



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 06:42 PM EDT

PDB ID : 3U61 / pdb_00003u61
Title : Structure of T4 Bacteriophage Clamp Loader Bound To Closed Clamp, DNA and ATP Analog and ADP
Authors : Kelch, B.A.; Makino, D.L.; O'Donnell, M.; Kuriyan, J.
Deposited on : 2011-10-11
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

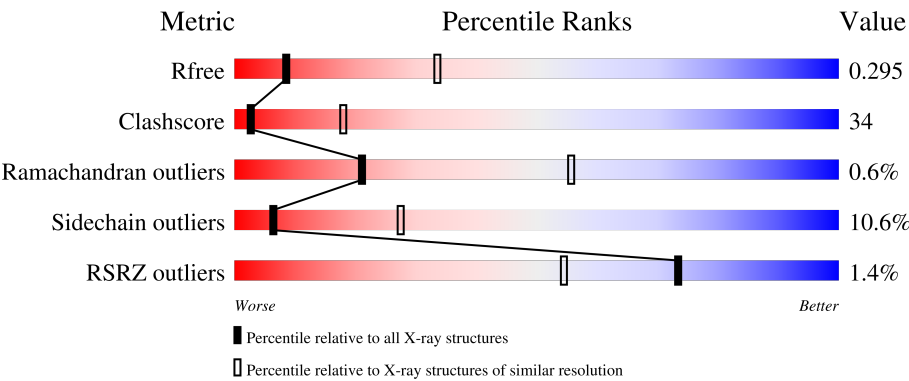
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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.



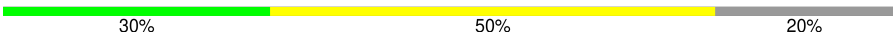
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	B	324	2% 38%50%6%6%
1	C	324	% 42%48%7%..
1	D	324	2% 44%44%10%..
1	E	324	2% 41%41%8%9%
2	A	199	% 30%51%7%.11%

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Mol	Chain	Length	Quality of chain
3	F	228	
3	G	228	
3	H	228	
4	I	20	
5	J	10	

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
6	ADP	B	700	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16748 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 DNA polymerase accessory protein 44.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	305	Total	C	N	O	S	0	0	0
			2407	1525	412	454	16			
1	C	319	Total	C	N	O	S	0	0	0
			2503	1583	430	473	17			
1	D	320	Total	C	N	O	S	0	0	0
			2514	1590	432	475	17			
1	E	294	Total	C	N	O	S	0	0	0
			2292	1451	394	432	15			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP P04526
B	-3	PRO	-	expression tag	UNP P04526
B	-2	GLY	-	expression tag	UNP P04526
B	-1	GLY	-	expression tag	UNP P04526
B	0	SER	-	expression tag	UNP P04526
C	-4	GLY	-	expression tag	UNP P04526
C	-3	PRO	-	expression tag	UNP P04526
C	-2	GLY	-	expression tag	UNP P04526
C	-1	GLY	-	expression tag	UNP P04526
C	0	SER	-	expression tag	UNP P04526
D	-4	GLY	-	expression tag	UNP P04526
D	-3	PRO	-	expression tag	UNP P04526
D	-2	GLY	-	expression tag	UNP P04526
D	-1	GLY	-	expression tag	UNP P04526
D	0	SER	-	expression tag	UNP P04526
E	-4	GLY	-	expression tag	UNP P04526
E	-3	PRO	-	expression tag	UNP P04526
E	-2	GLY	-	expression tag	UNP P04526
E	-1	GLY	-	expression tag	UNP P04526
E	0	SER	-	expression tag	UNP P04526

- Molecule 2 is a protein called DNA polymerase accessory protein 62.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	178	Total	C	N	O	S	0	0	0
			1416	909	233	268	6			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	188	GLY	-	expression tag	UNP P04527
A	189	LEU	-	expression tag	UNP P04527
A	190	GLU	-	expression tag	UNP P04527
A	191	HIS	-	expression tag	UNP P04527
A	192	HIS	-	expression tag	UNP P04527
A	193	HIS	-	expression tag	UNP P04527
A	194	HIS	-	expression tag	UNP P04527
A	195	HIS	-	expression tag	UNP P04527
A	196	HIS	-	expression tag	UNP P04527
A	197	HIS	-	expression tag	UNP P04527
A	198	HIS	-	expression tag	UNP P04527
A	199	HIS	-	expression tag	UNP P04527
A	200	HIS	-	expression tag	UNP P04527

- Molecule 3 is a protein called DNA polymerase processivity component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	228	Total	C	N	O	Se	0	0	0
			1750	1113	288	343	6			
3	H	228	Total	C	N	O	Se	0	0	0
			1750	1113	288	343	6			
3	F	222	Total	C	N	O	Se	0	0	0
			1699	1083	280	330	6			

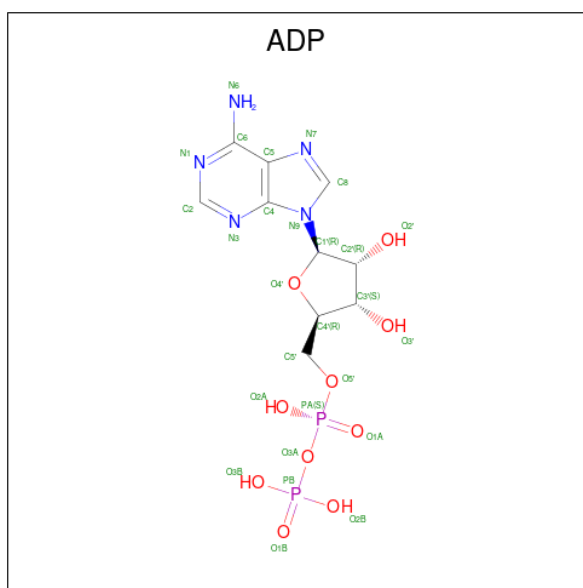
- Molecule 4 is a DNA chain called Template DNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	I	8	Total	C	N	O	P	0	0	0
			163	79	29	48	7			

- Molecule 5 is a DNA chain called Primer DNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	J	8	Total	C	N	O	P	0	0	0
			162	77	31	46	8			

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

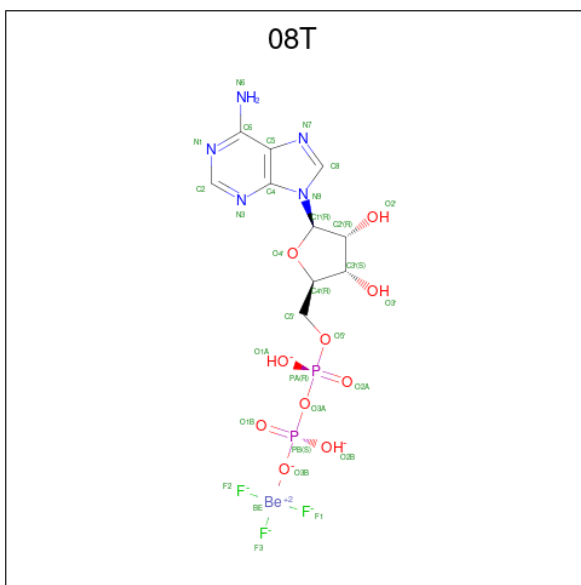


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Mg	0	0
			1	1		
7	C	1	Total	Mg	0	0
			1	1		
7	D	1	Total	Mg	0	0
			1	1		

- Molecule 8 is [[[(2R,3S,4R,5R)-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]oxy-oxidanyl-phosphoryl]oxy-tris(fluoranyl)beryllium (CCD ID: 08T) (formula: $C_{10}H_{14}BeF_3N_5O_{10}P_2$).

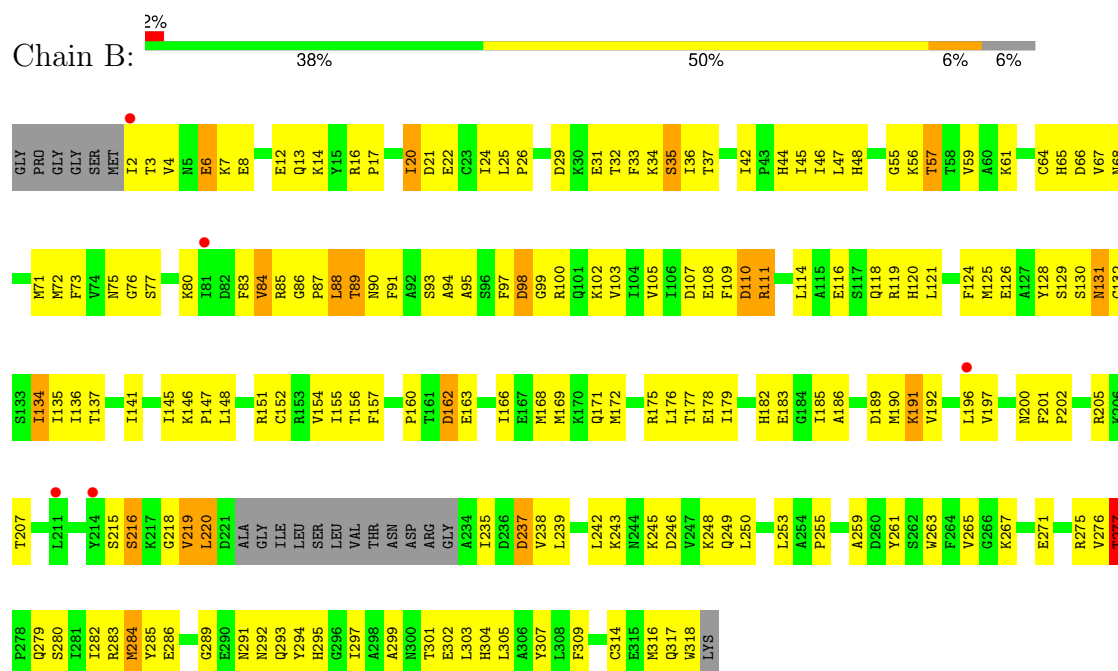


Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
8	C	1	Total 31	Be 1	C 10	F 3	N 5	O 10	P 2	0	0
8	D	1	Total 31	Be 1	C 10	F 3	N 5	O 10	P 2	0	0

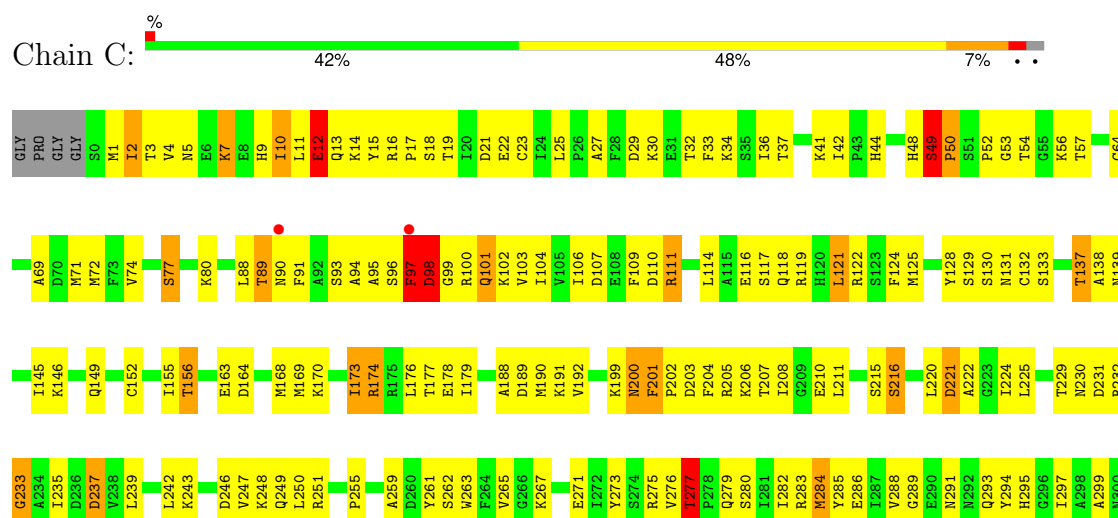
3 Residue-property plots

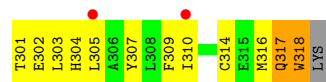
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: DNA polymerase accessory protein 44

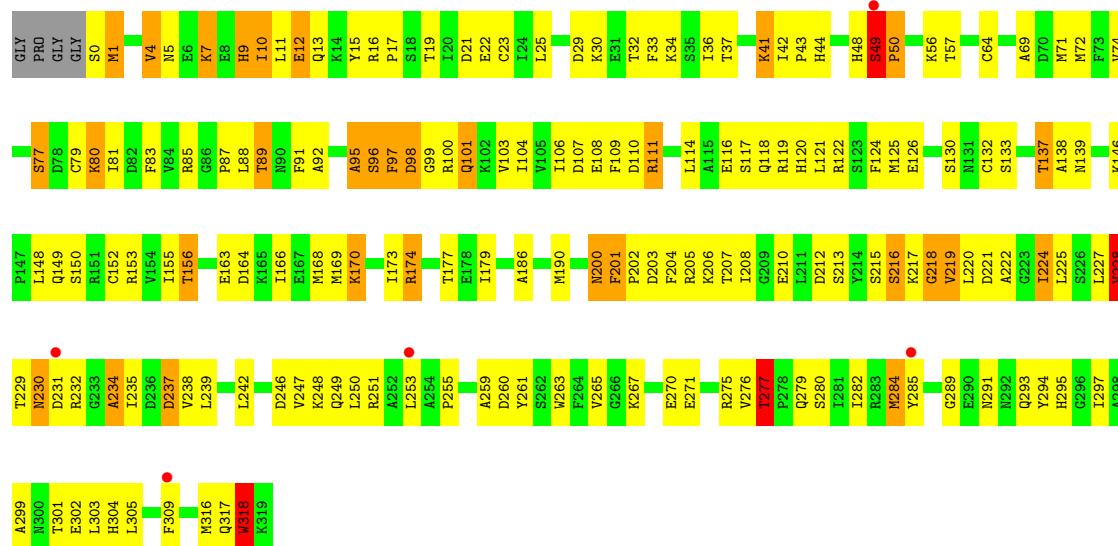
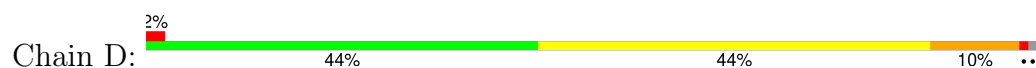


• Molecule 1: DNA polymerase accessory protein 44

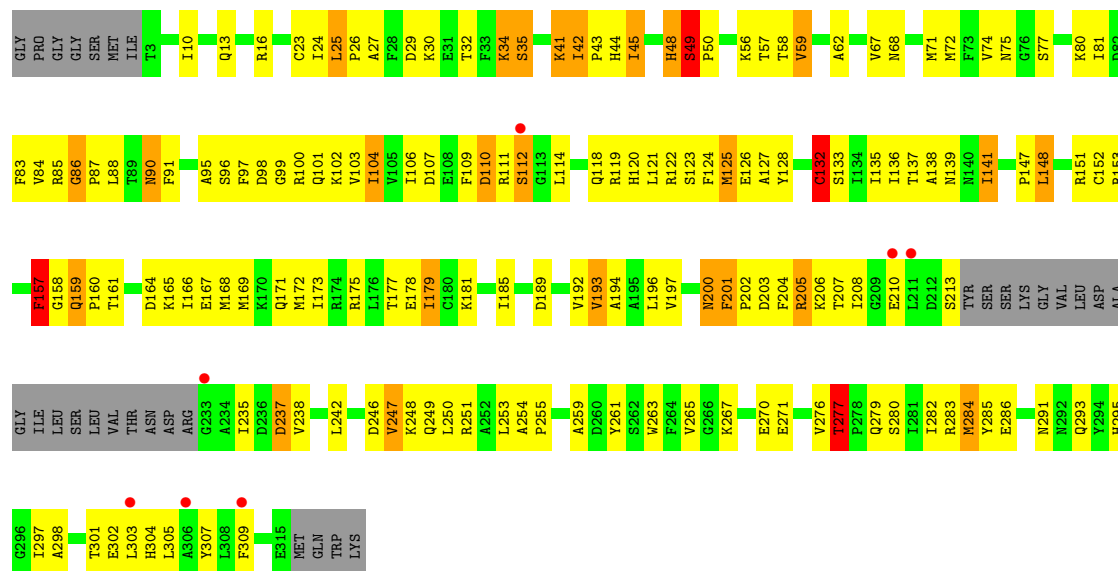
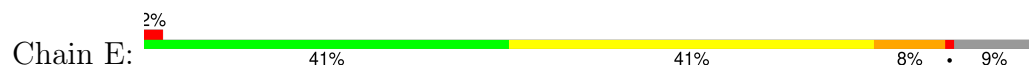




• Molecule 1: DNA polymerase accessory protein 44

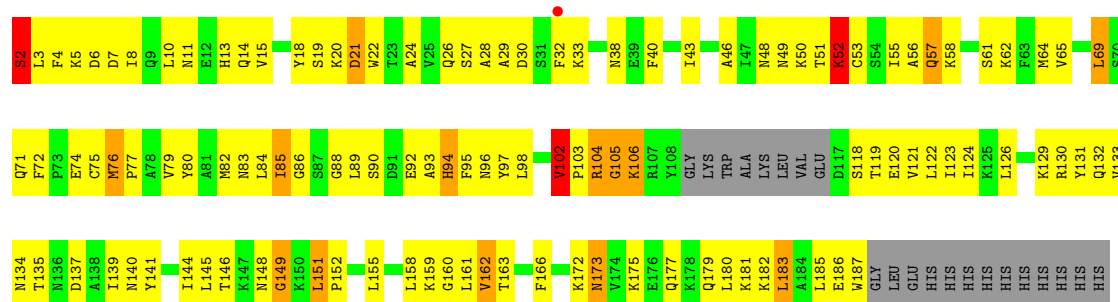


• Molecule 1: DNA polymerase accessory protein 44

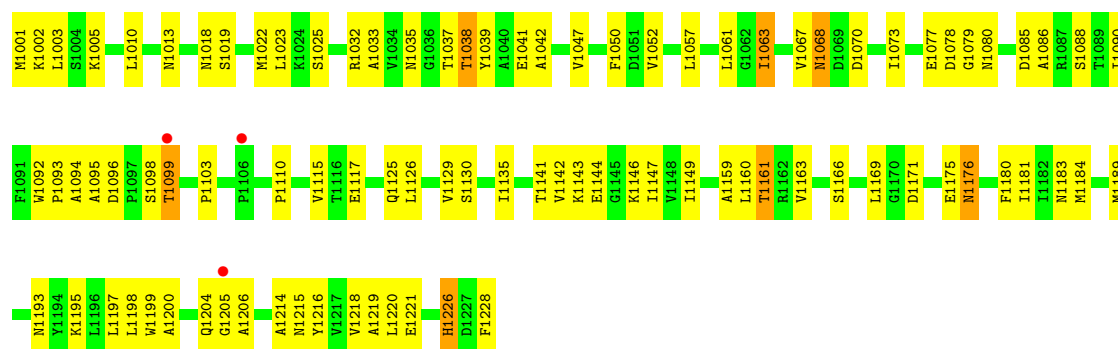


• Molecule 2: DNA polymerase accessory protein 62

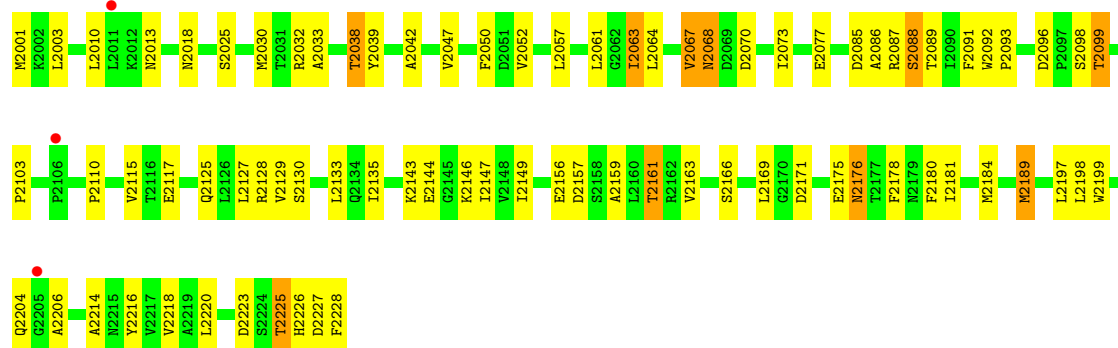




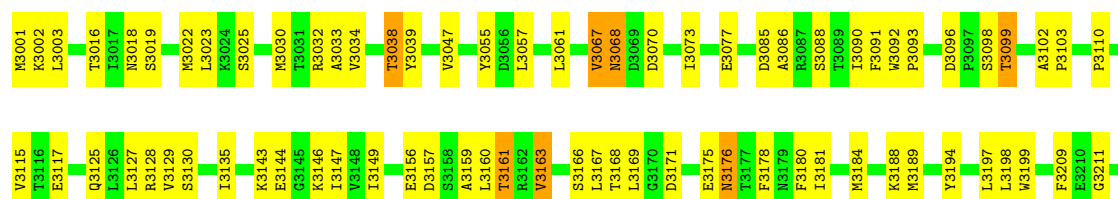
• Molecule 3: DNA polymerase processivity component

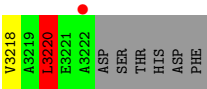


• Molecule 3: DNA polymerase processivity component



• Molecule 3: DNA polymerase processivity component





● Molecule 4: Template DNA strand



● Molecule 5: Primer DNA strand



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.30Å 137.27Å 222.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.65 – 3.20 47.65 – 3.20	Depositor EDS
% Data completeness (in resolution range)	96.2 (47.65-3.20) 96.1 (47.65-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.239 , 0.305 0.230 , 0.295	Depositor DCC
R_{free} test set	3572 reflections (7.12%)	wwPDB-VP
Wilson B-factor (Å ²)	73.1	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16748	wwPDB-VP
Average B, all atoms (Å ²)	106.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 08T, ADP, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	B	0.68	1/2450 (0.0%)	1.10	11/3303 (0.3%)
1	C	0.73	0/2546	1.15	19/3434 (0.6%)
1	D	0.70	0/2558	1.14	17/3449 (0.5%)
1	E	0.66	0/2331	1.17	18/3144 (0.6%)
2	A	0.59	0/1440	1.19	17/1938 (0.9%)
3	F	0.68	0/1721	0.96	2/2324 (0.1%)
3	G	0.76	0/1774	0.99	3/2395 (0.1%)
3	H	0.64	0/1774	0.94	1/2395 (0.0%)
4	I	0.49	0/182	1.15	0/280
5	J	0.47	0/181	1.27	0/276
All	All	0.68	1/16957 (0.0%)	1.09	88/22938 (0.4%)

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	C	0	1
1	D	0	1
1	E	0	2
2	A	0	2
3	F	0	1
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	219	VAL	CA-C	5.78	1.59	1.52

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	12	GLU	N-CA-C	-10.18	100.27	112.89
1	C	98	ASP	N-CA-C	-10.14	100.71	112.87
2	A	105	GLY	N-CA-C	9.04	124.80	110.87
1	C	12	GLU	N-CA-C	-8.87	101.89	112.89
2	A	151	LEU	CA-C-N	-8.68	110.87	119.64
2	A	151	LEU	C-N-CA	-8.68	110.87	119.64
1	C	230	ASN	N-CA-C	8.36	120.39	111.28
1	E	25	LEU	CA-C-N	8.36	128.41	119.89
1	E	25	LEU	C-N-CA	8.36	128.41	119.89
1	E	201	PHE	CA-C-N	-8.32	111.16	119.56
1	E	201	PHE	C-N-CA	-8.32	111.16	119.56
1	D	80	LYS	N-CA-C	-8.31	97.62	110.17
3	G	1226	HIS	N-CA-C	7.99	119.16	108.38
3	H	2135	ILE	CB-CA-C	-7.34	101.93	111.25
1	B	219	VAL	N-CA-C	7.25	117.89	107.88
3	G	1135	ILE	CB-CA-C	-6.83	102.57	111.25
2	A	173	ASN	N-CA-C	6.76	117.19	108.34
1	E	86	GLY	N-CA-C	6.75	126.11	112.34
1	E	157	PHE	N-CA-C	6.57	119.25	109.59
1	C	129	SER	N-CA-C	-6.56	105.10	113.23
1	D	79	CYS	CB-CA-C	-6.53	100.64	111.41
1	C	97	PHE	CB-CA-C	-6.48	97.53	110.42
2	A	162	VAL	N-CA-C	6.42	118.33	112.43
2	A	152	PRO	N-CA-C	-6.39	105.30	114.18
1	D	228	VAL	N-CA-C	6.33	116.37	110.42
1	C	80	LYS	N-CA-C	-6.32	100.63	110.17
1	B	34	LYS	N-CA-C	-6.32	104.48	111.36
1	D	318	TRP	N-CA-C	6.29	118.11	108.42
1	D	277	THR	CA-C-N	6.25	126.45	119.32
1	D	277	THR	C-N-CA	6.25	126.45	119.32
1	D	149	GLN	N-CA-C	-6.20	104.52	111.28
3	F	3220	LEU	CB-CA-C	-6.12	100.75	112.43
1	B	277	THR	CA-C-N	6.06	126.23	119.32
1	B	277	THR	C-N-CA	6.06	126.23	119.32
1	C	49	SER	N-CA-C	6.03	123.14	109.81
1	B	179	ILE	CB-CA-C	-6.01	104.27	111.97
3	F	3135	ILE	CB-CA-C	-5.99	103.65	111.25
1	D	95	ALA	N-CA-C	5.98	118.52	107.99
1	D	234	ALA	N-CA-C	5.97	123.52	110.80
2	A	172	LYS	N-CA-C	5.90	120.18	112.92
2	A	85	ILE	N-CA-C	5.88	118.44	111.09
1	E	247	VAL	N-CA-C	5.86	116.90	111.45
1	E	141	ILE	CB-CA-C	-5.84	104.25	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	57	GLN	N-CA-C	-5.82	105.95	113.16
1	D	49	SER	N-CA-C	5.81	122.65	109.81
1	E	159	GLN	N-CA-C	-5.79	99.26	108.82
1	B	128	TYR	N-CA-C	5.77	120.44	113.17
1	B	220	LEU	N-CA-C	5.72	118.57	109.24
1	C	277	THR	CA-C-N	5.70	125.82	119.32
1	C	277	THR	C-N-CA	5.70	125.82	119.32
1	C	7	LYS	N-CA-C	-5.69	105.92	112.92
1	C	14	LYS	N-CA-C	-5.64	105.22	111.71
1	E	159	GLN	CA-C-N	-5.64	113.90	119.93
1	E	159	GLN	C-N-CA	-5.64	113.90	119.93
1	E	49	SER	N-CA-C	5.62	122.23	109.81
1	E	277	THR	CA-C-N	5.56	125.66	119.32
1	E	277	THR	C-N-CA	5.56	125.66	119.32
1	C	149	GLN	N-CA-C	-5.51	105.17	111.07
1	B	86	GLY	N-CA-C	5.43	123.42	112.34
1	C	179	ILE	CB-CA-C	-5.41	104.99	112.24
3	G	1195	LYS	N-CA-C	-5.38	102.42	110.23
1	D	179	ILE	CB-CA-C	-5.36	105.06	112.24
1	D	201	PHE	CA-C-N	-5.32	113.25	119.32
1	D	201	PHE	C-N-CA	-5.32	113.25	119.32
1	E	34	LYS	N-CA-C	-5.32	105.38	111.07
1	D	111	ARG	N-CA-C	5.30	117.97	110.50
1	D	7	LYS	N-CA-C	-5.30	106.41	112.92
1	E	193	VAL	CB-CA-C	-5.27	105.07	111.87
1	B	134	ILE	N-CA-C	5.27	115.49	108.11
2	A	21	ASP	CB-CA-C	5.26	118.43	109.80
1	C	201	PHE	CA-C-N	-5.26	113.33	119.32
1	C	201	PHE	C-N-CA	-5.26	113.33	119.32
2	A	149	GLY	N-CA-C	-5.24	108.84	115.08
1	B	131	ASN	N-CA-C	5.21	119.33	112.92
1	C	54	THR	N-CA-C	5.21	119.61	113.16
1	B	98	ASP	N-CA-C	5.20	117.75	109.02
1	C	15	TYR	N-CA-C	5.19	119.31	112.92
1	E	205	ARG	N-CA-C	-5.16	105.09	111.33
2	A	76	MET	N-CA-C	5.14	121.16	109.81
1	C	173	ILE	CB-CA-C	-5.08	105.46	111.97
1	E	132	CYS	N-CA-C	5.08	116.90	109.24
2	A	27	SER	N-CA-C	-5.07	106.60	112.89
1	D	15	TYR	N-CA-C	5.04	119.11	112.92
2	A	72	PHE	CA-C-N	5.02	126.11	119.84
2	A	72	PHE	C-N-CA	5.02	126.11	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	111	ARG	N-CA-C	5.02	117.71	110.28
2	A	102	VAL	CA-C-N	5.01	126.11	119.84
2	A	102	VAL	C-N-CA	5.01	126.11	119.84

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	2	SER	Peptide
2	A	52	LYS	Peptide
1	C	128	TYR	Mainchain
1	D	217	LYS	Mainchain
1	E	157	PHE	Peptide
1	E	49	SER	Peptide
3	F	3220	LEU	Peptide

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	B	2407	0	2424	196	0
1	C	2503	0	2524	240	0
1	D	2514	0	2543	257	0
1	E	2292	0	2302	208	0
2	A	1416	0	1431	159	0
3	F	1699	0	1716	73	1
3	G	1750	0	1752	115	1
3	H	1750	0	1752	68	0
4	I	163	0	93	19	0
5	J	162	0	90	6	0
6	B	27	0	12	9	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	C	31	0	13	5	0
8	D	31	0	13	1	0
All	All	16748	0	16665	1118	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 34.

All (1118) 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:C:97:PHE:CD1	3:G:1204:GLN:HB3	1.57	1.40
1:C:9:HIS:CD2	1:D:41:LYS:HB3	1.73	1.22
1:D:174:ARG:HH11	1:D:174:ARG:CB	1.53	1.20
1:D:174:ARG:HB3	1:D:174:ARG:NH1	1.55	1.20
1:C:174:ARG:HB3	1:C:174:ARG:NH1	1.55	1.18
1:C:174:ARG:HH11	1:C:174:ARG:CB	1.58	1.15
1:C:97:PHE:CE1	3:G:1199:TRP:HZ3	1.66	1.14
1:C:97:PHE:CE1	3:G:1199:TRP:CZ3	2.41	1.08
2:A:145:LEU:HB2	2:A:151:LEU:HD23	1.36	1.07
1:C:97:PHE:CE1	3:G:1204:GLN:HB3	1.88	1.06
1:D:77:SER:HB3	1:E:120:HIS:HD2	1.18	1.06
1:C:9:HIS:HD2	1:D:41:LYS:CB	1.68	1.06
1:D:299:ALA:HB2	1:E:295:HIS:HD2	1.20	1.06
2:A:48:ASN:OD1	2:A:104:ARG:NH2	1.88	1.06
1:C:299:ALA:HB2	1:D:295:HIS:HD2	1.19	1.05
1:B:293:GLN:NE2	2:A:84:LEU:O	1.90	1.05
1:C:96:SER:O	1:C:97:PHE:CB	2.02	1.04
1:D:299:ALA:HB2	1:E:295:HIS:CD2	1.92	1.04
1:C:97:PHE:CE2	3:G:1205:GLY:C	2.34	1.04
1:B:95:ALA:HB2	3:F:3096:ASP:HB2	1.38	1.03
1:C:97:PHE:CZ	3:G:1205:GLY:CA	2.41	1.03
1:B:48:HIS:CE1	1:B:156:THR:HG23	1.93	1.02
1:B:71:MET:HE3	1:B:105:VAL:HG21	1.43	1.01
1:C:9:HIS:CD2	1:D:41:LYS:CB	2.42	1.00
1:D:219:VAL:HG12	1:D:220:LEU:H	1.25	0.99
1:E:91:PHE:CE1	1:E:102:LYS:HD2	1.97	0.99
1:D:77:SER:HB3	1:E:120:HIS:CD2	1.98	0.98
1:C:232:ARG:HA	1:C:263:TRP:CZ2	2.00	0.97
1:C:111:ARG:NE	1:D:116:GLU:OE1	1.98	0.96
1:C:192:VAL:HG11	1:C:220:LEU:HB3	1.47	0.96
1:C:96:SER:O	1:C:97:PHE:HB2	1.16	0.94
1:B:276:VAL:HA	1:B:318:TRP:HB3	1.50	0.94
1:B:299:ALA:HB1	1:C:262:SER:HB3	1.48	0.94
1:C:97:PHE:CZ	3:G:1205:GLY:C	2.46	0.94
1:C:97:PHE:CZ	3:G:1199:TRP:CZ3	2.55	0.94
1:D:299:ALA:CB	1:E:295:HIS:HD2	1.80	0.94
1:D:97:PHE:CE2	3:G:1094:ALA:HB3	2.03	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:105:GLY:O	2:A:106:LYS:NZ	2.00	0.93
1:B:16:ARG:NH2	6:B:700:ADP:H5'2	1.84	0.92
1:B:277:THR:HG22	1:B:317:GLN:O	1.67	0.92
1:C:97:PHE:HD1	3:G:1204:GLN:HB3	1.15	0.92
2:A:120:GLU:HA	2:A:123:ILE:HD12	1.51	0.92
1:C:297:ILE:HD13	1:D:297:ILE:HD11	1.50	0.92
1:C:318:TRP:CZ2	1:C:318:TRP:CZ3	2.55	0.92
1:C:16:ARG:NH2	8:C:700:08T:O2A	2.03	0.91
1:D:97:PHE:CE2	3:G:1079:GLY:C	2.49	0.91
2:A:155:LEU:CG	2:A:183:LEU:HD21	2.02	0.90
1:E:173:ILE:HG12	1:E:197:VAL:HG21	1.52	0.90
1:C:48:HIS:NE2	1:C:156:THR:HB	1.87	0.89
1:C:275:ARG:O	1:C:318:TRP:HD1	1.56	0.89
1:E:303:LEU:HD21	2:A:79:VAL:HG12	1.54	0.89
1:E:77:SER:HA	1:E:111:ARG:HD3	1.53	0.89
1:C:299:ALA:HB2	1:D:295:HIS:CD2	2.07	0.89
1:E:99:GLY:HA3	3:H:2204:GLN:HG2	1.54	0.88
1:C:97:PHE:CZ	3:G:1199:TRP:HZ3	1.91	0.88
1:B:56:LYS:HE2	6:B:700:ADP:O3B	1.73	0.88
1:D:97:PHE:CE2	3:G:1079:GLY:O	2.27	0.88
1:D:72:MET:HE2	3:H:2156:GLU:HA	1.54	0.88
1:C:188:ALA:HB3	1:C:221:ASP:HA	1.55	0.87
1:D:49:SER:HB3	1:D:50:PRO:C	2.00	0.87
1:E:111:ARG:HG2	1:E:112:SER:H	1.38	0.87
1:D:29:ASP:HA	1:D:32:THR:HG22	1.57	0.86
1:D:186:ALA:HB3	1:D:219:VAL:HG22	1.55	0.86
1:B:56:LYS:NZ	1:B:108:GLU:OE2	2.09	0.86
1:D:48:HIS:NE2	1:D:156:THR:HB	1.90	0.86
1:C:318:TRP:N	1:C:318:TRP:HE3	1.73	0.85
1:C:97:PHE:CD1	3:G:1204:GLN:CB	2.53	0.85
1:E:83:PHE:O	1:E:87:PRO:HD2	1.77	0.85
1:C:49:SER:HB3	1:C:50:PRO:C	2.01	0.85
3:F:3068:ASN:ND2	3:F:3085:ASP:OD2	2.10	0.84
1:C:9:HIS:HD2	1:D:41:LYS:HB2	1.41	0.84
2:A:145:LEU:HB3	2:A:151:LEU:HB3	1.59	0.84
1:B:183:GLU:HB3	1:B:185:ILE:HG13	1.59	0.84
1:C:29:ASP:HA	1:C:32:THR:HG22	1.58	0.84
1:D:174:ARG:HH11	1:D:174:ARG:HB3	0.71	0.84
2:A:155:LEU:HG	2:A:183:LEU:HD21	1.60	0.83
1:B:95:ALA:HB2	3:F:3096:ASP:CB	2.08	0.83
1:E:124:PHE:HE1	1:E:128:TYR:CE2	1.95	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:GLU:O	1:B:7:LYS:HG2	1.76	0.83
1:B:293:GLN:HE22	2:A:84:LEU:C	1.86	0.83
1:C:275:ARG:O	1:C:318:TRP:CD1	2.30	0.83
1:D:97:PHE:HE2	3:G:1094:ALA:CB	1.92	0.83
3:H:2068:ASN:ND2	3:H:2085:ASP:OD2	2.12	0.83
1:B:276:VAL:HA	1:B:318:TRP:CB	2.09	0.83
1:E:124:PHE:CE1	1:E:128:TYR:CE2	2.67	0.83
1:B:16:ARG:HH21	6:B:700:ADP:H5'2	1.41	0.82
1:B:126:GLU:OE2	1:B:151:ARG:NH2	2.10	0.82
1:D:97:PHE:CE2	3:G:1094:ALA:CB	2.62	0.82
1:D:275:ARG:O	1:D:318:TRP:HD1	1.62	0.82
1:E:172:MET:HE2	1:E:204:PHE:HD2	1.45	0.82
1:C:72:MET:HE1	3:G:1035:ASN:CB	2.09	0.81
1:D:116:GLU:OE2	1:D:119:ARG:NH1	2.13	0.81
2:A:13:HIS:CE1	2:A:32:PHE:CE2	2.69	0.81
1:B:186:ALA:HB3	1:B:219:VAL:HG22	1.64	0.80
1:E:91:PHE:HE1	1:E:102:LYS:HD2	1.44	0.80
1:B:37:THR:HG21	1:B:66:ASP:HB3	1.61	0.80
1:B:55:GLY:O	1:B:59:VAL:HG23	1.83	0.79
1:C:95:ALA:O	1:C:96:SER:C	2.26	0.79
1:E:109:PHE:CE2	1:E:118:GLN:HG2	2.16	0.79
2:A:80:TYR:CZ	2:A:84:LEU:HD11	2.17	0.78
1:E:124:PHE:CE1	1:E:128:TYR:HE2	2.01	0.78
1:E:119:ARG:HD3	1:E:122:ARG:HH21	1.49	0.78
2:A:69:LEU:HD12	2:A:98:LEU:HD22	1.65	0.78
1:E:13:GLN:HG2	2:A:131:TYR:CD1	2.19	0.78
2:A:55:ILE:HD11	2:A:92:GLU:HA	1.66	0.78
1:D:0:SER:OG	1:D:1:MET:HE2	1.84	0.78
1:D:186:ALA:HB3	1:D:219:VAL:CG2	2.13	0.77
1:C:97:PHE:CZ	3:G:1205:GLY:HA2	2.20	0.77
1:D:218:GLY:O	1:D:219:VAL:HB	1.83	0.77
3:G:1032:ARG:HG2	3:G:1103:PRO:HD3	1.66	0.77
1:D:186:ALA:N	1:D:219:VAL:HA	1.99	0.77
1:C:97:PHE:CE1	3:G:1205:GLY:N	2.53	0.77
1:D:97:PHE:HB3	3:G:1078:ASP:O	1.85	0.77
1:E:251:ARG:HH21	2:A:71:GLN:NE2	1.83	0.77
1:C:97:PHE:CZ	3:G:1205:GLY:N	2.54	0.76
1:D:222:ALA:O	1:D:225:LEU:HB3	1.84	0.76
3:H:2143:LYS:HG2	3:H:2144:GLU:HG3	1.65	0.76
1:C:174:ARG:HB3	1:C:174:ARG:HH11	0.69	0.76
1:E:95:ALA:HB3	3:H:2220:LEU:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:219:VAL:HG12	1:D:220:LEU:N	2.00	0.76
1:C:318:TRP:HE3	1:C:318:TRP:H	1.32	0.76
1:E:173:ILE:HG23	1:E:193:VAL:HG11	1.68	0.76
1:B:95:ALA:HB2	3:F:3096:ASP:N	2.00	0.76
2:A:120:GLU:O	2:A:124:ILE:HG13	1.84	0.76
1:D:95:ALA:HB2	3:G:1095:ALA:C	2.11	0.76
2:A:177:GLN:NE2	3:F:3156:GLU:HG2	2.02	0.75
2:A:177:GLN:HE21	3:F:3156:GLU:HG2	1.50	0.75
1:B:71:MET:HE3	1:B:105:VAL:CG2	2.16	0.75
1:C:318:TRP:N	1:C:318:TRP:CE3	2.54	0.75
1:D:97:PHE:C	1:D:99:GLY:H	1.90	0.75
1:D:186:ALA:CB	1:D:219:VAL:HG22	2.16	0.75
1:E:172:MET:CE	1:E:204:PHE:HD2	2.00	0.75
3:F:3143:LYS:HG2	3:F:3144:GLU:HG3	1.67	0.75
1:C:119:ARG:HB3	1:C:122:ARG:NH1	2.01	0.75
1:D:119:ARG:HB3	1:D:122:ARG:NH1	2.01	0.75
1:C:89:THR:HA	1:C:124:PHE:HE2	1.52	0.74
1:E:121:LEU:O	1:E:125:MET:HG3	1.86	0.74
1:B:189:ASP:O	1:B:192:VAL:HG12	1.88	0.74
1:B:95:ALA:CB	3:F:3096:ASP:HB2	2.16	0.74
1:C:97:PHE:HE2	3:G:1206:ALA:CB	2.00	0.74
1:C:97:PHE:CE2	3:G:1205:GLY:O	2.39	0.74
2:A:145:LEU:CB	2:A:151:LEU:HD23	2.14	0.74
1:C:97:PHE:CE1	3:G:1204:GLN:CB	2.70	0.74
1:D:85:ARG:NH2	4:I:6:DC:OP1	2.20	0.74
2:A:13:HIS:CE1	2:A:32:PHE:CZ	2.76	0.74
1:B:248:LYS:HG2	1:C:273:TYR:OH	1.87	0.74
1:D:219:VAL:CG1	1:D:220:LEU:H	1.98	0.74
3:F:3016:THR:O	3:F:3188:LYS:NZ	2.18	0.73
1:D:97:PHE:C	1:D:99:GLY:N	2.45	0.73
1:D:294:TYR:HD2	1:E:293:GLN:NE2	1.87	0.73
1:C:97:PHE:HA	3:G:1204:GLN:HG2	1.69	0.73
1:D:276:VAL:HG23	1:D:318:TRP:HB3	1.70	0.73
3:G:1068:ASN:ND2	3:G:1085:ASP:OD2	2.22	0.73
1:D:106:ILE:HG21	1:D:109:PHE:CD1	2.24	0.73
1:C:279:GLN:O	1:C:282:ILE:HG22	1.88	0.72
1:E:178:GLU:O	1:E:181:LYS:HB2	1.89	0.72
1:C:206:LYS:HE3	1:D:152:CYS:O	1.89	0.72
1:E:111:ARG:HG2	1:E:112:SER:N	2.04	0.72
2:A:155:LEU:HD11	2:A:183:LEU:HD11	1.71	0.72
1:E:121:LEU:HD23	1:E:124:PHE:HD2	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:129:LYS:HZ2	2:A:161:LEU:HD21	1.53	0.72
1:E:99:GLY:HA3	3:H:2204:GLN:CG	2.20	0.71
1:D:97:PHE:CZ	3:G:1079:GLY:O	2.43	0.71
1:E:173:ILE:HG23	1:E:193:VAL:CG1	2.19	0.71
1:E:251:ARG:HH21	2:A:71:GLN:HE22	1.36	0.71
1:E:99:GLY:CA	3:H:2204:GLN:HG2	2.20	0.71
2:A:14:GLN:HB3	2:A:18:TYR:CE2	2.25	0.71
1:C:97:PHE:HE2	3:G:1206:ALA:HB2	1.54	0.71
1:E:303:LEU:CD2	2:A:79:VAL:HG12	2.20	0.71
1:D:50:PRO:HA	1:D:139:ASN:O	1.91	0.71
1:E:49:SER:OG	1:E:50:PRO:HA	1.91	0.71
2:A:82:MET:HE3	2:A:97:TYR:CG	2.25	0.71
1:B:56:LYS:HA	1:B:157:PHE:HE2	1.55	0.70
1:C:97:PHE:CZ	3:G:1199:TRP:CE3	2.78	0.70
1:C:176:LEU:HD22	1:C:211:LEU:HD22	1.72	0.70
1:D:110:ASP:HB3	1:D:138:ALA:HB1	1.73	0.70
1:C:21:ASP:HA	1:C:30:LYS:HZ3	1.55	0.70
1:B:17:PRO:HG2	6:B:700:ADP:C2	2.27	0.70
1:C:106:ILE:HG21	1:C:109:PHE:CD1	2.26	0.70
3:H:2013:ASN:OD1	3:H:2216:TYR:OH	2.07	0.70
1:B:314:CYS:SG	1:C:282:ILE:HD11	2.32	0.70
1:D:72:MET:HE2	3:H:2156:GLU:CA	2.21	0.70
1:C:119:ARG:HB3	1:C:122:ARG:HH12	1.55	0.70
1:D:186:ALA:HB3	1:D:219:VAL:HG13	1.73	0.70
1:E:251:ARG:NE	2:A:71:GLN:OE1	2.25	0.70
1:C:57:THR:CG2	1:C:137:THR:HG21	2.22	0.70
2:A:129:LYS:NZ	2:A:161:LEU:HD21	2.06	0.70
1:C:277:THR:HG22	1:C:317:GLN:O	1.93	0.69
1:D:279:GLN:O	1:D:282:ILE:HG22	1.91	0.69
1:E:279:GLN:O	1:E:282:ILE:HG22	1.92	0.69
1:C:225:LEU:O	1:C:225:LEU:HD12	1.93	0.69
2:A:146:THR:HG23	2:A:151:LEU:HD21	1.74	0.69
1:B:148:LEU:O	1:B:152:CYS:HB2	1.93	0.69
1:D:206:LYS:HE3	1:E:152:CYS:O	1.93	0.69
1:D:16:ARG:NH2	8:D:700:08T:O2A	2.26	0.69
1:C:72:MET:HE2	3:G:1035:ASN:HA	1.75	0.69
1:D:218:GLY:O	1:D:219:VAL:CB	2.40	0.69
1:B:48:HIS:CE1	1:B:156:THR:CG2	2.75	0.68
1:B:162:ASP:O	1:B:166:ILE:HG13	1.94	0.68
2:A:162:VAL:HG12	2:A:162:VAL:O	1.92	0.68
1:D:204:PHE:C	1:D:207:THR:HG22	2.19	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:11:LEU:HD22	1:D:212:ASP:HB2	1.75	0.68
1:B:279:GLN:O	1:B:282:ILE:HG22	1.93	0.68
1:E:121:LEU:HD23	1:E:124:PHE:CD2	2.28	0.68
2:A:13:HIS:HE1	2:A:32:PHE:CE2	2.12	0.68
1:D:89:THR:HA	1:D:124:PHE:HE2	1.59	0.68
2:A:82:MET:HG2	2:A:97:TYR:CD2	2.29	0.68
1:E:96:SER:HB3	1:E:102:LYS:NZ	2.09	0.67
2:A:15:VAL:O	2:A:19:SER:OG	2.12	0.67
1:D:97:PHE:CD2	3:G:1079:GLY:C	2.71	0.67
1:D:216:SER:HB3	1:E:35:SER:OG	1.93	0.67
1:D:277:THR:HG22	1:D:317:GLN:O	1.94	0.67
1:E:119:ARG:HD3	1:E:122:ARG:NH2	2.10	0.67
1:B:85:ARG:HD3	2:A:22:TRP:CE3	2.30	0.67
1:B:316:MET:HB3	1:B:318:TRP:CZ3	2.29	0.67
1:C:97:PHE:C	1:C:99:GLY:N	2.51	0.67
1:C:204:PHE:C	1:C:207:THR:HG22	2.19	0.67
3:G:1143:LYS:HG2	3:G:1144:GLU:HG3	1.75	0.67
1:C:50:PRO:HA	1:C:139:ASN:O	1.95	0.67
1:C:97:PHE:HZ	3:G:1205:GLY:HA2	1.59	0.67
1:E:200:ASN:OD1	1:E:200:ASN:N	2.26	0.67
1:B:8:GLU:HB3	1:B:14:LYS:HB2	1.76	0.67
1:B:37:THR:CG2	1:B:66:ASP:HB3	2.25	0.67
1:B:83:PHE:O	1:B:87:PRO:HD2	1.95	0.67
1:C:177:THR:OG1	1:C:190:MET:HE1	1.95	0.67
2:A:155:LEU:CD2	2:A:183:LEU:HD21	2.24	0.67
1:E:111:ARG:HB3	1:E:114:LEU:HD12	1.76	0.67
1:D:297:ILE:HG22	1:E:293:GLN:O	1.95	0.67
1:C:232:ARG:CA	1:C:263:TRP:CZ2	2.77	0.66
1:E:86:GLY:O	1:E:90:ASN:HB2	1.95	0.66
1:C:116:GLU:OE2	1:C:119:ARG:NH1	2.27	0.66
1:E:251:ARG:NH2	2:A:71:GLN:NE2	2.44	0.66
1:D:263:TRP:CZ2	1:D:267:LYS:HG3	2.31	0.66
1:E:30:LYS:O	1:E:34:LYS:HG2	1.94	0.66
1:C:263:TRP:CZ2	1:C:267:LYS:HG3	2.31	0.66
1:E:169:MET:O	1:E:173:ILE:HG13	1.96	0.66
2:A:177:GLN:NE2	2:A:181:LYS:HZ1	1.94	0.66
3:H:2176:ASN:HB3	3:H:2227:ASP:OD1	1.95	0.66
4:I:8:DA:H2	5:J:3:DT:H3	1.43	0.66
1:C:110:ASP:HB3	1:C:138:ALA:HB1	1.76	0.65
1:D:186:ALA:HB3	1:D:219:VAL:CG1	2.27	0.65
1:E:56:LYS:HD2	1:E:137:THR:HG23	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:189:ASP:O	1:E:192:VAL:HG12	1.95	0.65
2:A:30:ASP:O	2:A:33:LYS:HG2	1.95	0.65
3:H:2181:ILE:HD12	3:H:2223:ASP:HB2	1.77	0.65
1:B:285:TYR:CE1	2:A:93:ALA:HB1	2.31	0.65
2:A:74:GLU:CD	2:A:104:ARG:HD3	2.21	0.65
1:E:124:PHE:HE1	1:E:128:TYR:CD2	2.14	0.65
1:C:97:PHE:HD1	3:G:1204:GLN:CB	2.02	0.65
3:H:2030:MSE:SE	3:H:2103:PRO:HG2	2.47	0.65
1:E:263:TRP:CZ2	1:E:267:LYS:HG3	2.31	0.65
1:D:95:ALA:HB2	3:G:1096:ASP:N	2.11	0.65
1:B:303:LEU:HD21	1:C:288:VAL:HG12	1.79	0.65
1:C:72:MET:HE1	3:G:1035:ASN:HB3	1.78	0.65
1:D:186:ALA:H	1:D:219:VAL:HA	1.59	0.65
1:E:91:PHE:CZ	1:E:102:LYS:HB3	2.32	0.65
1:B:172:MET:O	1:B:176:LEU:HG	1.96	0.64
1:D:57:THR:CG2	1:D:137:THR:HG21	2.26	0.64
1:D:297:ILE:HD13	1:E:297:ILE:HD11	1.79	0.64
1:B:75:ASN:OD1	1:B:76:GLY:N	2.29	0.64
4:I:1:DG:H2''	4:I:2:DG:C8	2.31	0.64
1:B:299:ALA:HB1	1:C:262:SER:CB	2.27	0.64
1:C:72:MET:HE1	3:G:1035:ASN:HB2	1.78	0.64
1:D:119:ARG:HB3	1:D:122:ARG:HH12	1.61	0.64
1:B:42:ILE:HD12	1:B:103:VAL:HG21	1.80	0.64
1:C:176:LEU:HD22	1:C:211:LEU:CD2	2.26	0.64
1:C:91:PHE:HB2	3:G:1035:ASN:HB2	1.78	0.64
2:A:82:MET:HE3	2:A:97:TYR:CD2	2.33	0.64
1:C:21:ASP:HA	1:C:30:LYS:NZ	2.12	0.64
3:F:3096:ASP:HB3	3:F:3099:THR:HG23	1.79	0.64
1:B:276:VAL:HG23	1:B:318:TRP:HB3	1.80	0.64
3:G:1096:ASP:HB3	3:G:1099:THR:HG23	1.80	0.64
1:B:289:GLY:C	2:A:85:ILE:HG23	2.23	0.64
1:D:21:ASP:HA	1:D:30:LYS:NZ	2.13	0.64
1:B:218:GLY:O	1:B:219:VAL:HG23	1.97	0.63
1:E:124:PHE:CE1	1:E:128:TYR:CD2	2.87	0.63
4:I:7:DT:H1'	4:I:8:DA:H5'	1.79	0.63
1:D:276:VAL:HG23	1:D:318:TRP:CG	2.33	0.63
1:D:204:PHE:HA	1:D:207:THR:CG2	2.27	0.63
1:D:297:ILE:HG23	1:E:297:ILE:HG13	1.81	0.63
3:H:2159:ALA:HB3	3:H:2161:THR:HG22	1.81	0.63
1:B:95:ALA:HB2	3:F:3096:ASP:CA	2.28	0.63
1:C:97:PHE:C	1:C:99:GLY:H	2.04	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:ILE:HD13	1:D:297:ILE:CD1	2.27	0.63
1:D:57:THR:CG2	1:D:107:ASP:OD1	2.47	0.63
2:A:76:MET:N	2:A:77:PRO:HD2	2.13	0.63
1:B:172:MET:HE2	1:B:207:THR:CG2	2.29	0.63
2:A:82:MET:O	2:A:86:GLY:HA3	1.99	0.62
1:C:204:PHE:HA	1:C:207:THR:CG2	2.29	0.62
1:D:9:HIS:HD2	1:E:41:LYS:CB	2.11	0.62
2:A:155:LEU:HG	2:A:183:LEU:CD2	2.29	0.62
1:D:77:SER:CB	1:E:120:HIS:CD2	2.81	0.62
1:D:109:PHE:HE2	1:D:118:GLN:HG2	1.64	0.62
1:E:75:ASN:ND2	2:A:135:THR:HG23	2.14	0.62
1:E:168:MET:HE2	1:E:201:PHE:CZ	2.35	0.62
3:H:2226:HIS:ND1	3:H:2228:PHE:HB2	2.15	0.62
1:D:224:ILE:HA	1:D:227:LEU:HG	1.82	0.62
3:F:3001:MSE:HE3	3:F:3003:LEU:HD21	1.81	0.62
3:G:1159:ALA:HB3	3:G:1161:THR:HG22	1.80	0.62
1:D:49:SER:N	1:D:56:LYS:HD3	2.15	0.62
1:C:49:SER:N	1:C:56:LYS:HD3	2.14	0.62
1:B:95:ALA:HB2	3:F:3096:ASP:H	1.65	0.61
2:A:133:VAL:HG12	2:A:134:ASN:N	2.15	0.61
1:B:93:SER:OG	3:F:3055:TYR:CE1	2.42	0.61
1:E:298:ALA:HB1	2:A:83:ASN:ND2	2.15	0.61
2:A:49:ASN:O	2:A:50:LYS:HG2	2.00	0.61
1:D:294:TYR:CD2	1:E:293:GLN:NE2	2.68	0.61
2:A:155:LEU:HD21	2:A:183:LEU:HD21	1.82	0.61
1:B:263:TRP:CZ2	1:B:267:LYS:HG3	2.35	0.61
1:E:110:ASP:OD1	1:E:138:ALA:HA	2.01	0.61
1:B:111:ARG:HB3	1:B:114:LEU:HD12	1.81	0.61
2:A:122:LEU:O	2:A:126:LEU:HB2	2.01	0.61
1:D:276:VAL:HG23	1:D:318:TRP:CB	2.30	0.61
1:D:200:ASN:N	1:D:200:ASN:OD1	2.33	0.60
2:A:177:GLN:NE2	2:A:181:LYS:NZ	2.49	0.60
3:H:2096:ASP:HB3	3:H:2099:THR:HG23	1.82	0.60
3:F:3030:MSE:SE	3:F:3103:PRO:HG2	2.51	0.60
3:F:3159:ALA:HB3	3:F:3161:THR:HG22	1.83	0.60
4:I:1:DG:H2"	4:I:2:DG:H8	1.65	0.60
1:C:57:THR:CG2	1:C:107:ASP:OD1	2.49	0.60
1:E:284:MET:HG3	1:E:285:TYR:N	2.16	0.60
2:A:75:CYS:C	2:A:77:PRO:HD2	2.25	0.60
1:E:307:TYR:CD2	2:A:80:TYR:CD1	2.88	0.60
2:A:126:LEU:HD21	2:A:158:LEU:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:97:PHE:CE1	3:G:1204:GLN:C	2.80	0.60
1:E:167:GLU:O	1:E:171:GLN:HG3	2.02	0.60
2:A:130:ARG:HG2	2:A:158:LEU:HD11	1.83	0.60
1:B:110:ASP:OD1	1:B:110:ASP:N	2.28	0.60
1:B:172:MET:HE2	1:B:207:THR:HG21	1.82	0.60
1:D:97:PHE:HE2	3:G:1094:ALA:HB2	1.65	0.60
1:D:44:HIS:CE1	1:D:133:SER:HA	2.37	0.59
1:E:111:ARG:CG	1:E:112:SER:H	2.13	0.59
1:B:65:HIS:O	1:B:68:ASN:N	2.22	0.59
1:C:5:ASN:O	1:C:7:LYS:N	2.34	0.59
1:C:201:PHE:O	1:C:202:PRO:C	2.45	0.59
1:D:44:HIS:HE1	1:D:133:SER:HA	1.67	0.59
1:D:80:LYS:NZ	1:E:85:ARG:HH12	1.99	0.59
1:D:97:PHE:CD1	3:G:1079:GLY:HA3	2.37	0.59
1:E:75:ASN:HD21	2:A:135:THR:HG23	1.67	0.59
1:E:235:ILE:O	1:E:235:ILE:HG22	2.02	0.59
1:B:91:PHE:O	1:B:102:LYS:NZ	2.35	0.59
1:C:229:THR:O	1:C:233:GLY:CA	2.50	0.59
2:A:19:SER:HB3	3:F:3034:VAL:HB	1.84	0.59
1:B:151:ARG:HG2	1:B:151:ARG:O	2.02	0.59
1:D:200:ASN:HD22	1:D:206:LYS:HB3	1.67	0.59
1:D:232:ARG:O	1:D:263:TRP:CZ2	2.56	0.59
2:A:69:LEU:CD1	2:A:98:LEU:HD22	2.31	0.59
3:G:1226:HIS:ND1	3:G:1228:PHE:HB2	2.18	0.59
1:E:109:PHE:HE2	1:E:118:GLN:HG2	1.65	0.59
2:A:22:TRP:O	2:A:26:GLN:HB2	2.03	0.59
1:D:277:THR:HG23	1:D:280:SER:HB2	1.84	0.59
1:D:21:ASP:HA	1:D:30:LYS:HZ3	1.65	0.59
1:E:111:ARG:HB3	1:E:114:LEU:CD1	2.32	0.59
1:B:72:MET:HE1	1:B:91:PHE:HB2	1.85	0.59
1:B:109:PHE:CE2	1:B:118:GLN:HG2	2.37	0.59
1:C:97:PHE:CE2	3:G:1206:ALA:HB2	2.35	0.59
1:D:29:ASP:HA	1:D:32:THR:CG2	2.33	0.59
1:D:297:ILE:O	1:E:295:HIS:O	2.20	0.59
3:F:3096:ASP:O	3:F:3099:THR:HG23	2.03	0.59
1:C:310:ILE:HG12	1:D:285:TYR:CD2	2.38	0.59
1:E:166:ILE:O	1:E:169:MET:HB2	2.03	0.59
1:D:205:ARG:NH2	1:E:151:ARG:NH1	2.50	0.58
1:B:292:ASN:ND2	2:A:88:GLY:O	2.36	0.58
3:G:1110:PRO:HB2	3:G:1199:TRP:CD1	2.38	0.58
1:C:277:THR:HG21	1:C:317:GLN:HG2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:ARG:HH21	1:B:120:HIS:HE1	1.50	0.58
1:C:97:PHE:CD1	3:G:1199:TRP:HZ3	2.20	0.58
1:C:97:PHE:CE2	3:G:1206:ALA:N	2.71	0.58
2:A:71:GLN:OE1	2:A:71:GLN:HA	2.03	0.58
3:H:2110:PRO:HB2	3:H:2199:TRP:CD1	2.38	0.58
1:B:299:ALA:HB2	1:C:295:HIS:HD2	1.69	0.58
3:F:3146:LYS:HA	3:F:3171:ASP:HA	1.85	0.58
1:B:61:LYS:HG3	1:B:71:MET:HE1	1.85	0.58
1:D:201:PHE:O	1:D:202:PRO:C	2.46	0.58
1:B:89:THR:CG2	3:F:3055:TYR:OH	2.52	0.57
1:E:122:ARG:HB3	1:E:151:ARG:HH21	1.67	0.57
3:H:2032:ARG:HG2	3:H:2103:PRO:HD3	1.85	0.57
1:B:289:GLY:HA3	2:A:85:ILE:CG2	2.34	0.57
1:D:1:MET:HE2	1:D:1:MET:H	1.69	0.57
2:A:173:ASN:OD1	2:A:175:LYS:HB3	2.04	0.57
1:C:109:PHE:HE2	1:C:118:GLN:HG2	1.69	0.57
1:D:57:THR:HG22	1:D:107:ASP:OD1	2.04	0.57
1:D:284:MET:HG3	1:D:285:TYR:N	2.20	0.57
1:E:56:LYS:HD2	1:E:137:THR:CG2	2.34	0.57
1:E:203:ASP:CG	1:E:206:LYS:HB2	2.29	0.57
3:F:3180:PHE:HD2	3:F:3198:LEU:HD13	1.70	0.57
1:B:20:ILE:HD12	1:B:20:ILE:O	2.03	0.57
1:E:172:MET:HE3	1:E:204:PHE:HB2	1.86	0.57
2:A:2:SER:O	2:A:3:LEU:HB3	2.04	0.57
1:C:297:ILE:O	1:D:295:HIS:O	2.23	0.57
1:E:307:TYR:HB2	2:A:76:MET:HE1	1.85	0.57
2:A:82:MET:HG2	2:A:97:TYR:HD2	1.69	0.57
3:H:2176:ASN:OD1	3:H:2176:ASN:N	2.37	0.57
1:E:48:HIS:CD2	1:E:141:ILE:HD11	2.40	0.57
1:E:81:ILE:HG21	4:I:3:DT:H3'	1.85	0.57
1:B:177:THR:OG1	1:B:190:MET:HE1	2.05	0.57
1:E:107:ASP:HA	1:E:137:THR:HB	1.86	0.57
1:C:109:PHE:CE2	1:C:118:GLN:HG2	2.40	0.57
1:D:299:ALA:CB	1:E:295:HIS:CD2	2.68	0.57
1:B:4:VAL:HG23	1:B:4:VAL:O	2.04	0.56
1:C:95:ALA:HB2	3:G:1220:LEU:O	2.05	0.56
1:C:97:PHE:HE2	3:G:1205:GLY:C	2.09	0.56
1:C:188:ALA:HB3	1:C:220:LEU:O	2.04	0.56
1:D:95:ALA:O	1:D:96:SER:C	2.48	0.56
1:D:80:LYS:HE2	1:E:85:ARG:CZ	2.35	0.56
3:G:1146:LYS:HA	3:G:1171:ASP:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:MET:HE1	1:B:152:CYS:SG	2.45	0.56
1:D:204:PHE:HA	1:D:207:THR:HG22	1.86	0.56
3:H:2001:MSE:HE3	3:H:2003:LEU:HD21	1.86	0.56
3:H:2146:LYS:HA	3:H:2171:ASP:HA	1.86	0.56
1:B:46:ILE:HG12	1:B:136:ILE:HB	1.88	0.56
1:D:235:ILE:HG22	1:D:235:ILE:O	2.03	0.56
1:E:303:LEU:HD21	2:A:79:VAL:CG1	2.32	0.56
3:G:1057:LEU:O	3:G:1061:LEU:HG	2.04	0.56
3:F:3110:PRO:HB2	3:F:3199:TRP:CD1	2.40	0.56
1:D:80:LYS:NZ	1:E:85:ARG:NH1	2.52	0.56
1:D:80:LYS:HB3	4:I:5:DT:OP2	2.05	0.56
1:C:32:THR:O	1:C:36:ILE:HG13	2.06	0.56
1:C:29:ASP:HA	1:C:32:THR:CG2	2.34	0.56
1:C:90:ASN:HB2	3:G:1035:ASN:ND2	2.21	0.56
1:D:316:MET:O	1:D:318:TRP:CZ3	2.59	0.56
1:E:277:THR:HG23	1:E:280:SER:HB2	1.88	0.56
1:C:57:THR:HG22	1:C:107:ASP:OD1	2.06	0.56
1:D:9:HIS:HD2	1:E:41:LYS:HB2	1.71	0.56
1:D:97:PHE:CD2	3:G:1080:ASN:N	2.74	0.56
1:D:228:VAL:HG12	1:D:229:THR:N	2.20	0.56
1:B:16:ARG:NH2	6:B:700:ADP:C5'	2.65	0.55
1:C:44:HIS:HE1	1:C:133:SER:HA	1.71	0.55
2:A:43:ILE:HG23	2:A:95:PHE:HE1	1.71	0.55
1:C:77:SER:HB3	1:D:120:HIS:ND1	2.21	0.55
1:C:90:ASN:O	3:G:1037:THR:HG21	2.06	0.55
1:E:16:ARG:HG3	1:E:58:THR:HG23	1.87	0.55
1:B:125:MET:HG2	1:B:134:ILE:HD12	1.88	0.55
1:C:235:ILE:HG22	1:C:235:ILE:O	2.06	0.55
1:D:119:ARG:O	1:D:122:ARG:HG2	2.06	0.55
1:E:83:PHE:CE2	1:E:88:LEU:HD11	2.42	0.55
1:C:33:PHE:O	1:C:37:THR:HG23	2.06	0.55
1:C:44:HIS:CE1	1:C:133:SER:HA	2.42	0.55
1:D:177:THR:OG1	1:D:190:MET:HE1	2.06	0.55
3:G:1147:ILE:HG22	3:G:1169:LEU:HD12	1.88	0.55
1:B:85:ARG:NH2	2:A:26:GLN:HG2	2.21	0.55
1:E:172:MET:HB3	1:E:204:PHE:HE2	1.72	0.55
2:A:155:LEU:CD1	2:A:183:LEU:HD21	2.36	0.55
3:G:1042:ALA:HB2	3:G:1214:ALA:HB2	1.89	0.55
1:B:111:ARG:CB	1:B:114:LEU:HD12	2.37	0.55
1:C:246:ASP:OD2	1:C:249:GLN:HG3	2.07	0.55
1:D:297:ILE:CG2	1:E:293:GLN:O	2.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MET:HE2	1:C:178:GLU:OE1	2.07	0.55
1:B:3:THR:HG23	1:B:22:GLU:OE1	2.06	0.55
1:D:98:ASP:HB2	1:D:100:ARG:HG3	1.88	0.55
3:G:1200:ALA:HB1	3:G:1226:HIS:NE2	2.22	0.55
1:D:216:SER:CB	1:E:35:SER:OG	2.54	0.55
1:E:24:ILE:O	1:E:25:LEU:HD23	2.07	0.55
1:B:277:THR:HG23	1:B:280:SER:HB2	1.88	0.55
1:C:204:PHE:O	1:C:207:THR:HG22	2.06	0.55
2:A:55:ILE:O	2:A:56:ALA:HB3	2.06	0.55
5:J:6:DA:H2''	5:J:7:DC:O5'	2.06	0.55
1:E:68:ASN:O	1:E:100:ARG:HB3	2.06	0.54
1:B:293:GLN:CD	2:A:85:ILE:HA	2.32	0.54
1:D:205:ARG:NH2	1:E:151:ARG:HH12	2.05	0.54
2:A:57:GLN:HG3	2:A:58:LYS:HG3	1.88	0.54
2:A:182:LYS:O	2:A:185:LEU:HB3	2.06	0.54
1:B:237:ASP:OD1	1:B:237:ASP:N	2.40	0.54
1:C:72:MET:CE	3:G:1035:ASN:CB	2.83	0.54
1:C:72:MET:CE	3:G:1035:ASN:HA	2.37	0.54
1:C:284:MET:HG3	1:C:285:TYR:N	2.21	0.54
1:C:57:THR:HG22	1:C:137:THR:HG21	1.89	0.54
1:C:110:ASP:OD1	1:D:122:ARG:NH2	2.41	0.54
3:H:2033:ALA:HB2	3:H:2038:THR:HG23	1.89	0.54
3:H:2180:PHE:HD2	3:H:2198:LEU:HD13	1.73	0.54
1:D:33:PHE:O	1:D:37:THR:HG23	2.08	0.54
1:D:291:ASN:ND2	1:D:304:HIS:CE1	2.76	0.54
1:B:284:MET:HG3	1:B:285:TYR:N	2.23	0.54
1:D:109:PHE:CE2	1:D:118:GLN:HG2	2.43	0.54
1:E:59:VAL:HG21	1:E:157:PHE:CZ	2.43	0.54
1:E:158:GLY:O	1:E:159:GLN:HG2	2.07	0.54
1:B:235:ILE:O	1:B:235:ILE:HG22	2.08	0.54
1:C:192:VAL:CG1	1:C:220:LEU:HB3	2.28	0.54
3:H:2067:VAL:HG12	3:H:2085:ASP:OD2	2.08	0.54
1:B:275:ARG:O	1:B:318:TRP:HB2	2.08	0.53
1:B:163:GLU:HA	1:B:166:ILE:HD12	1.90	0.53
1:E:48:HIS:CE1	1:E:141:ILE:HG13	2.43	0.53
1:E:96:SER:HB3	1:E:102:LYS:CE	2.38	0.53
1:C:49:SER:HB3	1:C:50:PRO:O	2.08	0.53
1:E:237:ASP:N	1:E:237:ASP:OD1	2.41	0.53
1:C:97:PHE:O	3:G:1204:GLN:OE1	2.26	0.53
1:C:203:ASP:C	1:C:203:ASP:OD1	2.51	0.53
3:G:1090:ILE:HG23	3:H:2133:LEU:HD11	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:2225:THR:O	3:H:2226:HIS:HB3	2.08	0.53
1:C:277:THR:HG23	1:C:280:SER:HB2	1.91	0.53
1:B:85:ARG:HH21	2:A:26:GLN:HG2	1.74	0.53
1:C:5:ASN:C	1:C:7:LYS:H	2.17	0.53
1:C:119:ARG:CB	1:C:122:ARG:NH1	2.71	0.53
1:D:69:ALA:HB1	1:D:103:VAL:HG23	1.90	0.53
1:D:204:PHE:O	1:D:207:THR:HG22	2.09	0.53
1:D:250:LEU:HD13	1:D:309:PHE:HB3	1.90	0.53
1:E:172:MET:HB3	1:E:204:PHE:CE2	2.44	0.53
1:E:307:TYR:CE2	2:A:80:TYR:CZ	2.97	0.53
3:G:1018:ASN:C	3:G:1018:ASN:OD1	2.52	0.53
1:B:56:LYS:HA	1:B:157:PHE:CE2	2.42	0.53
1:C:237:ASP:N	1:C:237:ASP:OD1	2.41	0.53
1:C:250:LEU:HD13	1:C:309:PHE:HB3	1.89	0.53
1:C:277:THR:CG2	1:C:317:GLN:HG2	2.39	0.53
1:D:64:CYS:HB2	1:D:71:MET:HE2	1.90	0.53
2:A:82:MET:HE1	2:A:89:LEU:HD11	1.90	0.53
1:B:80:LYS:O	1:B:84:VAL:HG23	2.09	0.53
1:B:85:ARG:HD3	2:A:22:TRP:CD2	2.44	0.53
1:C:10:ILE:CG2	1:C:13:GLN:HB2	2.39	0.53
1:C:294:TYR:HD2	1:D:293:GLN:NE2	2.07	0.53
1:C:303:LEU:CD2	1:D:265:VAL:HG12	2.39	0.53
1:E:201:PHE:HB3	1:E:202:PRO:HD3	1.90	0.53
1:C:191:LYS:HB2	1:C:225:LEU:HD22	1.90	0.52
1:C:3:THR:HG21	1:C:18:SER:HB3	1.91	0.52
1:C:204:PHE:HA	1:C:207:THR:HG22	1.92	0.52
3:H:2096:ASP:O	3:H:2099:THR:HG23	2.09	0.52
1:C:2:ILE:HG13	1:C:178:GLU:HG2	1.91	0.52
1:C:13:GLN:NE2	1:D:126:GLU:HG2	2.24	0.52
1:E:172:MET:CE	1:E:204:PHE:CD2	2.89	0.52
1:B:242:LEU:HD12	1:B:250:LEU:HD11	1.91	0.52
1:C:229:THR:O	1:C:233:GLY:HA3	2.10	0.52
1:D:169:MET:O	1:D:173:ILE:HG13	2.09	0.52
1:E:80:LYS:O	1:E:84:VAL:HG23	2.09	0.52
3:G:1176:ASN:OD1	3:G:1176:ASN:N	2.42	0.52
3:F:3022:MSE:HE3	3:F:3023:LEU:O	2.09	0.52
3:F:3096:ASP:HB3	3:F:3099:THR:CG2	2.39	0.52
1:B:32:THR:O	1:B:36:ILE:HG13	2.10	0.52
1:C:64:CYS:SG	1:C:71:MET:HG3	2.50	0.52
1:D:80:LYS:HZ3	1:E:85:ARG:HH12	1.55	0.52
1:E:99:GLY:N	3:H:2204:GLN:HG2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:250:LEU:HD13	1:E:309:PHE:HB3	1.91	0.52
3:G:1077:GLU:CD	3:G:1077:GLU:H	2.18	0.52
3:H:2147:ILE:HG22	3:H:2169:LEU:HD12	1.92	0.52
1:B:316:MET:CB	1:B:318:TRP:CZ3	2.93	0.52
1:C:12:GLU:O	8:C:700:08T:O3'	2.28	0.52
3:G:1001:MSE:HE3	3:G:1003:LEU:HD21	1.91	0.52
3:H:2057:LEU:O	3:H:2061:LEU:HG	2.10	0.52
3:F:3092:TRP:CG	3:F:3093:PRO:HD2	2.44	0.52
1:D:276:VAL:HA	1:D:318:TRP:HB2	1.92	0.52
1:B:250:LEU:HD13	1:B:309:PHE:HB3	1.92	0.52
1:C:42:ILE:H	1:C:101:GLN:HE22	1.57	0.52
1:E:44:HIS:ND1	1:E:125:MET:HE3	2.25	0.52
1:E:307:TYR:HE2	2:A:80:TYR:CZ	2.28	0.52
1:C:53:GLY:O	8:C:700:08T:H14	2.09	0.51
2:A:2:SER:O	2:A:3:LEU:CB	2.58	0.51
1:B:277:THR:HG23	1:B:280:SER:CB	2.41	0.51
1:C:291:ASN:ND2	1:C:304:HIS:CE1	2.78	0.51
1:D:208:ILE:HG22	1:D:208:ILE:O	2.10	0.51
2:A:40:PHE:CD2	2:A:64:MET:HE2	2.45	0.51
2:A:135:THR:O	2:A:139:ILE:HG12	2.10	0.51
1:C:192:VAL:HG13	1:C:220:LEU:HD23	1.92	0.51
1:D:10:ILE:CG2	1:D:13:GLN:HB2	2.39	0.51
1:E:97:PHE:HD2	3:H:2206:ALA:HB2	1.76	0.51
1:E:307:TYR:CD2	2:A:80:TYR:CE1	2.98	0.51
1:E:45:ILE:HB	1:E:135:ILE:HG12	1.92	0.51
3:H:2087:ARG:O	3:F:3168:THR:N	2.39	0.51
1:B:29:ASP:O	1:B:33:PHE:CD2	2.64	0.51
1:B:90:ASN:O	1:B:94:ALA:N	2.34	0.51
1:D:277:THR:HG23	1:D:280:SER:CB	2.41	0.51
1:E:42:ILE:HG22	1:E:43:PRO:O	2.11	0.51
1:C:96:SER:O	1:C:97:PHE:CG	2.63	0.51
1:C:89:THR:HA	1:C:124:PHE:CE2	2.40	0.51
1:D:119:ARG:CB	1:D:122:ARG:NH1	2.74	0.51
1:E:26:PRO:HB2	1:E:29:ASP:HB2	1.93	0.51
1:E:42:ILE:O	1:E:133:SER:OG	2.26	0.51
3:H:2001:MSE:HG3	3:H:2073:ILE:HB	1.92	0.51
1:C:98:ASP:HB2	1:C:100:ARG:HG3	1.91	0.51
1:D:44:HIS:CD2	1:D:125:MET:HE3	2.46	0.51
1:D:186:ALA:CB	1:D:219:VAL:HG13	2.39	0.51
2:A:11:ASN:OD1	2:A:14:GLN:HG3	2.10	0.51
5:J:10:DC:C5'	5:J:10:DC:H6	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:16:ARG:O	1:B:17:PRO:C	2.52	0.51
1:B:111:ARG:HB3	1:B:114:LEU:CD1	2.40	0.51
1:C:94:ALA:O	1:C:131:ASN:ND2	2.43	0.51
1:D:9:HIS:HD1	1:D:10:ILE:N	2.09	0.51
1:E:298:ALA:HA	2:A:84:LEU:HA	1.93	0.51
3:H:2067:VAL:CG1	3:H:2085:ASP:OD2	2.59	0.51
1:B:294:TYR:OH	1:E:297:ILE:HD13	2.11	0.50
2:A:140:ASN:O	2:A:144:ILE:HG13	2.10	0.50
1:C:57:THR:HG21	1:C:107:ASP:OD1	2.11	0.50
1:D:57:THR:HG21	1:D:107:ASP:OD1	2.09	0.50
1:E:96:SER:HB3	1:E:102:LYS:HE2	1.91	0.50
1:B:243:LYS:HG2	1:B:318:TRP:NE1	2.26	0.50
1:B:291:ASN:ND2	1:B:304:HIS:CE1	2.79	0.50
1:C:251:ARG:NH2	1:D:270:GLU:HG3	2.26	0.50
1:D:204:PHE:CA	1:D:207:THR:HG22	2.41	0.50
1:C:242:LEU:HD12	1:C:250:LEU:HD11	1.92	0.50
1:D:13:GLN:HE22	1:E:126:GLU:HB3	1.76	0.50
1:E:25:LEU:HB2	1:E:30:LYS:HG3	1.93	0.50
3:F:3001:MSE:HG3	3:F:3073:ILE:HB	1.94	0.50
1:B:307:TYR:CG	1:C:289:GLY:HA3	2.46	0.50
1:D:237:ASP:OD1	1:D:237:ASP:N	2.43	0.50
1:D:242:LEU:HD12	1:D:250:LEU:HD11	1.94	0.50
1:D:246:ASP:OD2	1:D:249:GLN:HG3	2.12	0.50
3:G:1032:ARG:HD3	3:G:1103:PRO:HA	1.94	0.50
1:C:13:GLN:HE21	1:C:16:ARG:NH1	2.09	0.50
1:C:163:GLU:CD	1:C:163:GLU:H	2.20	0.50
1:E:307:TYR:CE2	2:A:80:TYR:CE2	3.00	0.50
3:G:1001:MSE:HG3	3:G:1073:ILE:HB	1.93	0.50
1:C:69:ALA:HB1	1:C:103:VAL:HG23	1.94	0.50
1:C:299:ALA:CB	1:D:295:HIS:HD2	2.07	0.50
1:D:80:LYS:NZ	4:I:4:DG:OP2	2.44	0.50
2:A:52:LYS:O	2:A:53:CYS:HB3	2.10	0.50
3:H:2042:ALA:HB2	3:H:2214:ALA:HB2	1.93	0.50
1:D:64:CYS:SG	1:D:71:MET:HG3	2.52	0.50
1:D:164:ASP:O	1:D:168:MET:HG3	2.11	0.50
1:D:261:TYR:CZ	1:D:265:VAL:HG21	2.46	0.50
1:E:124:PHE:CD1	1:E:128:TYR:CE2	3.00	0.50
2:A:133:VAL:HG12	2:A:134:ASN:H	1.76	0.50
3:F:3018:ASN:C	3:F:3018:ASN:OD1	2.54	0.50
3:F:3057:LEU:O	3:F:3061:LEU:HG	2.12	0.50
1:B:67:VAL:HG12	1:B:67:VAL:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:13:GLN:NE2	1:E:126:GLU:HB3	2.27	0.50
1:D:221:ASP:OD1	1:D:224:ILE:HG13	2.12	0.50
1:E:24:ILE:HD13	1:E:172:MET:HG2	1.93	0.50
1:E:298:ALA:HB1	2:A:83:ASN:HD21	1.77	0.50
3:H:2125:GLN:O	3:H:2129:VAL:HG23	2.12	0.50
1:B:59:VAL:HG21	1:B:157:PHE:HZ	1.77	0.49
1:B:131:ASN:O	1:B:132:CYS:HB3	2.12	0.49
1:B:95:ALA:CB	3:F:3096:ASP:N	2.73	0.49
1:C:13:GLN:HE21	1:C:16:ARG:HH12	1.59	0.49
1:C:97:PHE:HE2	3:G:1206:ALA:N	2.11	0.49
1:C:297:ILE:CD1	1:D:297:ILE:HD11	2.32	0.49
1:E:59:VAL:HG21	1:E:157:PHE:HZ	1.77	0.49
1:E:59:VAL:O	1:E:62:ALA:HB3	2.12	0.49
3:G:1189:MSE:H	3:G:1189:MSE:SE	2.46	0.49
1:B:83:PHE:CE1	1:B:88:LEU:HD13	2.47	0.49
1:B:91:PHE:CZ	1:B:102:LYS:HB3	2.46	0.49
1:C:12:GLU:CD	1:D:153:ARG:HH12	2.20	0.49
1:C:203:ASP:OD1	1:C:205:ARG:N	2.44	0.49
1:C:255:PRO:HB3	1:C:302:GLU:CD	2.37	0.49
1:D:97:PHE:CZ	3:G:1079:GLY:C	2.91	0.49
1:E:81:ILE:HG22	4:I:3:DT:P	2.53	0.49
1:E:101:GLN:HG2	1:E:103:VAL:HG23	1.94	0.49
1:E:242:LEU:HD12	1:E:250:LEU:HD11	1.94	0.49
3:G:1096:ASP:OD2	3:G:1098:SER:OG	2.28	0.49
3:H:2092:TRP:CG	3:H:2093:PRO:HD2	2.47	0.49
1:B:97:PHE:O	1:B:98:ASP:OD1	2.30	0.49
1:C:49:SER:HB2	1:C:56:LYS:CE	2.43	0.49
1:C:215:SER:O	1:C:216:SER:C	2.55	0.49
1:B:4:VAL:O	1:B:4:VAL:CG2	2.60	0.49
1:D:186:ALA:HB3	1:D:219:VAL:CB	2.41	0.49
1:E:276:VAL:HG22	1:E:277:THR:H	1.78	0.49
1:D:276:VAL:CG2	1:D:318:TRP:HB3	2.38	0.49
1:E:122:ARG:HB3	1:E:151:ARG:NH2	2.27	0.49
2:A:5:LYS:O	2:A:6:ASP:HB2	2.13	0.49
3:H:2089:THR:HB	3:F:3166:SER:HB3	1.93	0.49
3:F:3127:LEU:HD23	3:F:3184:MSE:HE1	1.94	0.49
1:B:168:MET:O	1:B:169:MET:C	2.54	0.49
1:B:285:TYR:OH	2:A:93:ALA:HA	2.11	0.49
1:C:10:ILE:HG22	1:C:13:GLN:HB2	1.95	0.49
1:C:29:ASP:CA	1:C:32:THR:HG22	2.37	0.49
1:C:106:ILE:CG2	1:C:109:PHE:CD1	2.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:261:TYR:CZ	1:C:265:VAL:HG21	2.48	0.49
1:D:10:ILE:HG22	1:D:13:GLN:HB2	1.95	0.49
2:A:104:ARG:CZ	2:A:105:GLY:HA2	2.43	0.49
2:A:159:LYS:O	2:A:162:VAL:HG23	2.13	0.49
3:H:2089:THR:N	3:F:3166:SER:O	2.35	0.49
1:B:246:ASP:OD2	1:B:249:GLN:HG3	2.12	0.48
2:A:149:GLY:C	2:A:151:LEU:H	2.20	0.48
1:B:261:TYR:CZ	1:B:265:VAL:HG21	2.48	0.48
1:D:174:ARG:CB	1:D:174:ARG:NH1	2.37	0.48
2:A:93:ALA:O	2:A:96:ASN:N	2.46	0.48
1:B:83:PHE:HE1	1:B:88:LEU:HD13	1.78	0.48
6:B:700:ADP:N3	6:B:700:ADP:H2'	2.26	0.48
1:E:124:PHE:O	1:E:127:ALA:N	2.46	0.48
1:E:291:ASN:ND2	1:E:304:HIS:CE1	2.81	0.48
8:C:700:08T:N3	8:C:700:08T:C2'	2.72	0.48
1:E:67:VAL:HG12	1:E:67:VAL:O	2.13	0.48
1:D:277:THR:CG2	1:D:317:GLN:O	2.62	0.48
3:F:3033:ALA:HB2	3:F:3038:THR:HG23	1.95	0.48
3:F:3115:VAL:HG22	3:F:3197:LEU:HD22	1.96	0.48
1:C:111:ARG:CZ	1:D:116:GLU:OE1	2.61	0.48
1:C:164:ASP:O	1:C:168:MET:HG3	2.13	0.48
3:F:3147:ILE:HG22	3:F:3169:LEU:HD12	1.96	0.48
3:F:3149:ILE:O	3:F:3166:SER:HA	2.13	0.48
1:B:93:SER:O	3:F:3099:THR:HG21	2.13	0.48
1:B:169:MET:SD	1:B:197:VAL:HG12	2.53	0.48
2:A:74:GLU:OE1	2:A:104:ARG:HD3	2.13	0.48
1:B:189:ASP:OD1	1:B:191:LYS:HG3	2.13	0.48
1:C:42:ILE:H	1:C:101:GLN:NE2	2.12	0.48
1:D:13:GLN:HE21	1:D:16:ARG:HH12	1.60	0.48
1:D:17:PRO:HB3	1:D:22:GLU:HG2	1.94	0.48
1:D:106:ILE:CG2	1:D:109:PHE:CD1	2.95	0.48
1:E:261:TYR:CZ	1:E:265:VAL:HG21	2.48	0.48
3:H:2115:VAL:HG22	3:H:2197:LEU:HD22	1.96	0.48
3:G:1085:ASP:OD1	3:G:1086:ALA:N	2.47	0.48
3:G:1115:VAL:HG22	3:G:1197:LEU:HD22	1.96	0.48
1:B:2:ILE:HD13	1:B:178:GLU:HG2	1.95	0.48
1:B:73:PHE:CD1	1:B:73:PHE:C	2.91	0.48
1:C:200:ASN:OD1	1:C:200:ASN:N	2.46	0.48
1:D:49:SER:HB3	1:D:50:PRO:O	2.12	0.48
1:D:72:MET:HE3	1:D:91:PHE:CG	2.48	0.48
1:E:148:LEU:HD12	1:E:148:LEU:HA	1.74	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:1050:PHE:CE2	3:G:1052:VAL:HB	2.49	0.48
1:B:20:ILE:HG12	1:B:33:PHE:HB2	1.96	0.47
1:C:204:PHE:CA	1:C:207:THR:HG22	2.44	0.47
1:D:33:PHE:CE1	1:D:155:ILE:HD13	2.49	0.47
2:A:155:LEU:HD11	2:A:183:LEU:HD21	1.96	0.47
3:G:1180:PHE:HD2	3:G:1198:LEU:HD13	1.78	0.47
3:F:3077:GLU:H	3:F:3077:GLU:CD	2.21	0.47
3:F:3002:LYS:O	3:F:3003:LEU:HD23	2.14	0.47
3:F:3096:ASP:OD2	3:F:3098:SER:OG	2.32	0.47
4:I:2:DG:N2	5:J:9:DC:N3	2.60	0.47
1:B:55:GLY:HA2	6:B:700:ADP:O1A	2.14	0.47
3:F:3090:ILE:HG22	3:F:3091:PHE:N	2.29	0.47
1:C:276:VAL:HG22	1:C:277:THR:H	1.79	0.47
1:E:13:GLN:HG2	2:A:131:TYR:HD1	1.72	0.47
1:B:64:CYS:SG	1:B:71:MET:HG3	2.54	0.47
1:B:85:ARG:O	1:B:89:THR:HB	2.14	0.47
3:H:2096:ASP:HB3	3:H:2099:THR:CG2	2.44	0.47
1:B:121:LEU:C	1:B:121:LEU:HD23	2.39	0.47
1:D:97:PHE:CE2	3:G:1080:ASN:HA	2.49	0.47
1:D:166:ILE:O	1:D:170:LYS:HG3	2.14	0.47
1:E:255:PRO:HA	1:E:302:GLU:HG3	1.97	0.47
3:H:2180:PHE:CE2	3:H:2198:LEU:HB3	2.50	0.47
1:B:31:GLU:O	1:B:35:SER:HB2	2.15	0.47
1:C:91:PHE:HD1	3:G:1035:ASN:O	1.98	0.47
1:C:125:MET:HE1	1:C:152:CYS:SG	2.55	0.47
1:C:277:THR:HG23	1:C:280:SER:CB	2.45	0.47
8:C:700:08T:N3	8:C:700:08T:H6	2.30	0.47
1:E:98:ASP:OD2	1:E:100:ARG:NH2	2.48	0.47
1:E:159:GLN:O	1:E:160:PRO:C	2.57	0.47
1:E:277:THR:HG23	1:E:280:SER:CB	2.45	0.47
3:G:1096:ASP:HB3	3:G:1099:THR:CG2	2.43	0.47
3:F:3085:ASP:OD1	3:F:3086:ALA:N	2.47	0.47
3:F:3189:MSE:SE	3:F:3189:MSE:H	2.48	0.47
4:I:1:DG:C2	4:I:2:DG:C4	3.03	0.47
1:C:200:ASN:HD22	1:C:206:LYS:HB3	1.80	0.47
1:D:218:GLY:O	1:D:219:VAL:HG23	2.14	0.47
1:E:49:SER:OG	1:E:139:ASN:HA	2.15	0.47
1:B:20:ILE:HG22	1:B:66:ASP:OD2	2.16	0.47
1:C:17:PRO:HB3	1:C:22:GLU:HG2	1.97	0.47
1:C:49:SER:HB2	1:C:56:LYS:NZ	2.30	0.47
2:A:10:LEU:HA	2:A:14:GLN:OE1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:85:ARG:O	1:D:89:THR:HB	2.15	0.46
1:D:276:VAL:HG22	1:D:277:THR:H	1.80	0.46
1:E:72:MET:HE1	1:E:91:PHE:HB2	1.98	0.46
3:G:1092:TRP:CG	3:G:1093:PRO:HD2	2.50	0.46
3:F:3159:ALA:O	3:F:3160:LEU:HB2	2.15	0.46
1:B:37:THR:O	1:B:37:THR:HG22	2.16	0.46
3:H:2077:GLU:CD	3:H:2077:GLU:H	2.24	0.46
1:B:83:PHE:HA	1:B:87:PRO:HD2	1.96	0.46
1:D:44:HIS:CG	1:D:125:MET:HE3	2.51	0.46
1:D:125:MET:HE1	1:D:152:CYS:SG	2.55	0.46
1:D:303:LEU:CD2	1:E:265:VAL:HG12	2.46	0.46
3:H:2226:HIS:CE1	3:H:2228:PHE:HB2	2.49	0.46
1:B:293:GLN:OE1	2:A:85:ILE:HA	2.16	0.46
1:D:49:SER:HB2	1:D:56:LYS:NZ	2.31	0.46
5:J:10:DC:H6	5:J:10:DC:H5''	1.81	0.46
1:B:255:PRO:HA	1:B:302:GLU:HG3	1.98	0.46
1:C:188:ALA:CB	1:C:221:ASP:HA	2.37	0.46
1:C:276:VAL:HG22	1:C:277:THR:N	2.31	0.46
1:E:246:ASP:OD2	1:E:249:GLN:HG3	2.16	0.46
2:A:13:HIS:CE1	2:A:32:PHE:HE2	2.29	0.46
2:A:151:LEU:CD1	2:A:151:LEU:O	2.64	0.46
1:C:52:PRO:HG3	1:D:150:SER:HB2	1.97	0.46
1:D:13:GLN:HE21	1:D:16:ARG:NH1	2.13	0.46
1:D:29:ASP:CA	1:D:32:THR:HG22	2.37	0.46
1:E:56:LYS:CB	1:E:137:THR:HG23	2.46	0.46
1:E:303:LEU:HD11	2:A:76:MET:SD	2.54	0.46
3:G:1125:GLN:O	3:G:1129:VAL:HG23	2.16	0.46
1:B:145:ILE:HB	1:B:147:PRO:HD2	1.98	0.46
1:E:72:MET:HE3	1:E:72:MET:HB2	1.60	0.46
2:A:102:VAL:HA	2:A:103:PRO:HD3	1.77	0.46
1:C:97:PHE:HA	3:G:1204:GLN:CG	2.40	0.46
3:F:3001:MSE:CE	3:F:3003:LEU:HD21	2.45	0.46
1:B:17:PRO:HB3	1:B:22:GLU:HG2	1.98	0.46
1:E:56:LYS:HB3	1:E:137:THR:HG23	1.97	0.46
1:E:111:ARG:CG	1:E:112:SER:N	2.75	0.46
1:E:276:VAL:HG22	1:E:277:THR:N	2.31	0.46
3:H:2039:TYR:CD1	3:H:2039:TYR:C	2.94	0.46
3:F:3180:PHE:CE2	3:F:3198:LEU:HB3	2.50	0.46
1:B:90:ASN:O	1:B:94:ALA:CB	2.64	0.45
1:C:204:PHE:HA	1:C:207:THR:HG21	1.98	0.45
1:D:232:ARG:O	1:D:263:TRP:CH2	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:239:LEU:HD13	1:D:275:ARG:NH1	2.31	0.45
1:E:67:VAL:O	1:E:67:VAL:CG1	2.64	0.45
1:E:147:PRO:O	1:E:151:ARG:HG3	2.15	0.45
1:B:99:GLY:O	1:B:100:ARG:C	2.58	0.45
1:C:12:GLU:OE1	1:D:153:ARG:NH1	2.49	0.45
1:C:44:HIS:CG	1:C:125:MET:HE3	2.52	0.45
1:D:81:ILE:N	4:I:5:DT:OP1	2.49	0.45
1:E:74:VAL:HG12	1:E:75:ASN:O	2.16	0.45
3:G:1068:ASN:HB2	3:G:1070:ASP:OD1	2.16	0.45
3:F:3030:MSE:HE3	3:F:3103:PRO:HG2	1.97	0.45
1:B:25:LEU:HA	1:B:168:MET:HE3	1.97	0.45
1:B:46:ILE:HB	1:B:154:VAL:HG22	1.98	0.45
1:B:285:TYR:CZ	2:A:93:ALA:HB1	2.51	0.45
1:B:289:GLY:C	2:A:85:ILE:CG2	2.88	0.45
1:B:316:MET:CB	1:B:318:TRP:HZ3	2.29	0.45
1:C:95:ALA:O	1:C:97:PHE:N	2.49	0.45
2:A:102:VAL:O	2:A:102:VAL:HG22	2.17	0.45
1:B:64:CYS:O	1:B:65:HIS:C	2.58	0.45
1:B:219:VAL:CG1	1:B:220:LEU:N	2.78	0.45
1:C:261:TYR:CD1	1:C:295:HIS:CD2	3.04	0.45
1:C:307:TYR:CG	1:D:289:GLY:HA3	2.52	0.45
3:G:1022:MSE:HE3	3:G:1023:LEU:O	2.17	0.45
3:G:1033:ALA:HB2	3:G:1038:THR:HG23	1.99	0.45
3:H:2085:ASP:OD1	3:H:2086:ALA:N	2.49	0.45
1:B:146:LYS:N	1:B:147:PRO:CD	2.78	0.45
1:B:276:VAL:HG22	1:B:277:THR:H	1.81	0.45
1:D:42:ILE:H	1:D:101:GLN:HE22	1.64	0.45
1:D:186:ALA:H	1:D:219:VAL:CA	2.27	0.45
2:A:179:GLN:O	2:A:180:LEU:C	2.59	0.45
3:G:1141:THR:OG1	3:G:1142:VAL:N	2.50	0.45
3:F:3125:GLN:O	3:F:3129:VAL:HG23	2.16	0.45
1:B:44:HIS:HE2	1:B:129:SER:HB3	1.81	0.45
1:D:215:SER:O	1:D:216:SER:C	2.59	0.45
1:B:76:GLY:N	1:B:107:ASP:O	2.49	0.45
1:C:251:ARG:HH21	1:D:270:GLU:HG3	1.82	0.45
1:D:1:MET:HE3	1:D:1:MET:HB2	1.86	0.45
1:D:205:ARG:HD3	1:E:151:ARG:HA	1.98	0.45
1:E:161:THR:N	1:E:164:ASP:HB2	2.31	0.45
2:A:50:LYS:HE2	2:A:103:PRO:O	2.17	0.45
3:G:1189:MSE:HE3	3:G:1189:MSE:HB3	1.90	0.45
1:B:22:GLU:HG2	1:B:22:GLU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:SER:HB2	1:D:56:LYS:CE	2.47	0.45
1:E:112:SER:C	1:E:114:LEU:H	2.25	0.45
3:H:2096:ASP:OD2	3:H:2098:SER:OG	2.32	0.45
3:H:2127:LEU:HD23	3:H:2184:MSE:HE1	1.98	0.45
3:F:3130:SER:CB	3:F:3184:MSE:HE2	2.46	0.45
1:C:121:LEU:HA	1:C:124:PHE:HB3	1.98	0.45
1:D:218:GLY:O	1:D:219:VAL:CG2	2.65	0.45
1:E:42:ILE:HG12	1:E:67:VAL:HG21	1.99	0.45
1:E:106:ILE:HG21	1:E:109:PHE:CE1	2.51	0.45
1:E:124:PHE:O	1:E:127:ALA:HB3	2.17	0.45
3:F:3039:TYR:CD1	3:F:3039:TYR:C	2.95	0.45
1:B:59:VAL:HG21	1:B:157:PHE:CZ	2.52	0.45
1:D:242:LEU:CD1	1:D:250:LEU:HD21	2.47	0.45
1:E:204:PHE:O	1:E:205:ARG:C	2.59	0.45
2:A:80:TYR:OH	2:A:84:LEU:HD11	2.17	0.45
2:A:163:THR:O	2:A:166:PHE:N	2.46	0.45
1:D:206:LYS:HD2	1:D:206:LYS:HA	1.56	0.44
1:D:219:VAL:O	1:D:220:LEU:HD12	2.18	0.44
1:D:255:PRO:HA	1:D:302:GLU:HG3	1.99	0.44
2:A:24:ALA:O	2:A:28:ALA:N	2.50	0.44
3:G:1130:SER:CB	3:G:1184:MSE:HE2	2.46	0.44
1:B:276:VAL:HG22	1:B:277:THR:N	2.32	0.44
1:C:176:LEU:HD23	1:C:176:LEU:HA	1.71	0.44
1:C:294:TYR:HB3	1:D:293:GLN:HG2	2.00	0.44
1:D:107:ASP:O	1:D:108:GLU:C	2.60	0.44
2:A:160:GLY:O	3:H:2099:THR:HG22	2.17	0.44
3:H:2130:SER:CB	3:H:2184:MSE:HE2	2.47	0.44
3:F:3018:ASN:OD1	3:F:3019:SER:N	2.50	0.44
1:B:238:VAL:HG22	1:B:253:LEU:HD13	1.99	0.44
1:C:44:HIS:CD2	1:C:125:MET:CE	3.00	0.44
1:C:114:LEU:HD23	1:C:114:LEU:HA	1.62	0.44
1:D:23:CYS:O	1:D:30:LYS:HE2	2.17	0.44
3:G:1096:ASP:O	3:G:1099:THR:HG23	2.17	0.44
1:B:119:ARG:HE	2:A:33:LYS:HB3	1.82	0.44
1:B:243:LYS:HG2	1:B:318:TRP:HE1	1.82	0.44
1:D:246:ASP:CG	1:D:249:GLN:HG3	2.42	0.44
2:A:62:LYS:HG2	2:A:94:HIS:CD2	2.52	0.44
2:A:177:GLN:O	2:A:177:GLN:HG2	2.18	0.44
3:G:1160:LEU:CD1	3:G:1181:ILE:HD13	2.47	0.44
3:G:1221:GLU:H	3:G:1221:GLU:HG2	1.60	0.44
1:C:280:SER:HB3	1:C:316:MET:SD	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:HIS:CD2	1:E:41:LYS:CB	2.98	0.44
2:A:40:PHE:CE2	2:A:64:MET:HG3	2.52	0.44
2:A:64:MET:HE3	2:A:64:MET:HB3	1.79	0.44
2:A:151:LEU:O	2:A:151:LEU:HD12	2.15	0.44
2:A:162:VAL:O	2:A:162:VAL:CG1	2.61	0.44
1:C:34:LYS:HD2	1:C:34:LYS:HA	1.66	0.44
1:D:83:PHE:O	1:D:87:PRO:HD2	2.17	0.44
2:A:69:LEU:C	2:A:71:GLN:N	2.75	0.44
2:A:90:SER:C	2:A:92:GLU:N	2.71	0.44
2:A:163:THR:O	2:A:166:PHE:HB3	2.18	0.44
2:A:186:GLU:O	2:A:187:TRP:C	2.60	0.44
3:F:3176:ASN:OD1	3:F:3176:ASN:N	2.49	0.44
1:B:120:HIS:CD2	2:A:29:ALA:CB	3.01	0.44
1:B:215:SER:O	1:B:216:SER:C	2.59	0.44
1:B:239:LEU:O	1:B:243:LYS:HG3	2.18	0.44
1:B:261:TYR:CD1	1:B:295:HIS:CD2	3.05	0.44
1:B:275:ARG:O	1:B:318:TRP:CD1	2.71	0.44
1:C:174:ARG:NH1	1:C:174:ARG:CB	2.41	0.44
1:C:239:LEU:HD13	1:C:275:ARG:NH1	2.33	0.44
1:D:148:LEU:HD23	1:D:148:LEU:HA	1.77	0.44
2:A:69:LEU:C	2:A:71:GLN:H	2.25	0.44
2:A:92:GLU:O	2:A:95:PHE:HB3	2.18	0.44
3:G:1126:LEU:O	3:G:1130:SER:HB2	2.17	0.44
3:H:2157:ASP:OD1	3:H:2161:THR:HG23	2.17	0.44
3:F:3194:TYR:CE1	3:F:3211:GLY:HA3	2.53	0.44
1:B:284:MET:O	1:B:284:MET:HE2	2.18	0.44
1:C:297:ILE:CG2	1:D:297:ILE:HG13	2.47	0.44
1:D:72:MET:HE2	3:H:2156:GLU:CB	2.48	0.44
1:D:81:ILE:HG21	4:I:5:DT:H3'	1.99	0.44
1:D:318:TRP:N	1:D:318:TRP:CE3	2.85	0.44
3:G:1180:PHE:CE2	3:G:1198:LEU:HB3	2.53	0.44
1:B:48:HIS:HE1	1:B:156:THR:CG2	2.30	0.44
1:C:91:PHE:CZ	1:C:102:LYS:HD3	2.53	0.44
1:C:174:ARG:O	1:C:177:THR:HB	2.18	0.44
1:C:297:ILE:HG23	1:D:297:ILE:HG13	1.99	0.44
1:D:42:ILE:H	1:D:101:GLN:NE2	2.16	0.44
1:D:77:SER:OG	1:D:111:ARG:HD3	2.18	0.44
1:D:174:ARG:O	1:D:177:THR:HB	2.17	0.44
1:D:204:PHE:HA	1:D:207:THR:HG21	1.98	0.44
1:D:261:TYR:CD1	1:D:295:HIS:CD2	3.06	0.44
3:G:1039:TYR:CD1	3:G:1039:TYR:C	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:SER:OG	1:E:153:ARG:NE	2.50	0.43
1:D:318:TRP:N	1:D:318:TRP:HE3	2.16	0.43
1:E:83:PHE:CE2	1:E:88:LEU:CD1	3.00	0.43
1:E:261:TYR:CD1	1:E:295:HIS:CD2	3.06	0.43
3:H:2042:ALA:HB2	3:H:2214:ALA:CB	2.47	0.43
3:F:3090:ILE:CG2	3:F:3091:PHE:N	2.81	0.43
1:C:255:PRO:HA	1:C:302:GLU:HG3	2.00	0.43
1:D:32:THR:O	1:D:36:ILE:HG13	2.18	0.43
1:D:230:ASN:HD22	1:D:231:ASP:H	1.66	0.43
2:A:69:LEU:O	2:A:71:GLN:N	2.51	0.43
3:H:2091:PHE:CD2	3:F:3163:VAL:O	2.71	0.43
3:F:3022:MSE:HB3	3:F:3102:ALA:HB2	2.00	0.43
1:B:105:VAL:HG22	1:B:135:ILE:HD12	2.00	0.43
1:C:247:VAL:O	1:C:248:LYS:C	2.60	0.43
1:D:203:ASP:OD1	1:D:205:ARG:N	2.44	0.43
1:D:247:VAL:O	1:D:248:LYS:C	2.61	0.43
1:D:276:VAL:HG22	1:D:277:THR:N	2.33	0.43
1:E:204:PHE:HE1	1:E:208:ILE:HD11	1.83	0.43
2:A:80:TYR:O	2:A:83:ASN:HB3	2.18	0.43
3:G:1041:GLU:HG2	3:G:1215:ASN:HB2	2.00	0.43
3:H:2063:ILE:HA	3:H:2063:ILE:HD13	1.82	0.43
1:C:200:ASN:HD21	1:C:210:GLU:HG3	1.83	0.43
1:E:179:ILE:C	1:E:179:ILE:HD12	2.43	0.43
1:B:162:ASP:O	1:B:166:ILE:CG1	2.65	0.43
1:B:255:PRO:HB3	1:B:302:GLU:CD	2.43	0.43
1:D:186:ALA:O	1:D:219:VAL:HA	2.18	0.43
3:F:3189:MSE:HE2	3:F:3209:PHE:CG	2.53	0.43
1:D:88:LEU:HD22	1:D:104:ILE:HD13	2.01	0.43
1:D:251:ARG:NH2	1:E:270:GLU:HG3	2.33	0.43
1:E:27:ALA:N	1:E:164:ASP:OD1	2.46	0.43
2:A:118:SER:OG	2:A:119:THR:N	2.52	0.43
2:A:120:GLU:HG2	2:A:124:ILE:HD11	1.99	0.43
1:B:93:SER:CB	3:F:3055:TYR:CE1	3.01	0.43
1:C:2:ILE:HG13	1:C:178:GLU:CG	2.49	0.43
1:D:4:VAL:HG23	1:D:4:VAL:O	2.18	0.43
1:D:85:ARG:HH22	4:I:6:DC:P	2.40	0.43
1:E:173:ILE:HD13	1:E:194:ALA:HB2	1.99	0.43
1:E:213:SER:C	2:A:148:ASN:ND2	2.76	0.43
2:A:144:ILE:O	2:A:144:ILE:HG22	2.18	0.43
3:G:1018:ASN:OD1	3:G:1019:SER:N	2.51	0.43
3:G:1063:ILE:HD13	3:G:1063:ILE:HA	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:3128:ARG:HG3	3:F:3128:ARG:HH11	1.83	0.43
1:B:176:LEU:HA	1:B:176:LEU:HD23	1.75	0.43
2:A:145:LEU:HB2	2:A:151:LEU:CD2	2.26	0.43
1:B:8:GLU:HG2	1:B:13:GLN:C	2.44	0.43
1:B:98:ASP:OD1	1:B:98:ASP:C	2.61	0.43
1:B:121:LEU:O	1:B:124:PHE:HB3	2.19	0.43
1:B:141:ILE:HD12	1:B:154:VAL:HG11	2.01	0.43
1:B:162:ASP:OD1	1:B:162:ASP:N	2.51	0.43
1:B:276:VAL:HA	1:B:318:TRP:HB2	1.94	0.43
1:C:284:MET:HE2	1:C:284:MET:O	2.19	0.43
1:C:297:ILE:CG2	1:D:293:GLN:O	2.67	0.43
1:E:165:LYS:O	1:E:169:MET:CG	2.67	0.43
1:E:242:LEU:HD12	1:E:250:LEU:HD21	2.00	0.43
2:A:3:LEU:HG	2:A:3:LEU:O	2.19	0.43
3:G:1010:LEU:HA	3:G:1010:LEU:HD23	1.82	0.43
1:B:283:ARG:NH1	1:B:286:GLU:OE1	2.51	0.43
1:E:247:VAL:O	1:E:248:LYS:C	2.62	0.43
3:G:1110:PRO:HB2	3:G:1199:TRP:NE1	2.34	0.43
3:G:1183:ASN:HB2	3:G:1221:GLU:CD	2.44	0.43
1:B:172:MET:HE2	1:B:207:THR:HG23	2.01	0.42
1:C:44:HIS:CD2	1:C:125:MET:HE3	2.54	0.42
1:C:276:VAL:HA	1:C:318:TRP:HB3	2.01	0.42
1:D:33:PHE:CZ	1:D:155:ILE:HD13	2.54	0.42
1:E:124:PHE:CD1	1:E:128:TYR:HE2	2.33	0.42
3:G:1149:ILE:O	3:G:1166:SER:HA	2.19	0.42
1:C:97:PHE:HZ	3:G:1205:GLY:CA	2.11	0.42
1:C:314:CYS:SG	1:D:282:ILE:HD11	2.59	0.42
1:D:44:HIS:CD2	1:D:125:MET:CE	3.01	0.42
1:D:72:MET:HE1	1:D:91:PHE:HB2	2.01	0.42
1:D:80:LYS:CE	1:E:85:ARG:NH1	2.82	0.42
1:D:260:ASP:OD1	1:D:260:ASP:N	2.50	0.42
1:D:289:GLY:O	1:D:293:GLN:HB2	2.19	0.42
3:H:2010:LEU:HA	3:H:2010:LEU:HD23	1.75	0.42
4:I:2:DG:H1	5:J:9:DC:H42	1.67	0.42
1:B:246:ASP:CG	1:B:249:GLN:HG3	2.45	0.42
1:C:246:ASP:CG	1:C:249:GLN:HG3	2.44	0.42
1:D:9:HIS:ND1	1:D:10:ILE:N	2.67	0.42
1:D:163:GLU:H	1:D:163:GLU:CD	2.28	0.42
1:D:163:GLU:CD	1:D:163:GLU:N	2.77	0.42
1:E:255:PRO:HB3	1:E:302:GLU:CD	2.44	0.42
3:H:2018:ASN:OD1	3:H:2018:ASN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:GLN:NE2	2:A:84:LEU:C	2.60	0.42
1:B:294:TYR:HD1	1:B:297:ILE:HD12	1.84	0.42
1:D:92:ALA:HB2	1:D:124:PHE:CZ	2.54	0.42
2:A:145:LEU:O	2:A:148:ASN:N	2.52	0.42
3:F:3092:TRP:CD1	3:F:3093:PRO:HD2	2.54	0.42
1:B:26:PRO:HB3	1:B:160:PRO:HA	2.00	0.42
1:C:119:ARG:O	1:C:122:ARG:HG2	2.19	0.42
1:D:242:LEU:HD12	1:D:250:LEU:HD21	2.01	0.42
1:D:255:PRO:HB3	1:D:302:GLU:CD	2.45	0.42
1:E:84:VAL:HG13	1:E:88:LEU:HD22	2.00	0.42
3:H:2189:MSE:HE3	3:H:2189:MSE:HB3	1.99	0.42
1:C:208:ILE:O	1:C:208:ILE:HG22	2.19	0.42
1:E:165:LYS:HE3	1:E:165:LYS:HB2	1.88	0.42
2:A:65:VAL:HG11	2:A:98:LEU:HD13	2.01	0.42
3:G:1039:TYR:O	3:G:1216:TYR:HA	2.19	0.42
3:H:2068:ASN:HB2	3:H:2070:ASP:OD1	2.20	0.42
1:C:27:ALA:H	1:C:164:ASP:CG	2.28	0.42
1:D:114:LEU:HA	1:D:114:LEU:HD23	1.64	0.42
1:E:102:LYS:O	1:E:132:CYS:HA	2.19	0.42
3:H:2064:LEU:HD23	3:H:2064:LEU:HA	1.86	0.42
3:H:2068:ASN:ND2	3:H:2085:ASP:CG	2.76	0.42
4:I:1:DG:N2	4:I:2:DG:C4	2.88	0.42
1:B:285:TYR:HE2	2:A:96:ASN:HB2	1.84	0.42
1:C:64:CYS:HB2	1:C:71:MET:HE2	2.01	0.42
1:C:93:SER:OG	3:G:1221:GLU:OE1	2.24	0.42
1:C:222:ALA:HA	1:C:225:LEU:HB3	2.02	0.42
1:E:119:ARG:CD	1:E:122:ARG:HH21	2.27	0.42
2:A:132:GLN:C	2:A:133:VAL:HG23	2.45	0.42
2:A:181:LYS:O	2:A:182:LYS:C	2.60	0.42
3:G:1003:LEU:HD23	3:G:1003:LEU:HA	1.80	0.42
1:B:129:SER:O	1:B:130:SER:C	2.61	0.42
1:C:169:MET:O	1:C:173:ILE:HG13	2.20	0.42
1:E:283:ARG:NH1	1:E:286:GLU:OE1	2.53	0.42
2:A:137:ASP:O	2:A:141:TYR:N	2.52	0.42
1:B:98:ASP:OD1	1:B:99:GLY:N	2.53	0.42
1:B:148:LEU:HD23	1:B:148:LEU:HA	1.76	0.42
1:B:304:HIS:CE1	1:C:293:GLN:HG3	2.55	0.42
1:D:97:PHE:CB	3:G:1078:ASP:O	2.61	0.42
1:E:10:ILE:HD13	2:A:141:TYR:CD2	2.55	0.42
1:E:119:ARG:HA	1:E:122:ARG:HE	1.85	0.42
1:E:242:LEU:CD1	1:E:250:LEU:HD21	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:284:MET:O	1:E:284:MET:HE2	2.19	0.42
2:A:46:ALA:O	2:A:50:LYS:HA	2.20	0.42
3:H:2128:ARG:HG3	3:H:2128:ARG:NH1	2.35	0.42
1:C:304:HIS:CE1	1:D:293:GLN:HG3	2.55	0.41
1:D:34:LYS:HD2	1:D:34:LYS:HA	1.77	0.41
1:D:119:ARG:CA	1:D:122:ARG:HH11	2.33	0.41
1:E:167:GLU:OE1	1:E:167:GLU:HA	2.20	0.41
2:A:4:PHE:CG	3:F:3032:ARG:NH1	2.88	0.41
2:A:181:LYS:HZ1	3:F:3156:GLU:HA	1.85	0.41
3:H:2149:ILE:O	3:H:2166:SER:HA	2.20	0.41
1:B:6:GLU:O	1:B:7:LYS:CG	2.59	0.41
1:C:88:LEU:HD22	1:C:104:ILE:HD13	2.01	0.41
1:E:254:ALA:N	1:E:255:PRO:HD2	2.36	0.41
3:H:2128:ARG:HG3	3:H:2128:ARG:HH11	1.84	0.41
3:F:3067:VAL:HG12	3:F:3085:ASP:OD2	2.20	0.41
3:F:3147:ILE:CD1	3:F:3178:PHE:HZ	2.32	0.41
4:I:1:DG:H8	4:I:1:DG:H5'	1.85	0.41
1:B:24:ILE:C	1:B:25:LEU:HG	2.45	0.41
1:B:85:ARG:HH21	1:B:120:HIS:CE1	2.34	0.41
1:B:171:GLN:O	1:B:175:ARG:HB2	2.20	0.41
1:D:42:ILE:HG22	1:D:43:PRO:O	2.21	0.41
1:C:239:LEU:O	1:C:243:LYS:HG3	2.20	0.41
1:E:42:ILE:CG1	1:E:67:VAL:HG21	2.51	0.41
1:E:83:PHE:HE2	1:E:88:LEU:HD11	1.84	0.41
2:A:177:GLN:HE21	2:A:181:LYS:HZ1	1.67	0.41
3:H:2088:SER:HA	3:F:3166:SER:O	2.20	0.41
3:F:3160:LEU:CD1	3:F:3181:ILE:HD13	2.50	0.41
1:B:201:PHE:O	1:B:202:PRO:C	2.61	0.41
1:B:219:VAL:HG12	1:B:220:LEU:N	2.36	0.41
1:C:4:VAL:HG23	1:C:4:VAL:O	2.19	0.41
2:A:64:MET:O	2:A:65:VAL:C	2.62	0.41
3:G:1005:LYS:H	3:G:1005:LYS:HG2	1.70	0.41
3:G:1198:LEU:N	3:G:1198:LEU:HD23	2.35	0.41
1:B:205:ARG:NH2	6:B:700:ADP:O2B	2.53	0.41
1:C:163:GLU:CD	1:C:163:GLU:N	2.77	0.41
1:C:199:LYS:HE2	1:C:232:ARG:HE	1.86	0.41
1:C:206:LYS:HD2	1:C:206:LYS:HA	1.50	0.41
1:C:225:LEU:HD12	1:C:225:LEU:C	2.46	0.41
1:D:9:HIS:CD2	1:E:41:LYS:HB2	2.52	0.41
1:E:83:PHE:CD1	1:E:87:PRO:HG2	2.56	0.41
1:B:121:LEU:HD23	1:B:125:MET:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:316:MET:O	1:D:318:TRP:HZ3	2.03	0.41
1:E:172:MET:HE1	1:E:201:PHE:O	2.21	0.41
3:G:1130:SER:OG	3:G:1184:MSE:HE2	2.20	0.41
3:H:2088:SER:HA	3:F:3167:LEU:HA	2.02	0.41
1:C:23:CYS:O	1:C:30:LYS:HE2	2.21	0.41
1:C:94:ALA:HB1	3:G:1219:ALA:CB	2.51	0.41
1:C:283:ARG:NH1	1:C:286:GLU:OE1	2.52	0.41
1:D:88:LEU:HD23	1:D:88:LEU:HA	1.87	0.41
2:A:19:SER:O	2:A:20:LYS:HB2	2.20	0.41
3:G:1032:ARG:HG2	3:G:1103:PRO:CD	2.42	0.41
3:H:2147:ILE:CD1	3:H:2178:PHE:HZ	2.33	0.41
1:B:116:GLU:HA	1:B:119:ARG:NH1	2.36	0.41
1:D:80:LYS:HZ3	4:I:4:DG:P	2.44	0.41
1:E:104:ILE:HG22	1:E:106:ILE:HG13	2.02	0.41
1:E:238:VAL:HG22	1:E:253:LEU:HD13	2.02	0.41
2:A:4:PHE:CD2	3:F:3032:ARG:NH1	2.89	0.41
2:A:133:VAL:CG1	2:A:137:ASP:OD2	2.69	0.41
3:G:1002:LYS:O	3:G:1003:LEU:HD23	2.21	0.41
3:F:3068:ASN:HB2	3:F:3070:ASP:OD1	2.21	0.41
1:B:126:GLU:CD	1:B:151:ARG:NH2	2.77	0.41
1:E:98:ASP:C	3:H:2204:GLN:HG2	2.44	0.41
1:E:106:ILE:HG21	1:E:109:PHE:CD1	2.56	0.41
2:A:74:GLU:OE1	2:A:104:ARG:HG2	2.21	0.41
3:F:3128:ARG:HG3	3:F:3128:ARG:NH1	2.36	0.41
3:F:3157:ASP:OD1	3:F:3161:THR:HG23	2.21	0.41
1:C:10:ILE:O	1:C:10:ILE:HG23	2.20	0.40
1:D:5:ASN:C	1:D:7:LYS:H	2.29	0.40
1:D:203:ASP:OD1	1:D:203:ASP:C	2.64	0.40
1:E:173:ILE:HG23	1:E:193:VAL:HG12	1.99	0.40
1:E:238:VAL:HA	1:E:253:LEU:HD13	2.03	0.40
1:E:246:ASP:CG	1:E:249:GLN:HG3	2.45	0.40
3:G:1010:LEU:O	3:G:1013:ASN:HB3	2.21	0.40
1:C:3:THR:OG1	1:C:22:GLU:OE1	2.33	0.40
1:C:119:ARG:CA	1:C:122:ARG:HH11	2.34	0.40
1:D:238:VAL:HG22	1:D:253:LEU:HD13	2.03	0.40
1:D:261:TYR:CE1	1:D:265:VAL:HG21	2.56	0.40
1:B:83:PHE:HE1	1:B:88:LEU:CD1	2.33	0.40
1:B:238:VAL:HA	1:B:253:LEU:HD13	2.04	0.40
1:B:284:MET:O	1:B:284:MET:CE	2.70	0.40
1:C:118:GLN:HB3	1:C:145:ILE:CD1	2.51	0.40
1:E:34:LYS:HE3	1:E:34:LYS:HB3	1.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:123:ILE:H	2:A:123:ILE:HG13	1.75	0.40
3:H:2050:PHE:CE2	3:H:2052:VAL:HB	2.56	0.40
1:B:25:LEU:CA	1:B:168:MET:HE3	2.52	0.40
1:B:57:THR:HG23	6:B:700:ADP:O3B	2.22	0.40
1:B:243:LYS:O	1:B:245:LYS:HG3	2.21	0.40
1:C:189:ASP:OD1	1:C:191:LYS:HG3	2.22	0.40
1:D:238:VAL:HA	1:D:253:LEU:HD13	2.04	0.40
2:A:55:ILE:O	2:A:56:ALA:CB	2.70	0.40
1:B:89:THR:HG22	3:F:3055:TYR:OH	2.21	0.40
1:B:289:GLY:CA	2:A:85:ILE:CG2	3.00	0.40
1:C:33:PHE:CZ	1:C:155:ILE:HD13	2.57	0.40
1:E:71:MET:O	1:E:71:MET:HG2	2.21	0.40
1:E:196:LEU:HD23	1:E:196:LEU:HA	1.75	0.40
2:A:61:SER:O	2:A:62:LYS:C	2.65	0.40
4:I:1:DG:C2	4:I:2:DG:C5	3.10	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)
3:G:1193:ASN:OD1	3:F:3176:ASN:ND2[4_445]	2.12	0.08

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	B	301/324 (93%)	282 (94%)	18 (6%)	1 (0%)	36 68
1	C	317/324 (98%)	302 (95%)	11 (4%)	4 (1%)	9 40
1	D	318/324 (98%)	300 (94%)	13 (4%)	5 (2%)	7 36
1	E	290/324 (90%)	277 (96%)	12 (4%)	1 (0%)	36 68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	174/199 (87%)	140 (80%)	33 (19%)	1 (1%)	21	56
3	F	220/228 (96%)	217 (99%)	3 (1%)	0	100	100
3	G	226/228 (99%)	223 (99%)	3 (1%)	0	100	100
3	H	226/228 (99%)	222 (98%)	4 (2%)	0	100	100
All	All	2072/2179 (95%)	1963 (95%)	97 (5%)	12 (1%)	21	56

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	219	VAL
1	C	97	PHE
1	D	234	ALA
1	B	259	ALA
1	C	259	ALA
1	E	259	ALA
1	D	259	ALA
1	D	218	GLY
1	C	233	GLY
2	A	8	ILE
1	C	50	PRO
1	D	50	PRO

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	B	266/279 (95%)	238 (90%)	28 (10%)	6	28
1	C	276/279 (99%)	240 (87%)	36 (13%)	4	20
1	D	278/279 (100%)	240 (86%)	38 (14%)	3	18
1	E	250/279 (90%)	219 (88%)	31 (12%)	4	21
2	A	154/174 (88%)	141 (92%)	13 (8%)	10	38
3	F	183/183 (100%)	169 (92%)	14 (8%)	12	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	189/183 (103%)	175 (93%)	14 (7%)	13	43
3	H	189/183 (103%)	173 (92%)	16 (8%)	10	37
All	All	1785/1839 (97%)	1595 (89%)	190 (11%)	6	27

All (190) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	6	GLU
1	B	12	GLU
1	B	20	ILE
1	B	21	ASP
1	B	35	SER
1	B	45	ILE
1	B	47	LEU
1	B	57	THR
1	B	77	SER
1	B	84	VAL
1	B	88	LEU
1	B	89	THR
1	B	110	ASP
1	B	111	ARG
1	B	137	THR
1	B	155	ILE
1	B	162	ASP
1	B	182	HIS
1	B	191	LYS
1	B	196	LEU
1	B	200	ASN
1	B	216	SER
1	B	237	ASP
1	B	271	GLU
1	B	277	THR
1	B	284	MET
1	B	301	THR
1	B	305	LEU
1	C	2	ILE
1	C	10	ILE
1	C	11	LEU
1	C	12	GLU
1	C	19	THR
1	C	25	LEU

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Mol	Chain	Res	Type
1	C	41	LYS
1	C	49	SER
1	C	74	VAL
1	C	77	SER
1	C	89	THR
1	C	97	PHE
1	C	98	ASP
1	C	101	GLN
1	C	117	SER
1	C	121	LEU
1	C	130	SER
1	C	132	CYS
1	C	137	THR
1	C	146	LYS
1	C	156	THR
1	C	170	LYS
1	C	174	ARG
1	C	200	ASN
1	C	216	SER
1	C	221	ASP
1	C	224	ILE
1	C	231	ASP
1	C	237	ASP
1	C	271	GLU
1	C	277	THR
1	C	284	MET
1	C	301	THR
1	C	305	LEU
1	C	317	GLN
1	C	318	TRP
1	D	1	MET
1	D	4	VAL
1	D	9	HIS
1	D	10	ILE
1	D	12	GLU
1	D	19	THR
1	D	25	LEU
1	D	41	LYS
1	D	49	SER
1	D	74	VAL
1	D	77	SER
1	D	89	THR

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Mol	Chain	Res	Type
1	D	96	SER
1	D	97	PHE
1	D	98	ASP
1	D	101	GLN
1	D	117	SER
1	D	121	LEU
1	D	130	SER
1	D	132	CYS
1	D	137	THR
1	D	146	LYS
1	D	156	THR
1	D	170	LYS
1	D	174	ARG
1	D	200	ASN
1	D	210	GLU
1	D	216	SER
1	D	224	ILE
1	D	228	VAL
1	D	230	ASN
1	D	237	ASP
1	D	271	GLU
1	D	277	THR
1	D	284	MET
1	D	301	THR
1	D	305	LEU
1	D	318	TRP
1	E	23	CYS
1	E	32	THR
1	E	35	SER
1	E	41	LYS
1	E	42	ILE
1	E	45	ILE
1	E	48	HIS
1	E	57	THR
1	E	59	VAL
1	E	90	ASN
1	E	104	ILE
1	E	110	ASP
1	E	112	SER
1	E	123	SER
1	E	125	MET
1	E	132	CYS

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Mol	Chain	Res	Type
1	E	136	ILE
1	E	148	LEU
1	E	175	ARG
1	E	177	THR
1	E	179	ILE
1	E	185	ILE
1	E	200	ASN
1	E	207	THR
1	E	210	GLU
1	E	237	ASP
1	E	271	GLU
1	E	277	THR
1	E	284	MET
1	E	301	THR
1	E	305	LEU
2	A	2	SER
2	A	7	ASP
2	A	21	ASP
2	A	38	ASN
2	A	51	THR
2	A	52	LYS
2	A	69	LEU
2	A	94	HIS
2	A	102	VAL
2	A	104	ARG
2	A	106	LYS
2	A	121	VAL
2	A	183	LEU
3	G	1025	SER
3	G	1038	THR
3	G	1047	VAL
3	G	1063	ILE
3	G	1067	VAL
3	G	1068	ASN
3	G	1088	SER
3	G	1099	THR
3	G	1117	GLU
3	G	1161	THR
3	G	1163	VAL
3	G	1175	GLU
3	G	1176	ASN
3	G	1218	VAL

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Mol	Chain	Res	Type
3	H	2025	SER
3	H	2038	THR
3	H	2047	VAL
3	H	2063	ILE
3	H	2067	VAL
3	H	2068	ASN
3	H	2088	SER
3	H	2099	THR
3	H	2117	GLU
3	H	2161	THR
3	H	2163	VAL
3	H	2175	GLU
3	H	2176	ASN
3	H	2189	MSE
3	H	2218	VAL
3	H	2225	THR
3	F	3025	SER
3	F	3038	THR
3	F	3047	VAL
3	F	3067	VAL
3	F	3068	ASN
3	F	3088	SER
3	F	3099	THR
3	F	3117	GLU
3	F	3161	THR
3	F	3163	VAL
3	F	3175	GLU
3	F	3176	ASN
3	F	3218	VAL
3	F	3220	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	5	ASN
1	B	48	HIS
1	B	131	ASN
1	B	140	ASN
1	B	292	ASN
1	B	293	GLN
1	B	295	HIS
1	B	304	HIS

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Mol	Chain	Res	Type
1	C	9	HIS
1	C	13	GLN
1	C	101	GLN
1	C	171	GLN
1	C	200	ASN
1	C	291	ASN
1	C	295	HIS
1	C	304	HIS
1	D	13	GLN
1	D	101	GLN
1	D	140	ASN
1	D	171	GLN
1	D	230	ASN
1	D	291	ASN
1	D	293	GLN
1	D	295	HIS
1	E	48	HIS
1	E	65	HIS
1	E	120	HIS
1	E	293	GLN
1	E	295	HIS
2	A	13	HIS
2	A	26	GLN
2	A	177	GLN
3	G	1068	ASN
3	G	1150	ASN
3	G	1215	ASN
3	H	2068	ASN
3	H	2150	ASN
3	H	2190	GLN
3	H	2215	ASN
3	F	3068	ASN
3	F	3150	ASN
3	F	3215	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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
8	08T	C	700	7	31,33,33	2.90	15 (48%)	41,52,52	5.22	14 (34%)
8	08T	D	700	7	31,33,33	2.97	14 (45%)	41,52,52	5.55	18 (43%)
6	ADP	B	700	-	28,29,29	1.68	6 (21%)	43,45,45	2.13	13 (30%)

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
8	08T	C	700	7	-	1/16/38/38	0/3/3/3
8	08T	D	700	7	-	2/16/38/38	0/3/3/3
6	ADP	B	700	-	-	7/16/32/32	0/3/3/3

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	700	08T	F1-BE	-8.12	1.35	1.54
8	D	700	08T	F1-BE	-7.49	1.37	1.54
8	C	700	08T	F3-BE	-6.27	1.39	1.54
8	D	700	08T	F2-BE	-6.15	1.40	1.54
8	D	700	08T	F3-BE	-6.03	1.40	1.54
8	C	700	08T	F2-BE	-5.77	1.41	1.54
8	D	700	08T	C2'-C3'	-5.51	1.38	1.53
6	B	700	ADP	PA-O3A	5.34	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	700	08T	C2'-C3'	-4.94	1.40	1.53
8	D	700	08T	PB-O3A	-4.76	1.54	1.59
6	B	700	ADP	C5-C4	4.38	1.46	1.39
8	D	700	08T	C6-N6	4.19	1.44	1.34
8	C	700	08T	C6-N6	3.96	1.44	1.34
8	D	700	08T	C3'-C4'	-3.52	1.44	1.53
8	C	700	08T	C3'-C4'	-3.16	1.45	1.53
8	C	700	08T	PB-O3A	-3.08	1.56	1.59
8	C	700	08T	C5-N7	-3.06	1.33	1.39
8	D	700	08T	C5-N7	-3.01	1.33	1.39
8	D	700	08T	C8-N9	-2.84	1.32	1.37
8	C	700	08T	C4-N9	2.80	1.43	1.37
6	B	700	ADP	C5-N7	-2.67	1.34	1.39
8	C	700	08T	O4'-C4'	-2.58	1.39	1.45
8	C	700	08T	PA-O5'	-2.56	1.49	1.59
8	D	700	08T	C4-N9	2.55	1.43	1.37
8	C	700	08T	C4-N3	2.45	1.39	1.34
8	D	700	08T	C2'-C1'	-2.43	1.45	1.53
6	B	700	ADP	C8-N7	2.43	1.36	1.31
8	D	700	08T	O4'-C4'	-2.36	1.39	1.45
8	D	700	08T	C4-N3	2.35	1.38	1.34
8	C	700	08T	C2'-C1'	-2.28	1.46	1.53
6	B	700	ADP	C5-C6	2.28	1.47	1.41
8	D	700	08T	PA-O5'	-2.22	1.50	1.59
8	C	700	08T	C5-C4	2.21	1.43	1.39
8	C	700	08T	C8-N9	-2.14	1.33	1.37
6	B	700	ADP	C8-N9	-2.01	1.34	1.37

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	700	08T	C4-N9-C1'	-18.89	82.46	126.63
8	D	700	08T	C1'-N9-C8	17.29	165.48	127.09
8	C	700	08T	C4-N9-C1'	-16.83	87.26	126.63
8	C	700	08T	C1'-N9-C8	16.59	163.91	127.09
8	D	700	08T	C5-C4-N3	-14.02	107.41	126.72
8	D	700	08T	N3-C4-N9	13.46	150.06	127.17
8	C	700	08T	C5-C4-N3	-13.45	108.20	126.72
8	C	700	08T	N3-C4-N9	13.14	149.51	127.17
8	D	700	08T	C6-C5-C4	6.62	126.22	117.18
6	B	700	ADP	C5-C4-N3	-6.43	117.87	126.72
8	D	700	08T	C2-N3-C4	6.15	126.85	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	700	08T	C6-C5-C4	5.95	125.30	117.18
8	C	700	08T	C2-N3-C4	5.89	126.21	111.83
6	B	700	ADP	N3-C4-N9	5.55	136.61	127.17
8	C	700	08T	C3'-C2'-C1'	5.15	111.20	101.46
8	C	700	08T	N3-C2-N1	-4.67	121.51	128.58
8	D	700	08T	C6-C5-N7	-4.43	123.55	132.09
8	C	700	08T	C6-C5-N7	-4.36	123.69	132.09
8	D	700	08T	N3-C2-N1	-4.34	122.02	128.58
8	D	700	08T	O4'-C1'-C2'	-4.16	97.72	106.62
6	B	700	ADP	C2'-C1'-N9	-3.90	103.60	113.30
6	B	700	ADP	C2-N3-C4	3.86	121.27	111.83
8	D	700	08T	O4'-C1'-N9	-3.82	100.75	108.09
8	D	700	08T	C3'-C2'-C1'	3.56	108.20	101.46
6	B	700	ADP	N3-C2-N1	-3.38	123.47	128.58
8	C	700	08T	O4'-C1'-C2'	-3.31	99.54	106.62
8	C	700	08T	C5-C4-N9	-3.27	102.24	105.81
8	D	700	08T	C5-C4-N9	-3.21	102.31	105.81
8	C	700	08T	O5'-C5'-C4'	3.19	119.85	108.99
6	B	700	ADP	C4-N9-C8	3.00	108.89	105.74
6	B	700	ADP	C4-C5-N7	-2.91	107.26	110.58
6	B	700	ADP	N6-C6-N1	2.84	124.69	118.38
8	D	700	08T	C5-N7-C8	2.71	107.71	103.45
8	D	700	08T	C4-N9-C8	2.67	108.55	105.74
8	D	700	08T	O5'-C5'-C4'	2.63	117.95	108.99
6	B	700	ADP	O2A-PA-O1A	2.52	124.17	112.44
6	B	700	ADP	C5-N7-C8	2.51	107.39	103.45
8	C	700	08T	C5-N7-C8	2.33	107.11	103.45
8	D	700	08T	O4'-C4'-C5'	2.30	116.69	109.33
8	D	700	08T	N9-C8-N7	-2.29	110.69	113.94
8	D	700	08T	C5'-C4'-C3'	-2.22	107.21	115.21
6	B	700	ADP	N9-C8-N7	-2.11	110.94	113.94
6	B	700	ADP	C5-C6-N6	-2.07	118.17	123.29
6	B	700	ADP	O5'-PA-O1A	-2.06	100.77	108.94
8	C	700	08T	C4-N9-C8	2.04	107.88	105.74

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	700	ADP	PA-O3A-PB-O2B
6	B	700	ADP	PA-O3A-PB-O3B
6	B	700	ADP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
6	B	700	ADP	C5'-O5'-PA-O2A
6	B	700	ADP	C5'-O5'-PA-O3A
6	B	700	ADP	O4'-C4'-C5'-O5'
6	B	700	ADP	C3'-C4'-C5'-O5'
8	D	700	08T	O4'-C4'-C5'-O5'
8	D	700	08T	C3'-C4'-C5'-O5'
8	C	700	08T	C5'-O5'-PA-O1A

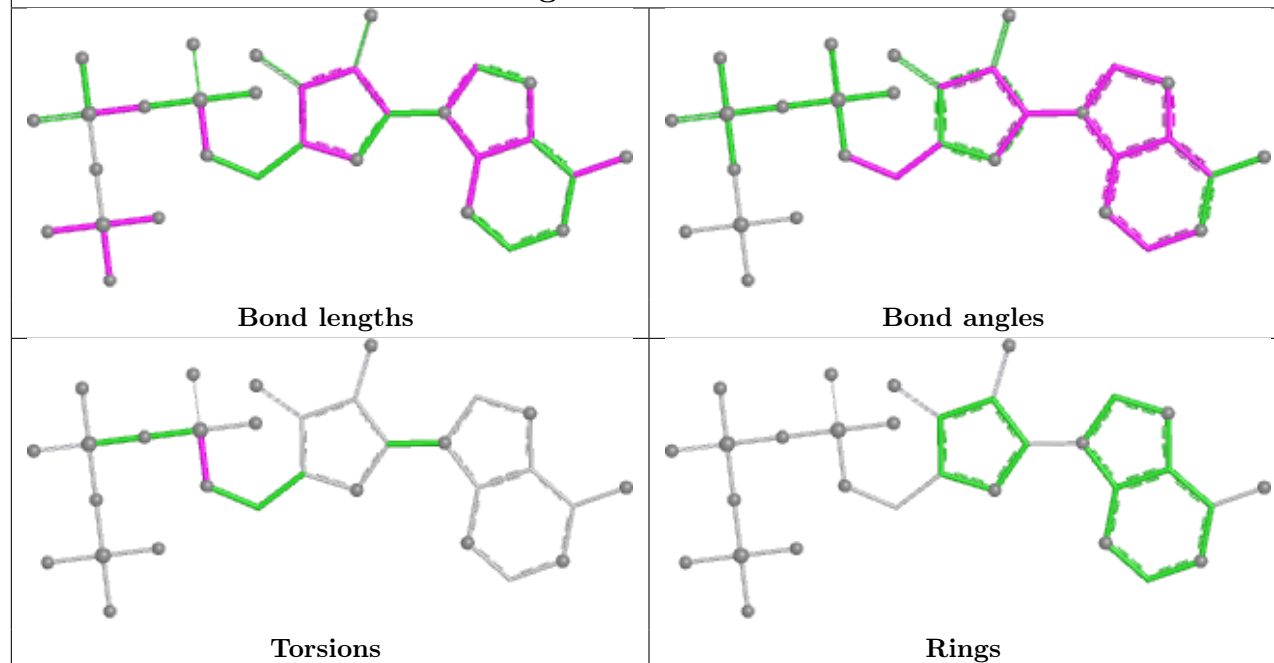
There are no ring outliers.

3 monomers are involved in 15 short contacts:

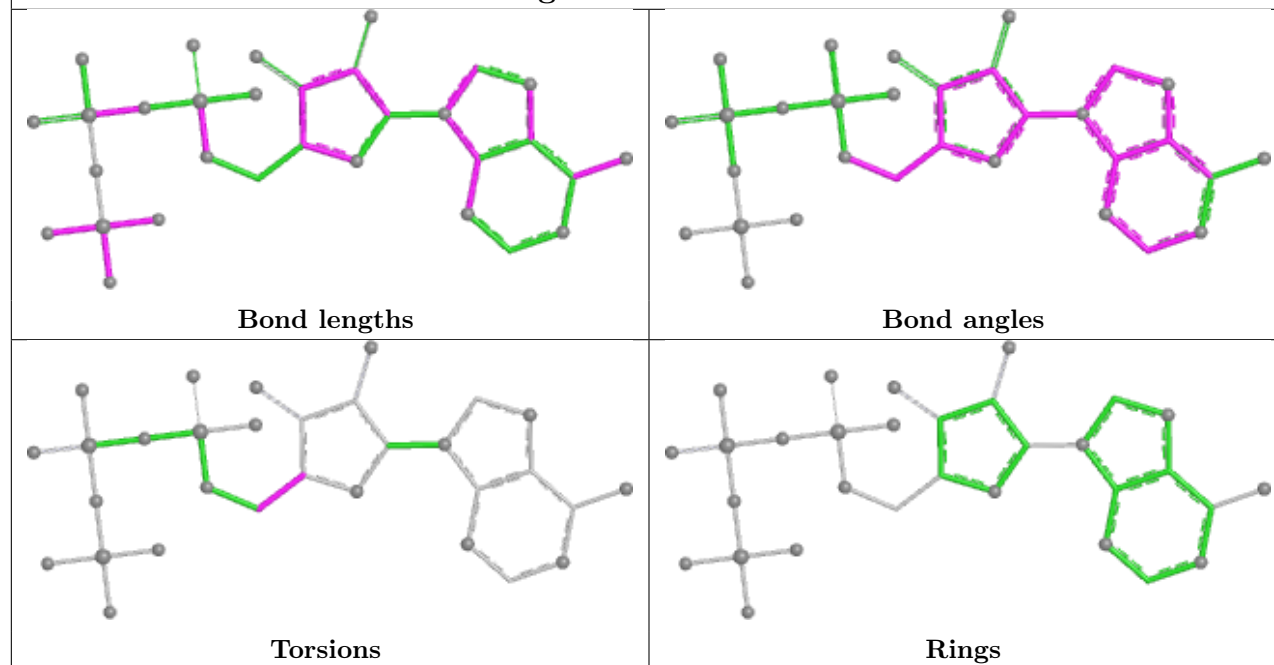
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	700	08T	5	0
8	D	700	08T	1	0
6	B	700	ADP	9	0

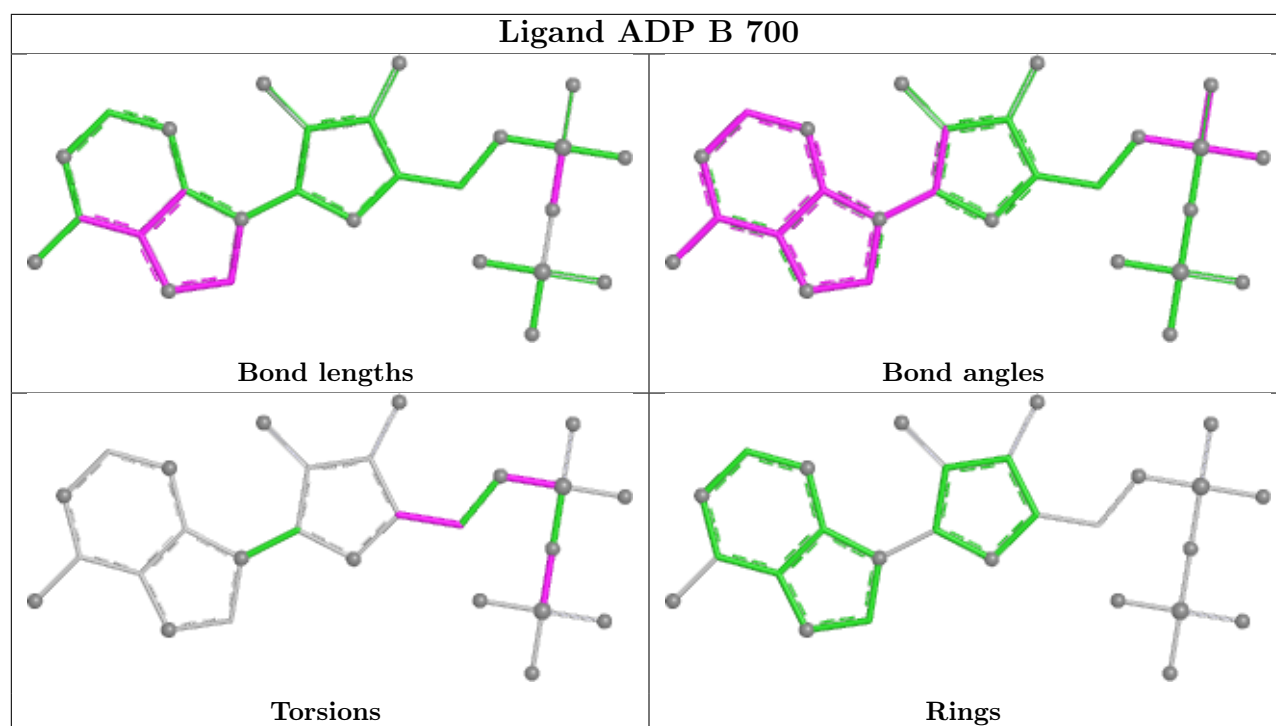
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand 08T C 700



Ligand 08T D 700





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	B	305/324 (94%)	-0.01	5 (1%) 70 51	81, 104, 150, 221	0
1	C	319/324 (98%)	-0.05	4 (1%) 75 55	57, 95, 144, 211	0
1	D	320/324 (98%)	-0.01	5 (1%) 70 51	54, 89, 179, 232	0
1	E	294/324 (90%)	0.00	7 (2%) 59 40	69, 117, 189, 246	0
2	A	178/199 (89%)	0.07	1 (0%) 85 73	81, 120, 181, 223	0
3	F	216/228 (94%)	-0.01	1 (0%) 87 76	70, 96, 159, 252	0
3	G	222/228 (97%)	-0.10	3 (1%) 73 54	58, 84, 130, 188	0
3	H	222/228 (97%)	-0.13	3 (1%) 73 54	71, 95, 143, 200	0
4	I	8/20 (40%)	-0.08	0 100 100	83, 92, 123, 127	0
5	J	8/10 (80%)	-0.17	0 100 100	107, 118, 140, 160	0
All	All	2092/2209 (94%)	-0.03	29 (1%) 73 54	54, 100, 167, 252	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	303	LEU	4.1
1	B	81	ILE	3.4
3	G	1099	THR	3.4
1	E	306	ALA	3.2
1	D	231	ASP	2.9
1	C	97	PHE	2.8
1	E	211	LEU	2.7
1	C	90	ASN	2.7
1	D	309	PHE	2.5
1	D	285	TYR	2.5
1	D	49	SER	2.4
3	G	1106	PRO	2.4
1	E	309	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	233	GLY	2.3
3	F	3222	ALA	2.2
1	E	112	SER	2.2
1	B	2	ILE	2.2
3	H	2205	GLY	2.2
2	A	32	PHE	2.2
1	B	214	TYR	2.2
3	H	2106	PRO	2.2
1	B	196	LEU	2.1
3	G	1205	GLY	2.1
1	D	253	LEU	2.1
1	C	305	LEU	2.1
1	C	310	ILE	2.1
1	E	210	GLU	2.1
3	H	2011	LEU	2.0
1	B	211	LEU	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](#)

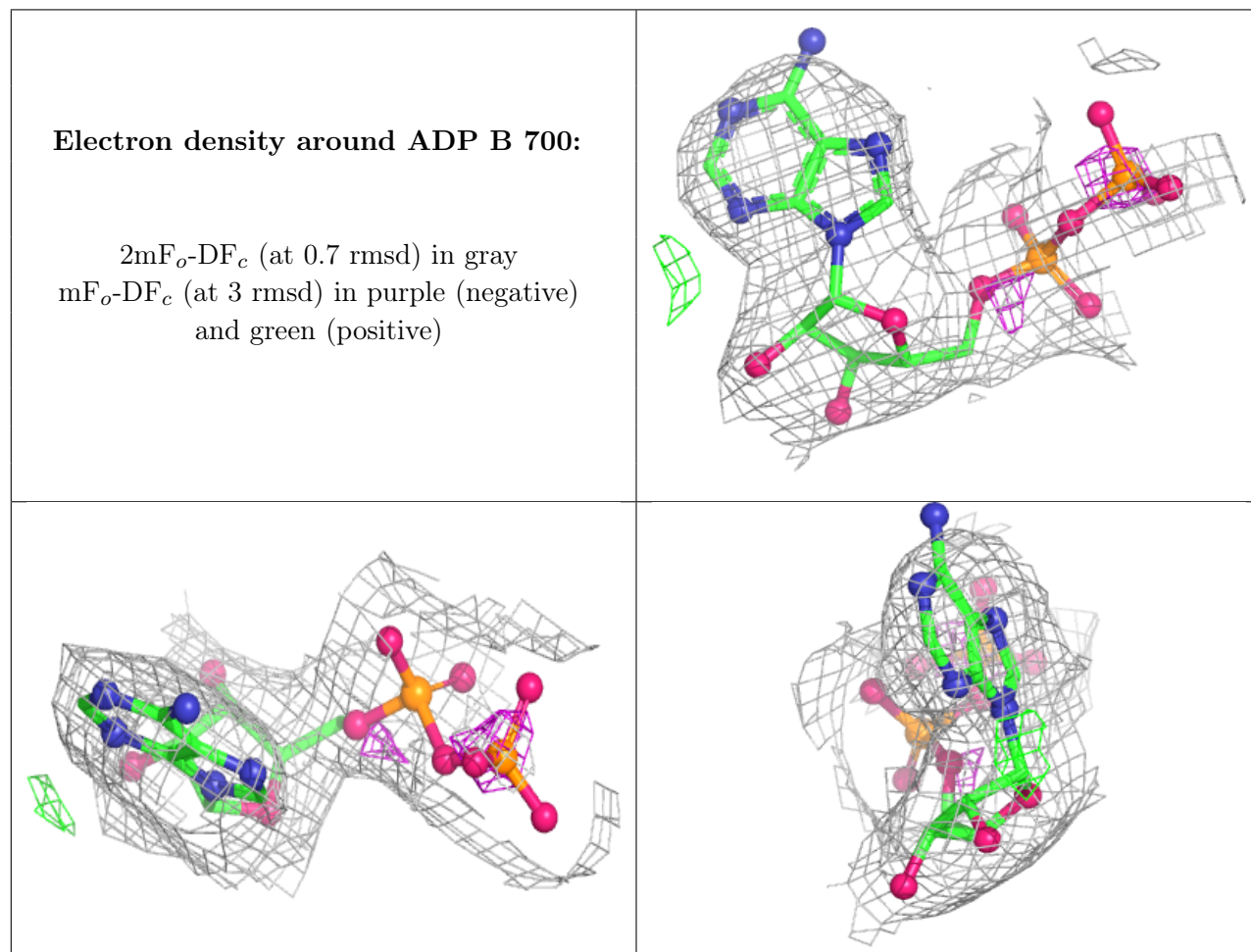
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

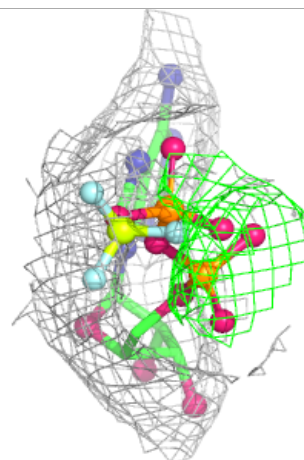
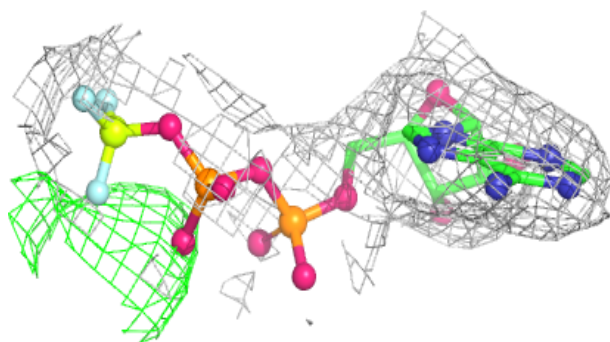
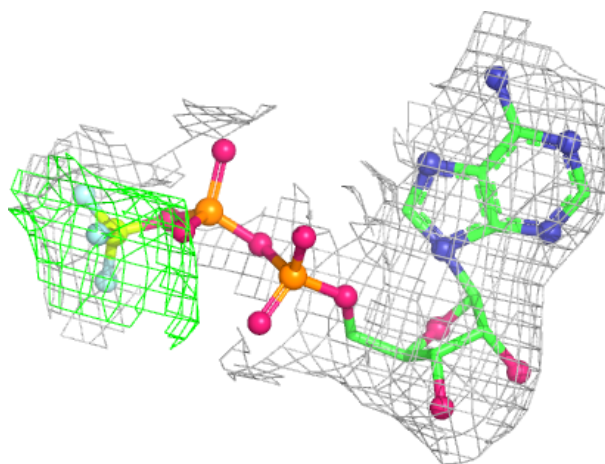
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	MG	D	800	1/1	0.76	0.29	83,83,83,83	0
7	MG	B	800	1/1	0.77	0.10	83,83,83,83	0
7	MG	C	800	1/1	0.87	0.18	83,83,83,83	0
6	ADP	B	700	27/27	0.90	0.07	83,83,83,83	0
8	08T	D	700	31/31	0.94	0.09	83,83,83,83	0
8	08T	C	700	31/31	0.96	0.09	83,83,83,83	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.



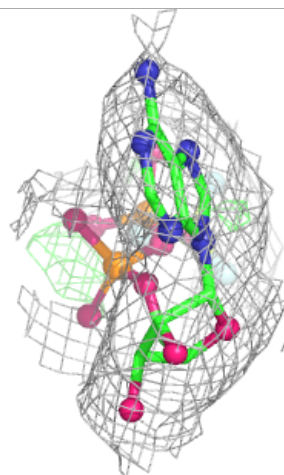
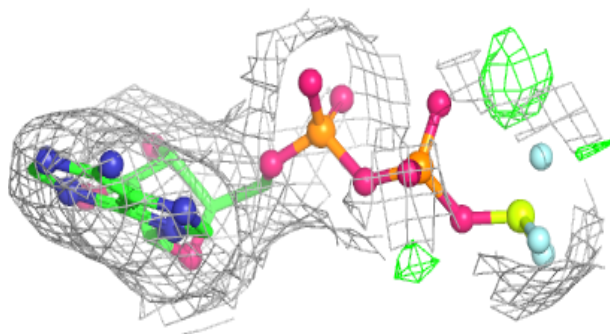
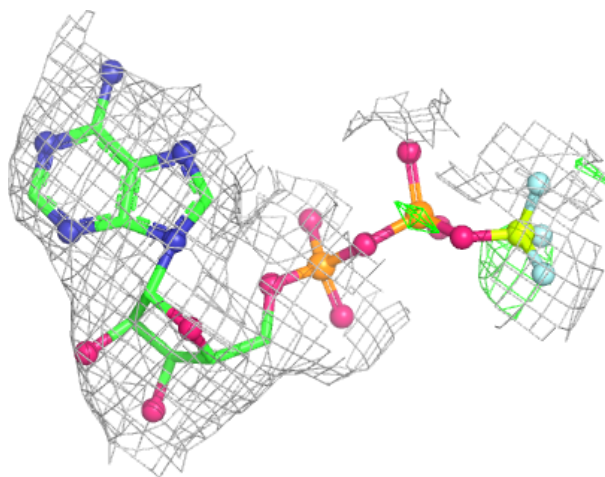
Electron density around 08T D 700:

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



Electron density around 08T C 700:

$2mF_o-DF_c$ (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.