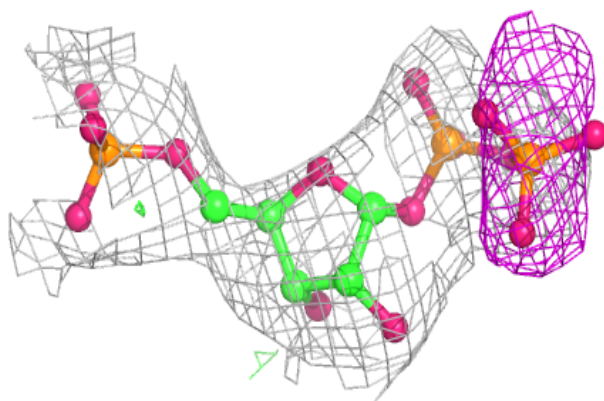
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	PO4	G	1001	5/5	0.68	0.44	127,127,127,127	0
3	PRP	G	4009	22/22	0.78	0.27	118,118,118,118	0
3	PRP	H	4010	22/22	0.81	0.25	138,138,138,138	0
3	PRP	F	4008	22/22	0.81	0.22	117,117,117,117	0
3	PRP	E	4007	22/22	0.84	0.22	113,113,113,113	0
4	PO4	F	1002	5/5	0.87	0.34	111,111,111,111	0

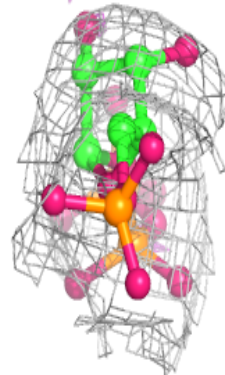
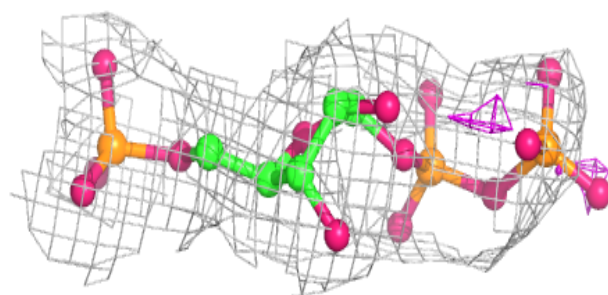
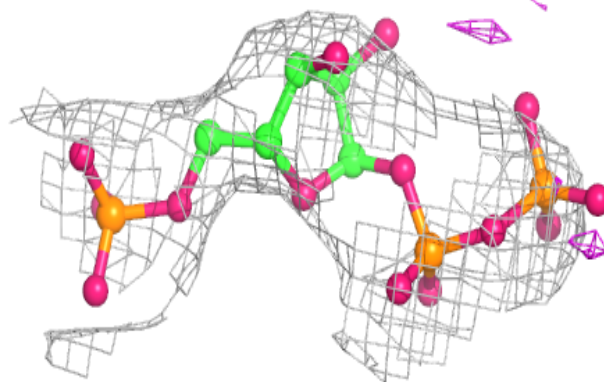
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PRP G 4009:

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

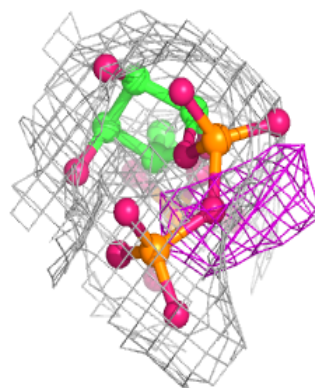
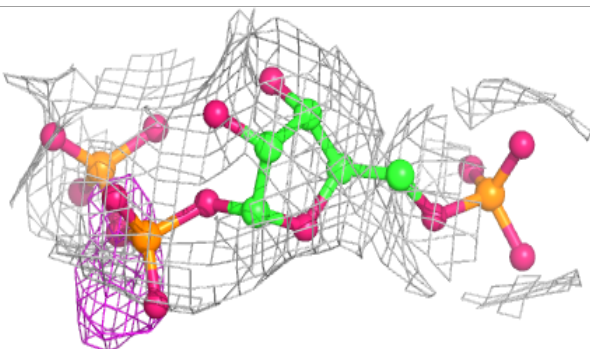
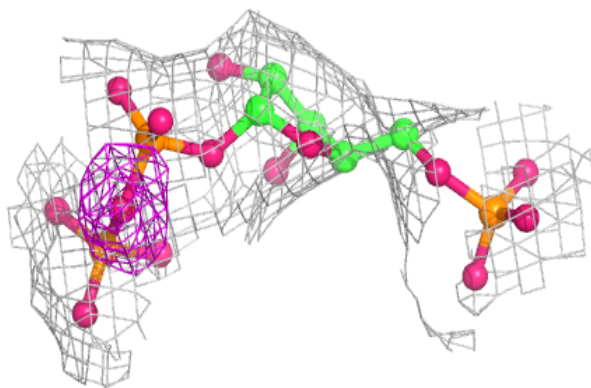
**Electron density around PRP H 4010:**

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

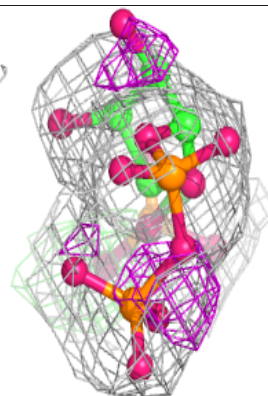
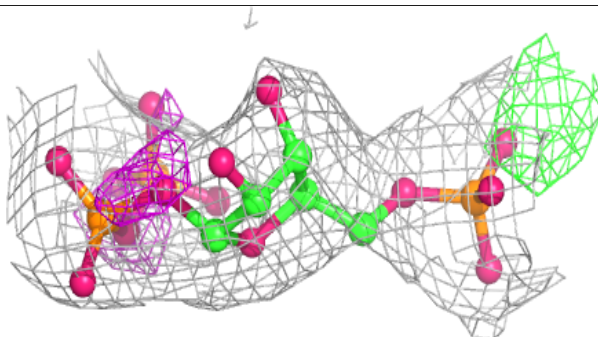
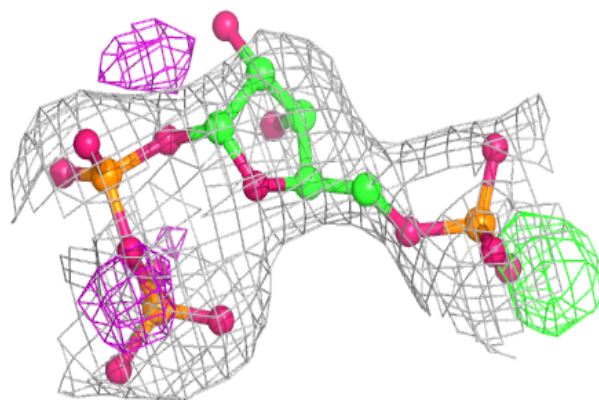


Electron density around PRP F 4008:

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

**Electron density around PRP E 4007:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.