



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 11:05 AM EDT

PDB ID : 7KEF
Title : RNA polymerase II elongation complex with unnatural base dTPT3, rNaM in swing state
Authors : Oh, J.; Wang, D.
Deposited on : 2020-10-10
Resolution : 3.89 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 : 2.35.1
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) : 2.35.1

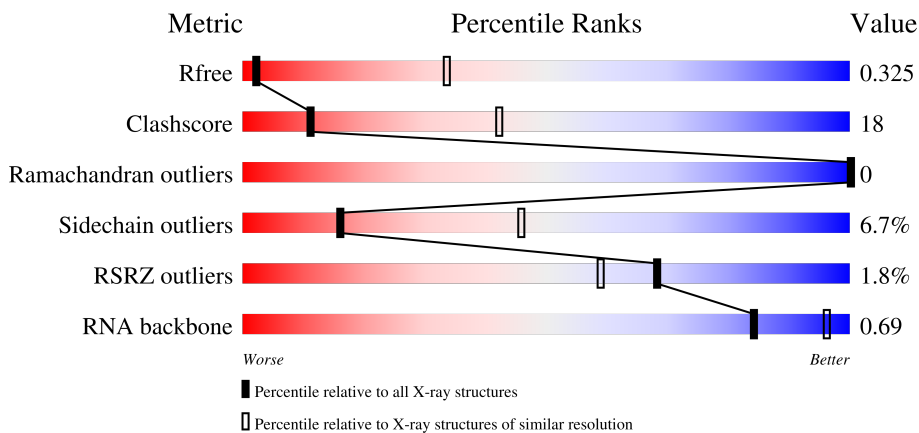
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.89 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.






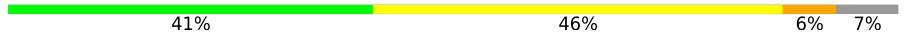

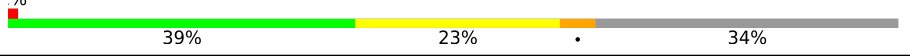

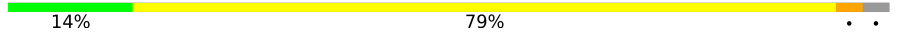

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)
RNA backbone	3102	1040 (4.76-3.00)

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	1733	 48% 30% 20%
2	B	1224	 51% 37% 10%
3	C	318	 53% 30% 16%
4	E	215	 67% 29%

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Mol	Chain	Length	Quality of chain
5	F	155	
6	H	146	
7	I	122	
8	J	70	
9	K	120	
10	L	70	
11	R	10	
12	T	29	
13	N	16	

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 29202 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-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1390	10920	6887	1913	2059	61	0	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	1106	8792	5568	1538	1631	55	0	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	266	2091	1315	348	415	13	0	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	E	214	1748	1108	308	321	11	0	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	F	84	679	434	115	127	3	0	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	H	133	1068	673	180	211	4	0	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	I	119	971	596	179	186	10	0	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	J	65	532	339	93	94	6	0	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	K	114	919	590	156	171	2	0	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	L	46	359	221	71	63	4	0	0	0

- Molecule 11 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
11	R	10	217	98	45	65	9	0	0	0

- Molecule 12 is a DNA chain called Template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
12	T	28	566	273	100	164	27	2	0	0	0

- Molecule 13 is a DNA chain called Non-template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
13	N	15	307	147	51	94	15	0	0	0

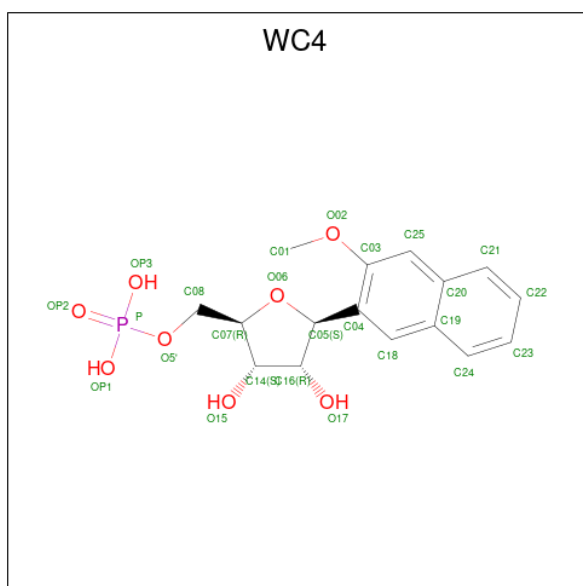
- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	2	Total	Zn	0	0
			2	2		
14	B	1	Total	Zn	0	0
			1	1		
14	C	1	Total	Zn	0	0
			1	1		
14	I	2	Total	Zn	0	0
			2	2		
14	J	1	Total	Zn	0	0
			1	1		
14	L	1	Total	Zn	0	0
			1	1		

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total	Mg	0	0
			1	1		

- Molecule 16 is (1S)-1,4-anhydro-1-(3-methoxynaphthalen-2-yl)-5-O-phosphono-D-ribose (three-letter code: WC4) (formula: C₁₆H₁₉O₈P) (labeled as "Ligand of Interest" by depositor).

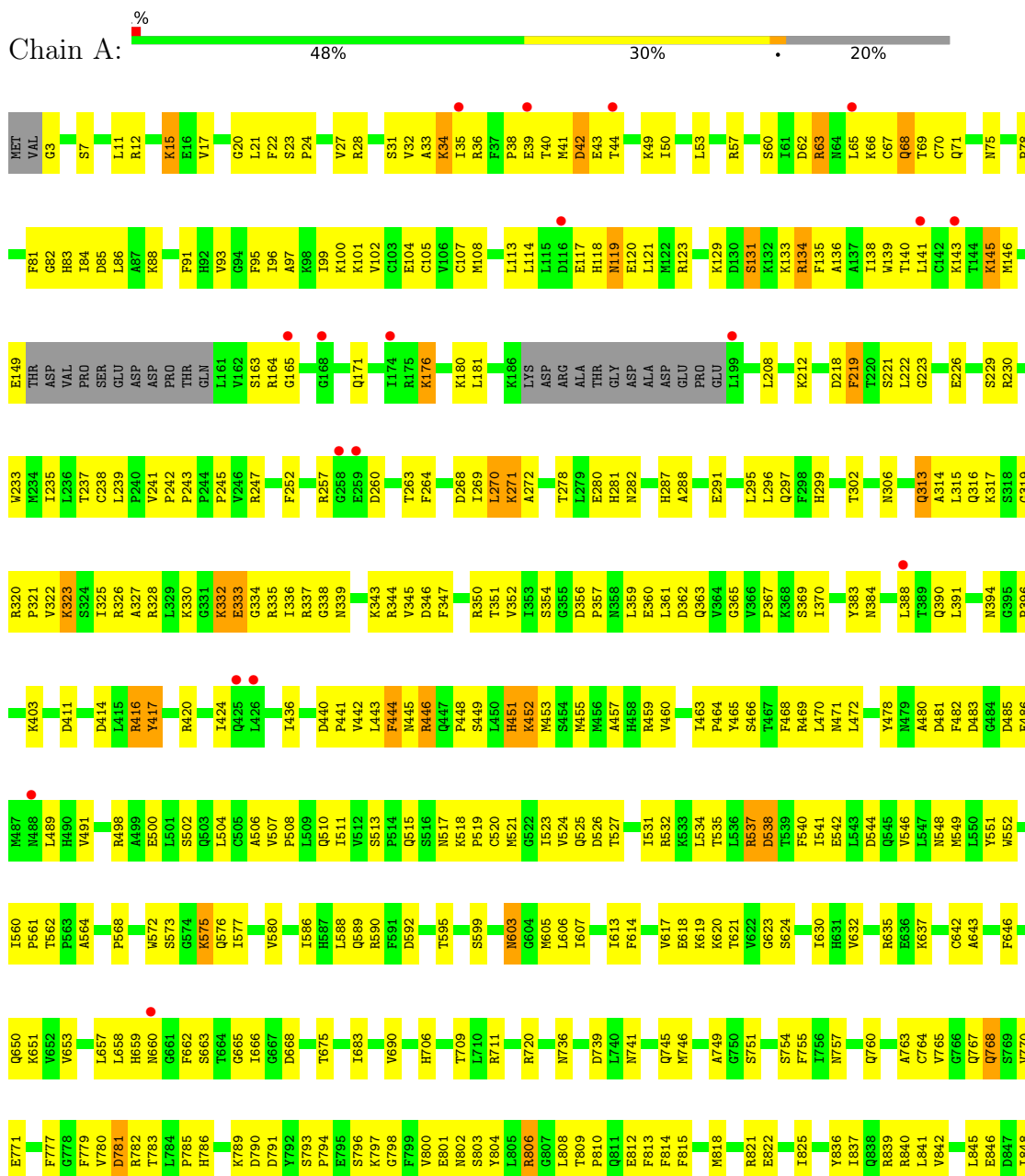


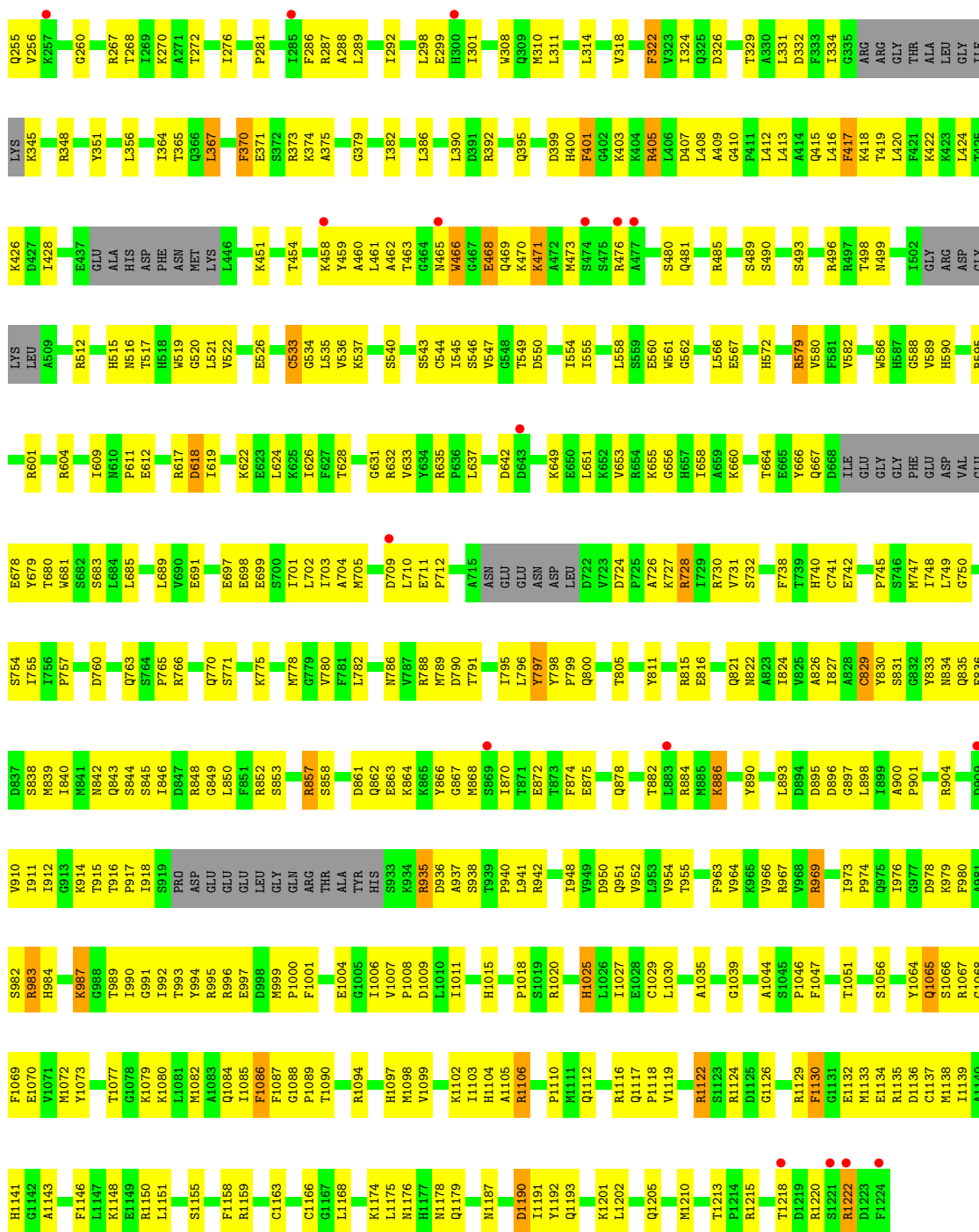
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	R	1	Total	C	O	P	0	0
			24	16	7	1		

3 Residue-property plots [i](#)

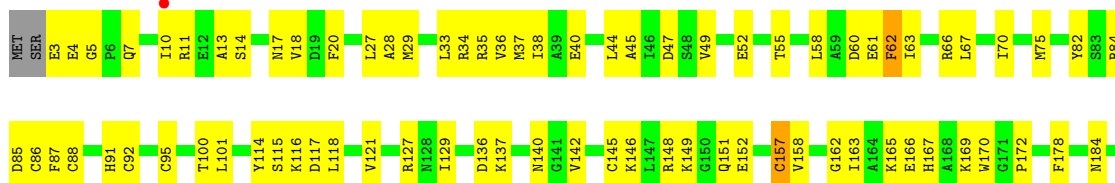
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

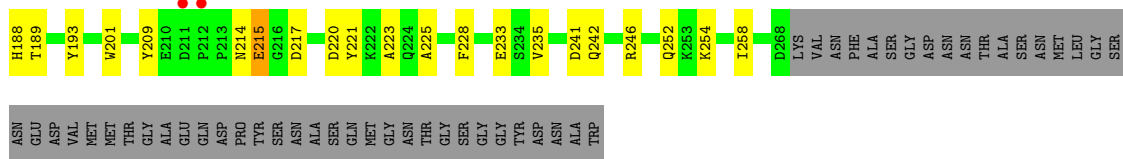
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1



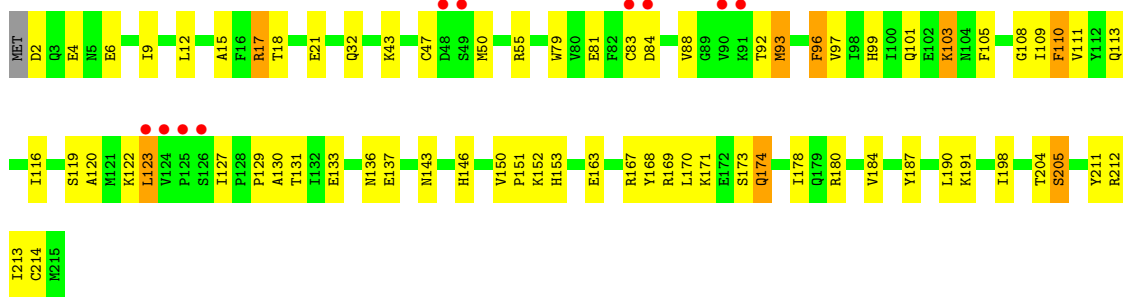


• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

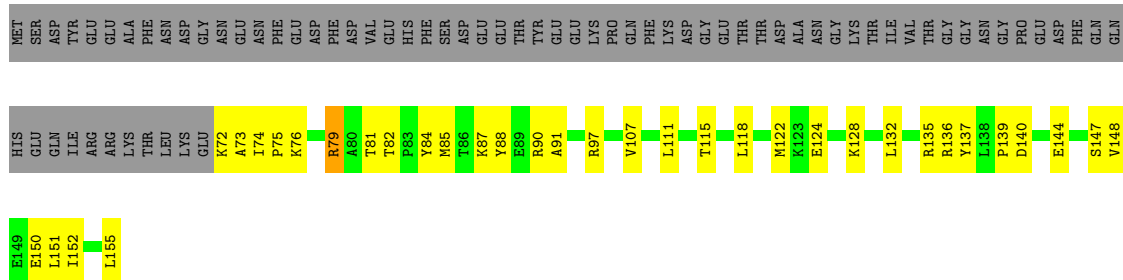
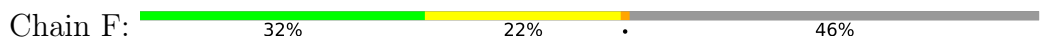




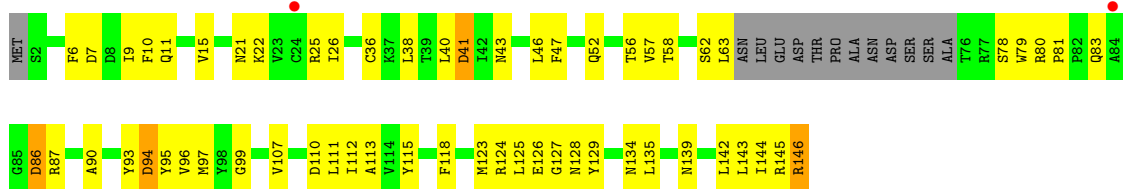
● Molecule 4: DNA-directed RNA polymerases I, II, and III subunit RPABC1



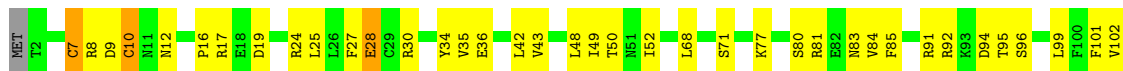
● Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC2

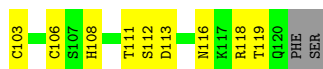


● Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC3



● Molecule 7: DNA-directed RNA polymerase II subunit RPB9

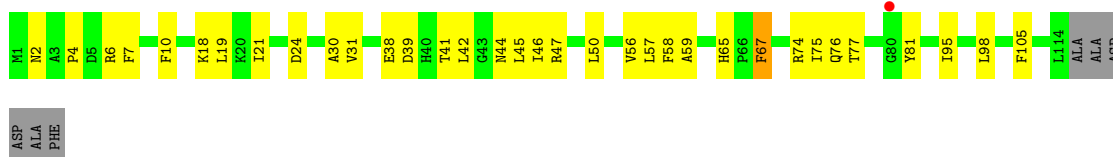




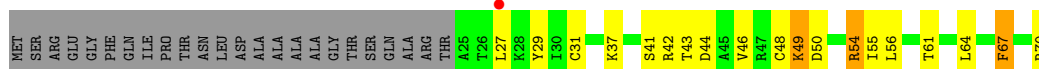
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC5



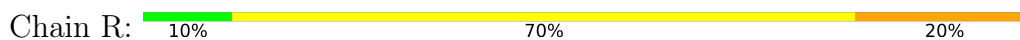
- Molecule 9: DNA-directed RNA polymerase II subunit RPB11



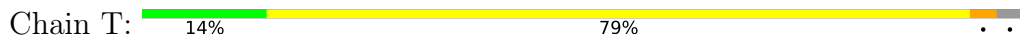
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 11: RNA



- Molecule 12: Template strand DNA



- Molecule 13: Non-template strand DNA



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	167.71Å 221.71Å 193.25Å 90.00° 101.78° 90.00°	Depositor
Resolution (Å)	48.70 – 3.89 48.70 – 3.89	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.70-3.89) 98.6 (48.70-3.89)	Depositor EDS
R_{merge}	1.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 3.88Å)	Xtrriage
Refinement program	PHENIX 1.13	Depositor
R, R_{free}	0.268 , 0.326 0.268 , 0.325	Depositor DCC
R_{free} test set	1979 reflections (3.17%)	wwPDB-VP
Wilson B-factor (Å ²)	107.6	Xtrriage
Anisotropy	0.316	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	29202	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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: MG, ZN, WC4, WC7

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	0.26	0/11113	0.48	1/15025 (0.0%)
2	B	0.26	0/8963	0.49	0/12086
3	C	0.26	0/2129	0.48	0/2886
4	E	0.26	0/1784	0.46	0/2402
5	F	0.26	0/691	0.43	0/933
6	H	0.26	0/1086	0.50	0/1470
7	I	0.27	0/989	0.47	0/1331
8	J	0.28	0/541	0.51	0/727
9	K	0.27	0/937	0.46	0/1265
10	L	0.25	0/361	0.57	0/481
11	R	0.41	0/244	1.08	1/380 (0.3%)
12	T	0.62	0/609	1.06	1/934 (0.1%)
13	N	0.55	0/342	1.35	1/526 (0.2%)
All	All	0.28	0/29789	0.53	4/40446 (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	2
13	N	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	N	17	DG	C5-C6-O6	-20.52	116.29	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	T	21	DC	O4'-C4'-C3'	-5.52	102.29	104.50
11	R	8	G	N3-C2-N2	-5.51	116.04	119.90
1	A	997	LEU	CA-CB-CG	5.40	127.71	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	332	LYS	Peptide
1	A	895	LYS	Peptide
13	N	17	DG	Sidechain

5.2 Too-close contacts [i](#)

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	10920	0	11003	438	0
2	B	8792	0	8823	397	0
3	C	2091	0	2049	77	0
4	E	1748	0	1765	50	0
5	F	679	0	701	27	0
6	H	1068	0	1040	41	0
7	I	971	0	929	29	0
8	J	532	0	543	36	0
9	K	919	0	929	35	0
10	L	359	0	378	13	0
11	R	217	0	110	13	0
12	T	566	0	305	34	0
13	N	307	0	172	6	1
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
15	A	1	0	0	0	0
16	R	24	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	29202	0	28747	1036	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 18.

All (1036) 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)
2:B:1094:ARG:NH2	2:B:1098:MET:SD	2.09	1.23
16:R:11:WC4:O06	16:R:11:WC4:C05	1.66	1.19
2:B:1094:ARG:HH12	2:B:1098:MET:HE2	0.98	1.11
2:B:1094:ARG:HH12	2:B:1098:MET:CE	1.65	1.10
1:A:508:PRO:HA	1:A:511:ILE:HG13	1.35	1.05
1:A:35:ILE:HD13	1:A:270:LEU:HD11	1.41	0.99
1:A:504:LEU:CD1	5:F:91:ALA:HB2	1.96	0.94
2:B:1094:ARG:NH1	2:B:1098:MET:HE2	1.84	0.92
1:A:414:ASP:OD2	1:A:416:ARG:NH2	2.02	0.91
1:A:463:ILE:HD13	1:A:464:PRO:O	1.72	0.90
2:B:1094:ARG:HH22	2:B:1098:MET:CE	1.86	0.88
2:B:405:ARG:HH21	2:B:632:ARG:CG	1.86	0.88
2:B:405:ARG:HH21	2:B:632:ARG:HG2	1.37	0.87
2:B:1094:ARG:NH1	2:B:1098:MET:CE	2.37	0.87
1:A:900:ASP:HA	1:A:926:GLN:HE22	1.40	0.86
4:E:93:MET:HG2	4:E:123:LEU:HD13	1.60	0.84
4:E:123:LEU:HD23	4:E:123:LEU:H	1.43	0.84
1:A:347:PHE:HB3	1:A:491:VAL:HG12	1.60	0.82
1:A:508:PRO:HA	1:A:511:ILE:CG1	2.10	0.81
8:J:7:CYS:HA	8:J:49:MET:HG2	1.63	0.80
2:B:128:LEU:HB3	2:B:167:ILE:HG13	1.63	0.80
1:A:3:GLY:HA2	2:B:1159:ARG:HD2	1.62	0.80
1:A:463:ILE:O	1:A:463:ILE:HD12	1.81	0.80
2:B:405:ARG:NH2	2:B:632:ARG:HG2	1.97	0.79
2:B:405:ARG:HE	2:B:632:ARG:HG2	1.47	0.79
1:A:504:LEU:HD11	5:F:91:ALA:HB2	1.64	0.79
1:A:35:ILE:HD12	1:A:35:ILE:O	1.83	0.78
1:A:335:ARG:HH12	2:B:1202:LEU:HD12	1.50	0.77
1:A:825:ILE:HD12	2:B:512:ARG:HB2	1.67	0.76
2:B:849:GLY:HA2	2:B:852:ARG:HE	1.50	0.76
8:J:9:SER:OG	8:J:45:CYS:SG	2.43	0.76
3:C:27:LEU:HA	3:C:228:PHE:HZ	1.47	0.76
1:A:504:LEU:HD13	5:F:91:ALA:HB2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:35:ARG:NH1	9:K:41:THR:OG1	2.18	0.75
1:A:71:GLN:HE22	2:B:1176:ASN:H	1.33	0.75
1:A:388:LEU:HA	1:A:391:LEU:HD12	1.69	0.75
2:B:731:VAL:HG13	2:B:732:SER:H	1.52	0.75
1:A:146:MET:HA	1:A:171:GLN:HE22	1.51	0.74
1:A:414:ASP:OD2	1:A:416:ARG:CZ	2.34	0.74
2:B:547:VAL:HG12	2:B:612:GLU:OE2	1.86	0.74
1:A:504:LEU:HD13	5:F:91:ALA:CB	2.17	0.74
11:R:5:A:H61	12:T:25:DC:H42	1.35	0.74
2:B:635:ARG:NH1	2:B:742:GLU:OE2	2.21	0.74
2:B:800:GLN:HB3	8:J:52:THR:HG22	1.69	0.74
1:A:999:VAL:HG12	1:A:1000:LEU:HD12	1.70	0.73
2:B:840:ILE:HG12	2:B:992:ILE:HG22	1.69	0.73
2:B:642:ASP:HA	2:B:649:LYS:HA	1.69	0.73
1:A:34:LYS:H	1:A:34:LYS:HD3	1.54	0.73
1:A:899:VAL:HG23	1:A:929:LEU:HD13	1.69	0.73
1:A:445:ASN:ND2	1:A:455:MET:SD	2.61	0.73
1:A:951:GLU:O	1:A:954:TRP:NE1	2.22	0.73
3:C:172:PRO:O	3:C:235:VAL:HG12	1.89	0.72
1:A:663:SER:HB2	2:B:1085:ILE:HG22	1.72	0.72
1:A:1267:MET:O	1:A:1271:ILE:HG23	1.89	0.72
8:J:6:ARG:HG2	8:J:13:VAL:HA	1.72	0.72
12:T:1:DC:O2	13:N:17:DG:N2	2.19	0.72
1:A:821:ARG:HH21	2:B:534:GLY:HA2	1.55	0.72
1:A:663:SER:OG	2:B:827:ILE:O	2.07	0.71
2:B:916:THR:O	2:B:935:ARG:NH2	2.22	0.71
8:J:18:TRP:O	8:J:21:TYR:HB3	1.91	0.71
3:C:254:LYS:NZ	9:K:38:GLU:OE1	2.24	0.71
2:B:1222:ARG:H	2:B:1222:ARG:HD2	1.54	0.71
5:F:79:ARG:NH1	5:F:150:GLU:OE1	2.25	0.70
2:B:911:ILE:HG22	2:B:912:ILE:HG13	1.73	0.70
2:B:987:LYS:NZ	11:R:10:A:OP1	2.24	0.70
5:F:128:LYS:NZ	5:F:151:LEU:O	2.24	0.70
2:B:755:ILE:O	2:B:983:ARG:NH1	2.24	0.70
1:A:504:LEU:CD1	5:F:91:ALA:CB	2.69	0.70
1:A:17:VAL:HG13	1:A:1419:ASP:HB3	1.74	0.70
1:A:1399:ARG:NH2	1:A:1417:GLU:OE2	2.25	0.69
1:A:1102:LYS:O	1:A:1106:ASN:ND2	2.26	0.69
2:B:822:ASN:HB2	8:J:52:THR:HG21	1.73	0.69
2:B:405:ARG:NE	2:B:632:ARG:HG2	2.06	0.69
4:E:151:PRO:HD2	4:E:153:HIS:HE1	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:GLY:HA3	1:A:469:ARG:HB2	1.75	0.69
1:A:1406:VAL:HA	1:A:1409:LEU:HD12	1.75	0.68
8:J:57:ILE:HA	8:J:60:PHE:HD2	1.57	0.68
2:B:942:ARG:NH2	12:T:24:DT:OP1	2.26	0.68
3:C:116:LYS:NZ	3:C:117:ASP:OD1	2.24	0.68
1:A:1342:GLU:HG3	4:E:198:ILE:HG21	1.75	0.68
4:E:127:ILE:HG22	4:E:129:PRO:HD2	1.74	0.68
2:B:996:ARG:NH1	3:C:38:ILE:HG23	2.08	0.68
6:H:96:VAL:HA	6:H:142:LEU:O	1.94	0.68
3:C:75:MET:O	3:C:246:ARG:NH2	2.27	0.67
2:B:26:THR:OG1	2:B:29:ASP:OD1	2.07	0.67
1:A:326:ARG:HG3	1:A:1406:VAL:HG11	1.76	0.67
1:A:1142:THR:HB	1:A:1271:ILE:HD11	1.75	0.67
9:K:56:VAL:HA	9:K:77:THR:HG23	1.75	0.67
1:A:323:LYS:HE2	1:A:328:ARG:HH21	1.60	0.67
1:A:114:LEU:HD13	1:A:145:LYS:HD2	1.76	0.67
1:A:93:VAL:HA	1:A:96:ILE:HG13	1.77	0.67
5:F:128:LYS:NZ	5:F:148:VAL:O	2.27	0.67
2:B:731:VAL:HG13	2:B:732:SER:N	2.09	0.67
4:E:143:ASN:ND2	4:E:187:TYR:OH	2.26	0.67
2:B:67:SER:OG	2:B:92:PHE:N	2.21	0.67
1:A:508:PRO:CA	1:A:511:ILE:HG13	2.19	0.66
2:B:995:ARG:NH1	2:B:997:GLU:OE2	2.28	0.66
3:C:166:GLU:O	9:K:6:ARG:NE	2.26	0.66
3:C:258:ILE:HD11	9:K:42:LEU:HD21	1.78	0.66
1:A:845:LEU:HD12	1:A:1069:ALA:HB2	1.76	0.66
2:B:1025:HIS:HE1	2:B:1090:THR:HG21	1.61	0.66
2:B:1094:ARG:NH2	2:B:1098:MET:CE	2.53	0.66
3:C:92:CYS:H	3:C:95:CYS:HB2	1.60	0.66
2:B:125:SER:HB2	2:B:169:ARG:HB3	1.78	0.66
6:H:110:ASP:O	6:H:128:ASN:ND2	2.28	0.66
6:H:95:TYR:HB3	6:H:144:ILE:HB	1.77	0.66
1:A:42:ASP:HA	1:A:50:ILE:HG23	1.77	0.66
1:A:449:SER:OG	2:B:1134:GLU:OE2	2.14	0.66
1:A:519:PRO:O	1:A:624:SER:OG	2.11	0.65
8:J:16:ASP:OD1	8:J:17:LYS:NZ	2.24	0.65
2:B:199:MET:SD	2:B:199:MET:N	2.64	0.65
6:H:146:ARG:O	6:H:146:ARG:NH1	2.29	0.65
1:A:1342:GLU:OE2	4:E:212:ARG:NH2	2.30	0.65
2:B:604:ARG:NH2	2:B:691:GLU:OE1	2.29	0.65
1:A:367:PRO:HB3	1:A:466:SER:HA	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:ARG:NH2	1:A:745:GLN:OE1	2.29	0.65
1:A:590:ARG:HE	1:A:621:THR:HG22	1.61	0.65
2:B:25:ILE:HD11	2:B:653:VAL:HB	1.79	0.65
2:B:999:MET:HG3	2:B:1000:PRO:HD2	1.79	0.65
2:B:1009:ASP:OD2	8:J:48:ARG:NH2	2.29	0.65
5:F:74:ILE:HG12	5:F:75:PRO:HD2	1.77	0.65
1:A:1209:MET:N	1:A:1209:MET:SD	2.70	0.64
1:A:1271:ILE:HD12	1:A:1271:ILE:O	1.97	0.64
1:A:660:ASN:ND2	2:B:1082:MET:SD	2.70	0.64
1:A:356:ASP:HB3	1:A:359:LEU:HD13	1.78	0.64
2:B:499:ASN:HA	2:B:536:VAL:HG12	1.78	0.64
2:B:628:THR:HA	2:B:632:ARG:HH21	1.62	0.64
2:B:1072:MET:SD	2:B:1085:ILE:HD11	2.37	0.64
1:A:1094:VAL:HA	1:A:1113:THR:HG21	1.80	0.64
2:B:664:THR:O	2:B:667:GLN:NE2	2.31	0.64
1:A:269:ILE:HG12	1:A:299:HIS:HB3	1.80	0.64
1:A:783:THR:O	2:B:516:ASN:ND2	2.31	0.64
1:A:839:ARG:NH1	2:B:1132:GLU:OE2	2.30	0.64
1:A:658:LEU:HD22	2:B:831:SER:H	1.61	0.64
1:A:1227:ILE:HG13	1:A:1239:ARG:HB2	1.80	0.64
2:B:1099:VAL:O	2:B:1103:ILE:N	2.30	0.63
1:A:20:GLY:N	2:B:1213:THR:O	2.28	0.63
1:A:35:ILE:HD13	1:A:270:LEU:CD1	2.25	0.63
2:B:268:THR:OG1	2:B:270:LYS:NZ	2.32	0.63
2:B:637:LEU:HD13	2:B:740:HIS:HB3	1.81	0.63
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.80	0.63
2:B:844:SER:O	2:B:848:ARG:N	2.29	0.63
1:A:442:VAL:HG12	1:A:491:VAL:HG23	1.80	0.63
1:A:351:THR:HB	2:B:1103:ILE:HG13	1.80	0.63
6:H:38:LEU:HD13	6:H:40:LEU:HD23	1.81	0.63
1:A:11:LEU:HD12	1:A:12:ARG:N	2.13	0.63
1:A:1143:LEU:HB3	1:A:1271:ILE:HG12	1.81	0.63
7:I:48:LEU:O	7:I:92:ARG:NH2	2.31	0.63
7:I:80:SER:OG	7:I:103:CYS:SG	2.57	0.63
2:B:1082:MET:HA	3:C:189:THR:HA	1.81	0.62
2:B:234:ILE:HG21	2:B:237:VAL:HG22	1.80	0.62
9:K:46:ILE:O	9:K:50:LEU:HB2	1.99	0.62
1:A:782:ARG:NH2	2:B:698:GLU:O	2.32	0.62
2:B:493:SER:OG	2:B:526:GLU:OE2	2.17	0.62
1:A:605:MET:HE1	1:A:607:ILE:HG13	1.80	0.62
1:A:343:LYS:NZ	2:B:1151:LEU:O	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:796:LEU:HB3	2:B:799:PRO:HG3	1.80	0.62
4:E:79:TRP:CZ2	4:E:99:HIS:NE2	2.68	0.62
1:A:338:GLY:HA2	2:B:1129:ARG:HH22	1.65	0.62
2:B:405:ARG:CZ	2:B:632:ARG:HG2	2.29	0.62
5:F:81:THR:OG1	5:F:144:GLU:OE1	2.15	0.62
2:B:238:ALA:HB3	2:B:256:VAL:HG12	1.81	0.62
2:B:1218:THR:O	2:B:1218:THR:HG22	2.00	0.62
3:C:36:VAL:HA	3:C:40:GLU:HG3	1.81	0.62
1:A:562:THR:O	1:A:576:GLN:NE2	2.33	0.62
2:B:356:LEU:O	2:B:374:LYS:NZ	2.31	0.61
2:B:839:MET:O	2:B:991:GLY:N	2.20	0.61
1:A:445:ASN:HD21	2:B:1134:GLU:HG3	1.65	0.61
1:A:1116:LEU:HG	1:A:1311:VAL:HG22	1.81	0.61
2:B:724:ASP:OD2	2:B:727:LYS:NZ	2.31	0.61
1:A:218:ASP:O	1:A:221:SER:OG	2.19	0.61
2:B:345:LYS:HB2	2:B:348:ARG:HH11	1.66	0.61
1:A:1289:ARG:NH1	1:A:1303:GLU:OE1	2.34	0.61
2:B:412:LEU:HB3	2:B:466:TRP:CH2	2.35	0.61
1:A:118:HIS:CD2	1:A:119:ASN:HD22	2.18	0.61
1:A:491:VAL:O	2:B:1150:ARG:NH2	2.34	0.60
1:A:1147:THR:HB	7:I:48:LEU:HD12	1.83	0.60
1:A:302:THR:O	1:A:306:ASN:ND2	2.34	0.60
2:B:50:SER:HG	2:B:410:GLY:H	1.46	0.60
1:A:482:PHE:O	2:B:989:THR:OG1	2.19	0.60
2:B:833:TYR:HD2	2:B:992:ILE:HG21	1.66	0.60
2:B:463:THR:O	2:B:480:SER:OG	2.17	0.60
2:B:1159:ARG:NH2	2:B:1193:GLN:OE1	2.35	0.60
2:B:100:PRO:O	2:B:180:TYR:OH	2.20	0.60
2:B:1106:ARG:NH1	2:B:1110:PRO:O	2.35	0.60
1:A:436:ILE:HD11	1:A:491:VAL:HG21	1.84	0.60
7:I:119:THR:HG22	7:I:119:THR:O	2.01	0.60
2:B:635:ARG:NH2	2:B:698:GLU:OE2	2.35	0.60
3:C:100:THR:HG23	3:C:121:VAL:HG21	1.82	0.60
1:A:840:ARG:HH21	1:A:1384:VAL:HG23	1.68	0.59
6:H:96:VAL:HG23	6:H:143:LEU:HD23	1.84	0.59
1:A:471:ASN:OD1	1:A:650:GLN:NE2	2.32	0.59
2:B:205:ILE:HG13	2:B:461:LEU:HB3	1.85	0.59
3:C:148:ARG:N	3:C:151:GLN:OE1	2.34	0.59
5:F:97:ARG:NE	5:F:124:GLU:OE1	2.29	0.59
2:B:348:ARG:O	2:B:351:TYR:HB3	2.02	0.59
4:E:55:ARG:NH2	4:E:113:GLN:OE1	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:ASP:OD2	6:H:22:LYS:N	2.28	0.59
1:A:1348:LEU:HD23	1:A:1372:VAL:HG13	1.85	0.59
2:B:416:LEU:HD22	2:B:466:TRP:HE1	1.68	0.59
2:B:969:ARG:HH21	3:C:61:GLU:H	1.51	0.59
9:K:39:ASP:OD2	9:K:41:THR:OG1	2.18	0.59
1:A:544:ASP:N	1:A:544:ASP:OD1	2.36	0.59
1:A:899:VAL:CG2	1:A:929:LEU:HD13	2.33	0.59
1:A:1224:LEU:HD11	1:A:1240:CYS:HB3	1.85	0.58
2:B:260:GLY:O	2:B:267:ARG:NH2	2.33	0.58
1:A:1325:THR:OG1	4:E:146:HIS:O	2.21	0.58
2:B:326:ASP:OD1	2:B:329:THR:OG1	2.21	0.58
2:B:468:GLU:OE1	2:B:469:GLN:N	2.36	0.58
2:B:833:TYR:HB2	2:B:840:ILE:HD11	1.85	0.58
2:B:1004:GLU:HB2	2:B:1006:ILE:HG12	1.84	0.58
1:A:242:PRO:HG2	1:A:247:ARG:HH21	1.68	0.58
1:A:463:ILE:HD12	1:A:463:ILE:C	2.24	0.58
1:A:1118:VAL:HA	1:A:1327:ILE:HG13	1.86	0.58
2:B:604:ARG:NH2	2:B:697:GLU:OE2	2.35	0.58
2:B:982:SER:OG	2:B:983:ARG:N	2.36	0.58
3:C:66:ARG:NH2	8:J:3:VAL:O	2.36	0.58
4:E:169:ARG:HB3	5:F:140:ASP:HB2	1.85	0.58
1:A:789:LYS:HG3	7:I:68:LEU:HD23	1.85	0.58
2:B:1104:HIS:HB2	2:B:1122:ARG:HD2	1.85	0.58
3:C:127:ARG:HB3	3:C:129:ILE:HD13	1.86	0.58
12:T:2:DT:H2'	12:T:3:DA:C4	2.39	0.57
2:B:34:ILE:HG21	2:B:747:MET:HE3	1.86	0.57
7:I:95:THR:HG22	7:I:96:SER:H	1.69	0.57
1:A:535:THR:HG21	1:A:617:VAL:HG23	1.86	0.57
1:A:588:LEU:HB3	1:A:607:ILE:HB	1.86	0.57
1:A:452:LYS:HE2	2:B:1141:HIS:HD2	1.69	0.57
2:B:522:VAL:HG11	2:B:537:LYS:HD2	1.87	0.57
2:B:996:ARG:HH12	3:C:38:ILE:HG23	1.68	0.57
2:B:1066:SER:OG	2:B:1067:ARG:NE	2.38	0.57
2:B:1094:ARG:CZ	2:B:1098:MET:CE	2.82	0.57
1:A:39:GLU:HB3	1:A:50:ILE:HD11	1.85	0.57
1:A:338:GLY:HA2	2:B:1129:ARG:NH2	2.20	0.57
1:A:951:GLU:OE2	1:A:953:ASN:ND2	2.36	0.57
1:A:113:LEU:HD12	1:A:113:LEU:H	1.68	0.57
1:A:709:THR:HG22	1:A:711:ARG:H	1.69	0.57
2:B:546:SER:OG	2:B:632:ARG:N	2.38	0.57
2:B:611:PRO:HB3	2:B:685:LEU:HD11	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1004:GLU:OE2	2:B:1064:TYR:OH	2.19	0.57
8:J:45:CYS:O	8:J:48:ARG:NH1	2.37	0.57
1:A:993:LEU:HD23	1:A:1022:LEU:HD21	1.85	0.57
2:B:227:LYS:H	2:B:395:GLN:NE2	2.03	0.57
2:B:332:ASP:OD1	2:B:348:ARG:NE	2.35	0.57
2:B:731:VAL:CG1	2:B:732:SER:H	2.18	0.57
7:I:34:TYR:HE2	7:I:36:GLU:HB2	1.70	0.57
1:A:485:ASP:OD1	11:R:10:A:O2'	2.14	0.57
1:A:599:SER:OG	1:A:603:ASN:O	2.16	0.57
1:A:1191:TRP:NE1	1:A:1257:ASP:OD1	2.35	0.57
2:B:901:PRO:HB3	2:B:951:GLN:HA	1.85	0.57
1:A:999:VAL:N	1:A:1011:GLN:OE1	2.32	0.56
2:B:222:ILE:HD13	2:B:403:LYS:HG2	1.87	0.56
3:C:116:LYS:HE3	3:C:140:ASN:HB3	1.86	0.56
3:C:258:ILE:HG23	9:K:19:LEU:HD11	1.87	0.56
1:A:443:LEU:HD21	1:A:455:MET:HE3	1.86	0.56
1:A:1170:ILE:O	1:A:1173:HIS:ND1	2.28	0.56
2:B:996:ARG:HG3	2:B:1007:VAL:HG11	1.86	0.56
9:K:24:ASP:OD1	9:K:74:ARG:NH1	2.38	0.56
1:A:32:VAL:O	1:A:57:ARG:NH1	2.36	0.56
1:A:896:ARG:HE	1:A:898:ARG:HB3	1.70	0.56
1:A:898:ARG:O	1:A:898:ARG:NH1	2.32	0.56
2:B:210:LYS:NZ	2:B:462:ALA:O	2.33	0.56
2:B:270:LYS:HA	2:B:281:PRO:HA	1.86	0.56
4:E:119:SER:HA	4:E:122:LYS:HD2	1.87	0.56
1:A:544:ASP:HB2	9:K:47:ARG:HH21	1.70	0.56
1:A:319:GLY:O	2:B:471:LYS:NZ	2.29	0.56
4:E:127:ILE:HB	4:E:130:ALA:HB3	1.88	0.56
1:A:335:ARG:NH1	2:B:1202:LEU:HD12	2.19	0.56
2:B:310:MET:HG3	2:B:386:LEU:HD13	1.88	0.56
1:A:363:GLN:HA	1:A:459:ARG:O	2.06	0.56
3:C:184:ASN:ND2	3:C:189:THR:O	2.39	0.56
2:B:827:ILE:HD12	2:B:1086:PHE:HD2	1.70	0.56
2:B:835:GLN:N	2:B:838:SER:OG	2.36	0.56
11:R:2:U:H2'	11:R:3:C:C6	2.41	0.56
1:A:212:LYS:O	1:A:212:LYS:NZ	2.32	0.56
3:C:100:THR:HG23	3:C:121:VAL:CG2	2.36	0.56
10:L:42:ARG:HG3	10:L:43:THR:HG23	1.88	0.56
2:B:1025:HIS:CE1	2:B:1090:THR:HG21	2.40	0.56
1:A:350:ARG:NH2	1:A:486:GLU:OE2	2.39	0.55
2:B:67:SER:HG	2:B:92:PHE:H	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:114:PRO:HG2	2:B:181:LEU:HD11	1.87	0.55
2:B:562:GLY:O	2:B:590:HIS:ND1	2.32	0.55
2:B:886:LYS:NZ	2:B:938:SER:O	2.39	0.55
4:E:6:GLU:O	4:E:9:ILE:HG13	2.06	0.55
12:T:25:DC:H2''	12:T:26:DG:H8	1.72	0.55
1:A:95:PHE:O	1:A:99:ILE:HG12	2.06	0.55
1:A:252:PHE:HB2	11:R:1:A:C6	2.41	0.55
1:A:899:VAL:HG21	1:A:929:LEU:HD22	1.88	0.55
1:A:1141:THR:HG23	1:A:1205:LYS:HE3	1.88	0.55
2:B:390:LEU:HB2	2:B:392:ARG:HG2	1.87	0.55
2:B:405:ARG:HH21	2:B:632:ARG:CD	2.18	0.55
5:F:90:ARG:HD3	5:F:155:LEU:HD12	1.87	0.55
1:A:465:TYR:HB3	2:B:976:ILE:HG13	1.88	0.55
1:A:1063:MET:SD	1:A:1436:ILE:HG13	2.47	0.55
1:A:781:ASP:OD1	7:I:91:ARG:NH1	2.39	0.55
2:B:893:LEU:HD13	2:B:897:GLY:HA2	1.89	0.55
1:A:840:ARG:NH2	1:A:1106:ASN:OD1	2.39	0.55
1:A:791:ASP:OD2	1:A:793:SER:OG	2.19	0.55
2:B:656:GLY:O	2:B:660:LYS:HG2	2.07	0.55
3:C:44:LEU:HD22	3:C:129:ILE:HG23	1.88	0.55
1:A:108:MET:SD	1:A:108:MET:N	2.79	0.55
1:A:383:TYR:HB3	5:F:115:THR:HB	1.88	0.55
2:B:866:TYR:HD2	2:B:870:ILE:HD11	1.72	0.55
7:I:111:THR:HG22	7:I:113:ASP:H	1.71	0.55
12:T:21:DC:C2	12:T:22:DT:H72	2.42	0.55
1:A:15:LYS:HB2	2:B:1220:ARG:HD3	1.88	0.55
12:T:19:DT:H2'	12:T:20:DC:C6	2.41	0.55
1:A:17:VAL:CG1	1:A:1419:ASP:HB3	2.37	0.54
1:A:360:GLU:OE2	1:A:651:LYS:NZ	2.38	0.54
1:A:857:ARG:CZ	5:F:139:PRO:HG3	2.37	0.54
2:B:1094:ARG:CZ	2:B:1098:MET:SD	2.89	0.54
1:A:866:PHE:HE1	4:E:211:TYR:H	1.54	0.54
3:C:47:ASP:OD1	10:L:70:ARG:NH2	2.40	0.54
7:I:71:SER:OG	7:I:83:ASN:OD1	2.25	0.54
1:A:101:LYS:HG3	1:A:139:TRP:CD1	2.42	0.54
1:A:345:VAL:HG21	2:B:1150:ARG:HD2	1.90	0.54
2:B:373:ARG:HG2	2:B:566:LEU:HD23	1.89	0.54
1:A:20:GLY:HA3	2:B:1215:ARG:HD2	1.89	0.54
6:H:111:LEU:HA	6:H:128:ASN:HB2	1.90	0.54
1:A:802:ASN:ND2	1:A:812:GLU:OE1	2.41	0.54
2:B:288:ALA:HB1	2:B:331:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:779:PHE:HB2	1:A:782:ARG:O	2.07	0.54
3:C:61:GLU:HA	10:L:67:PHE:HE2	1.72	0.54
1:A:780:VAL:O	1:A:789:LYS:NZ	2.28	0.54
2:B:103:ASN:HD22	2:B:109:THR:HB	1.72	0.54
2:B:1112:GLN:N	2:B:1117:GLN:O	2.39	0.54
4:E:21:GLU:OE1	4:E:146:HIS:NE2	2.40	0.54
1:A:35:ILE:CD1	1:A:270:LEU:HD21	2.38	0.54
1:A:777:PHE:CE1	1:A:797:LYS:HE2	2.43	0.54
1:A:785:PRO:HB2	2:B:703:ILE:HG12	1.90	0.54
2:B:1119:VAL:HG21	2:B:1124:ARG:HB2	1.90	0.54
1:A:1033:GLN:O	1:A:1036:ARG:NH1	2.40	0.54
2:B:763:GLN:HG2	2:B:765:PRO:HD2	1.90	0.54
2:B:1056:SER:OG	2:B:1066:SER:OG	2.19	0.54
1:A:803:SER:H	1:A:806:ARG:HB2	1.72	0.54
1:A:1206:ASP:O	1:A:1274:ARG:NH2	2.41	0.54
1:A:606:LEU:HD11	1:A:613:ILE:HD12	1.90	0.53
1:A:845:LEU:HD11	1:A:1371:LEU:HD23	1.91	0.53
1:A:446:ARG:HB3	1:A:478:TYR:HD2	1.73	0.53
1:A:1436:ILE:HD11	2:B:1139:ILE:HG23	1.91	0.53
2:B:496:ARG:NH2	2:B:540:SER:O	2.41	0.53
1:A:323:LYS:HE2	1:A:328:ARG:NH2	2.23	0.53
1:A:618:GLU:OE1	1:A:620:LYS:NZ	2.39	0.53
1:A:765:VAL:HG22	1:A:800:VAL:HB	1.90	0.53
1:A:390:GLN:NE2	1:A:394:ASN:OD1	2.41	0.53
2:B:896:ASP:OD2	10:L:29:TYR:OH	2.25	0.53
3:C:214:ASN:O	3:C:215:GLU:HG3	2.08	0.53
9:K:65:HIS:ND1	9:K:67:PHE:HB2	2.23	0.53
3:C:86:CYS:SG	3:C:87:PHE:N	2.81	0.53
9:K:18:LYS:NZ	9:K:38:GLU:OE2	2.39	0.53
1:A:919:ILE:HA	1:A:922:ASP:OD2	2.09	0.53
2:B:408:LEU:HG	2:B:545:ILE:HG21	1.91	0.53
4:E:97:VAL:O	4:E:101:GLN:NE2	2.39	0.53
7:I:106:CYS:SG	7:I:108:HIS:HB2	2.49	0.53
1:A:57:ARG:HB3	1:A:68:GLN:NE2	2.23	0.53
1:A:135:PHE:HA	1:A:138:ILE:HG22	1.89	0.53
1:A:361:LEU:HA	1:A:471:ASN:HD22	1.73	0.53
1:A:979:SER:OG	1:A:980:ASP:N	2.41	0.53
1:A:1146:VAL:HG23	1:A:1201:ALA:HB3	1.91	0.53
2:B:104:GLU:OE2	10:L:54:ARG:NE	2.28	0.53
2:B:771:SER:O	2:B:775:LYS:NZ	2.41	0.53
1:A:24:PRO:HD2	1:A:233:TRP:CD1	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:T:2:DT:H3	13:N:16:DA:H61	1.56	0.53
2:B:1046:PRO:HB2	2:B:1047:PHE:HD1	1.74	0.53
2:B:1135:ARG:NH2	2:B:1136:ASP:OD1	2.29	0.53
1:A:925:LEU:O	1:A:929:LEU:HG	2.08	0.52
2:B:498:THR:N	2:B:537:LYS:O	2.42	0.52
2:B:1065:GLN:OE1	2:B:1066:SER:N	2.42	0.52
1:A:260:ASP:OD1	1:A:263:THR:OG1	2.20	0.52
1:A:327:ALA:HA	1:A:330:LYS:HB2	1.91	0.52
2:B:39:ARG:HH22	2:B:664:THR:HG23	1.74	0.52
2:B:519:TRP:CE3	2:B:748:ILE:HD12	2.44	0.52
4:E:110:PHE:HD1	4:E:111:VAL:H	1.58	0.52
1:A:982:THR:N	1:A:985:ASP:OD2	2.39	0.52
2:B:412:LEU:HB3	2:B:466:TRP:HH2	1.73	0.52
4:E:108:GLY:O	4:E:133:GLU:N	2.33	0.52
4:E:205:SER:O	4:E:205:SER:OG	2.28	0.52
2:B:39:ARG:NH2	2:B:664:THR:O	2.42	0.52
2:B:790:ASP:O	2:B:858:SER:OG	2.24	0.52
1:A:949:ASP:OD1	1:A:949:ASP:N	2.41	0.52
1:A:1052:GLN:O	1:A:1056:SER:OG	2.13	0.52
2:B:976:ILE:O	2:B:990:ILE:HB	2.09	0.52
2:B:886:LYS:HG2	2:B:940:PRO:HG3	1.91	0.52
3:C:14:SER:N	3:C:17:ASN:O	2.43	0.52
1:A:65:LEU:H	1:A:66:LYS:HD2	1.75	0.52
1:A:396:PRO:HB3	1:A:403:LYS:HE2	1.91	0.52
1:A:1420:ASP:OD1	1:A:1422:ARG:NH2	2.42	0.52
2:B:169:ARG:N	2:B:454:THR:OG1	2.43	0.52
2:B:308:TRP:HA	2:B:311:LEU:HD12	1.91	0.52
1:A:798:GLY:HA2	1:A:815:PHE:CD1	2.45	0.52
1:A:1271:ILE:HD12	1:A:1271:ILE:C	2.31	0.52
1:A:1356:ILE:O	1:A:1361:SER:OG	2.27	0.52
2:B:276:ILE:HD13	2:B:334:ILE:HG23	1.92	0.52
12:T:19:DT:H2'	12:T:20:DC:H6	1.75	0.52
1:A:754:SER:OG	1:A:755:PHE:N	2.42	0.52
2:B:468:GLU:OE1	2:B:469:GLN:HB2	2.10	0.52
2:B:549:THR:HG22	2:B:550:ASP:H	1.75	0.52
4:E:17:ARG:NE	4:E:21:GLU:OE2	2.36	0.52
8:J:48:ARG:O	8:J:52:THR:OG1	2.14	0.52
1:A:586:ILE:HD11	1:A:637:LYS:HG3	1.92	0.51
1:A:1093:LYS:NZ	1:A:1307:GLU:OE2	2.42	0.51
2:B:878:GLN:O	2:B:882:THR:OG1	2.20	0.51
2:B:1174:LYS:O	2:B:1178:ASN:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:52:GLU:HA	10:L:64:LEU:HD13	1.92	0.51
1:A:513:SER:OG	1:A:515:GLN:O	2.18	0.51
1:A:1101:LEU:HD13	1:A:1355:VAL:HG11	1.92	0.51
2:B:1094:ARG:NH2	2:B:1098:MET:HE1	2.25	0.51
6:H:111:LEU:HD23	6:H:128:ASN:HB2	1.92	0.51
8:J:7:CYS:SG	8:J:11:GLY:N	2.84	0.51
1:A:526:ASP:HB2	2:B:835:GLN:HE22	1.74	0.51
1:A:840:ARG:NH2	1:A:1384:VAL:O	2.43	0.51
2:B:780:VAL:HG22	2:B:795:ILE:HG23	1.92	0.51
2:B:786:ASN:O	2:B:967:ARG:NH2	2.43	0.51
2:B:834:ASN:OD1	2:B:834:ASN:N	2.43	0.51
3:C:165:LYS:HD3	9:K:10:PHE:HB3	1.93	0.51
2:B:471:LYS:HD2	2:B:471:LYS:C	2.31	0.51
3:C:167:HIS:CD2	3:C:169:LYS:HG3	2.46	0.51
5:F:107:VAL:HG11	5:F:111:LEU:HD21	1.93	0.51
1:A:20:GLY:O	2:B:1213:THR:N	2.39	0.51
1:A:1343:ALA:HB2	4:E:150:VAL:HG22	1.92	0.51
2:B:301:ILE:HG12	2:B:379:GLY:HA2	1.92	0.51
5:F:72:LYS:HG2	5:F:73:ALA:H	1.75	0.51
1:A:357:PRO:HD2	2:B:833:TYR:CE1	2.46	0.51
1:A:517:ASN:ND2	1:A:1362:TYR:OH	2.43	0.51
1:A:632:VAL:HG13	1:A:962:ARG:HD3	1.92	0.51
1:A:821:ARG:NH2	2:B:534:GLY:HA2	2.23	0.51
1:A:868:TYR:CE1	1:A:1064:VAL:HG21	2.46	0.51
1:A:1329:THR:HB	1:A:1335:ILE:HD11	1.93	0.51
5:F:97:ARG:NH2	5:F:124:GLU:OE2	2.41	0.51
6:H:107:VAL:HB	6:H:111:LEU:HB2	1.92	0.51
1:A:370:ILE:HG23	2:B:1105:ALA:HB2	1.93	0.51
1:A:104:GLU:O	1:A:145:LYS:NZ	2.25	0.51
1:A:288:ALA:HB1	1:A:291:GLU:HG3	1.92	0.51
1:A:354:SER:O	1:A:470:LEU:N	2.43	0.51
3:C:84:ARG:HH22	3:C:163:ILE:HD11	1.75	0.51
1:A:779:PHE:HE1	1:A:785:PRO:HD3	1.76	0.51
1:A:896:ARG:HB3	1:A:898:ARG:HG3	1.93	0.51
2:B:520:GLY:HA3	2:B:635:ARG:NH1	2.25	0.51
2:B:874:PHE:CD2	2:B:914:LYS:HB3	2.45	0.51
3:C:5:GLY:O	3:C:7:GLN:NE2	2.44	0.51
6:H:99:GLY:HA3	6:H:118:PHE:HD2	1.76	0.51
9:K:58:PHE:O	9:K:75:ILE:HA	2.10	0.51
1:A:786:HIS:NE2	2:B:705:MET:SD	2.85	0.50
1:A:1287:TYR:CD1	1:A:1305:VAL:HG21	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:256:VAL:HG21	2:B:382:ILE:HD11	1.93	0.50
2:B:1143:ALA:HB1	2:B:1146:PHE:HB3	1.93	0.50
7:I:17:ARG:HE	7:I:28:GLU:HG2	1.76	0.50
12:T:15:DA:H2''	12:T:16:DC:H5'	1.94	0.50
1:A:441:PRO:HG3	1:A:498:ARG:HG3	1.93	0.50
2:B:39:ARG:HH21	2:B:667:GLN:HE22	1.58	0.50
10:L:46:VAL:HG12	10:L:56:LEU:HD21	1.92	0.50
1:A:346:ASP:OD1	2:B:1106:ARG:NH2	2.41	0.50
1:A:630:ILE:HG23	1:A:642:CYS:SG	2.52	0.50
1:A:848:ILE:HG22	1:A:1064:VAL:HG13	1.94	0.50
1:A:859:SER:O	1:A:1422:ARG:NH1	2.44	0.50
2:B:789:MET:SD	2:B:967:ARG:HB2	2.51	0.50
2:B:1077:THR:HG23	2:B:1079:LYS:H	1.75	0.50
1:A:709:THR:HG23	7:I:94:ASP:HA	1.94	0.50
1:A:1050:GLU:O	1:A:1054:LEU:HG	2.10	0.50
4:E:163:GLU:OE2	4:E:167:ARG:NE	2.44	0.50
1:A:846:GLU:OE2	2:B:1135:ARG:NH1	2.43	0.50
1:A:885:THR:HG23	1:A:1024:SER:HB2	1.93	0.50
2:B:195:CYS:HB3	2:B:782:LEU:HD13	1.92	0.50
2:B:424:LEU:O	2:B:428:ILE:HG23	2.11	0.50
2:B:554:ILE:HD12	2:B:609:ILE:HD11	1.92	0.50
3:C:167:HIS:HD2	3:C:169:LYS:HG3	1.77	0.50
1:A:842:VAL:HG11	2:B:1136:ASP:CG	2.32	0.50
3:C:145:CYS:SG	3:C:146:LYS:N	2.85	0.50
7:I:77:LYS:HB3	7:I:106:CYS:SG	2.51	0.50
1:A:926:GLN:HA	1:A:929:LEU:HD12	1.94	0.50
12:T:5:DC:H2''	12:T:6:DG:N7	2.25	0.50
1:A:7:SER:HB3	2:B:1159:ARG:NH2	2.27	0.50
1:A:322:VAL:HG12	1:A:323:LYS:H	1.76	0.50
1:A:351:THR:OG1	1:A:352:VAL:N	2.45	0.50
1:A:1120:LEU:HD23	1:A:1130:GLN:HG2	1.93	0.50
2:B:535:LEU:O	2:B:537:LYS:NZ	2.45	0.50
2:B:546:SER:OG	2:B:631:GLY:N	2.41	0.50
2:B:1163:CYS:HA	2:B:1191:ILE:HD12	1.94	0.50
1:A:465:TYR:CG	2:B:976:ILE:HG13	2.47	0.49
2:B:704:ALA:HB3	2:B:741:CYS:HB2	1.94	0.49
3:C:27:LEU:HB2	3:C:225:ALA:HB3	1.93	0.49
3:C:233:GLU:OE1	8:J:12:LYS:NZ	2.30	0.49
8:J:38:ARG:HB2	8:J:38:ARG:NH1	2.26	0.49
9:K:65:HIS:CE1	9:K:67:PHE:HB2	2.47	0.49
2:B:460:ALA:HB1	2:B:466:TRP:NE1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:THR:O	1:A:281:HIS:ND1	2.45	0.49
1:A:765:VAL:HG12	1:A:804:TYR:HD1	1.77	0.49
2:B:289:LEU:HD11	2:B:375:ALA:HB2	1.93	0.49
2:B:1035:ALA:O	2:B:1039:GLY:N	2.40	0.49
1:A:619:LYS:HG3	1:A:623:GLY:HA3	1.93	0.49
1:A:683:ILE:HG21	1:A:801:GLU:HG3	1.93	0.49
1:A:903:ASN:OD1	1:A:904:THR:N	2.45	0.49
2:B:29:ASP:HB3	2:B:658:ILE:HG21	1.93	0.49
2:B:287:ARG:NH1	2:B:292:ILE:O	2.45	0.49
2:B:680:THR:O	2:B:683:SER:OG	2.27	0.49
2:B:850:LEU:HB2	8:J:8:PHE:CG	2.47	0.49
3:C:55:THR:HG1	3:C:152:GLU:H	1.54	0.49
1:A:568:PRO:HG2	6:H:46:LEU:HB3	1.93	0.49
1:A:1364:ASN:OD1	1:A:1366:ARG:NE	2.42	0.49
2:B:121:ASN:HA	2:B:207:GLY:HA3	1.93	0.49
2:B:1046:PRO:HB2	2:B:1047:PHE:CD1	2.48	0.49
7:I:85:PHE:HD1	7:I:99:LEU:HD22	1.78	0.49
8:J:17:LYS:HB3	8:J:39:LEU:HD13	1.93	0.49
10:L:41:SER:OG	10:L:44:ASP:OD2	2.29	0.49
13:N:9:DT:H2''	13:N:10:DA:N7	2.27	0.49
1:A:532:ARG:HD3	1:A:749:ALA:HB2	1.94	0.49
1:A:1348:LEU:HG	1:A:1372:VAL:HG22	1.94	0.49
2:B:1029:CYS:SG	2:B:1088:GLY:HA3	2.52	0.49
4:E:178:ILE:HG22	4:E:214:CYS:HA	1.95	0.49
1:A:102:VAL:O	1:A:104:GLU:N	2.46	0.49
2:B:1130:PHE:HD2	2:B:1151:LEU:HD11	1.78	0.49
3:C:10:ILE:HD11	9:K:105:PHE:HE1	1.77	0.49
12:T:10:DA:H2'	12:T:11:DG:C8	2.48	0.49
1:A:149:GLU:O	1:A:163:SER:OG	2.24	0.49
1:A:534:LEU:HD11	1:A:541:ILE:HD11	1.94	0.49
1:A:540:PHE:HE1	6:H:43:ASN:HD22	1.60	0.49
2:B:232:SER:OG	2:B:234:ILE:O	2.22	0.49
2:B:582:VAL:HG22	2:B:626:ILE:HB	1.93	0.49
1:A:84:ILE:HD12	1:A:239:LEU:HB2	1.95	0.49
1:A:362:ASP:OD1	1:A:459:ARG:NH1	2.43	0.49
1:A:445:ASN:ND2	2:B:1134:GLU:HG3	2.28	0.49
6:H:11:GLN:NE2	6:H:52:GLN:OE1	2.44	0.49
2:B:861:ASP:OD1	2:B:862:GLN:N	2.46	0.49
1:A:40:THR:OG1	1:A:41:MET:N	2.46	0.48
2:B:617:ARG:HG2	2:B:619:ILE:HG13	1.93	0.48
8:J:64:ASN:N	8:J:65:PRO:HD2	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:ASN:O	1:A:745:GLN:HG2	2.13	0.48
2:B:458:LYS:O	2:B:462:ALA:HB2	2.13	0.48
2:B:619:ILE:HD12	2:B:619:ILE:H	1.78	0.48
3:C:101:LEU:HD13	3:C:118:LEU:HD23	1.94	0.48
2:B:745:PRO:O	2:B:748:ILE:HG22	2.14	0.48
1:A:369:SER:OG	9:K:2:ASN:ND2	2.47	0.48
1:A:657:LEU:HD11	2:B:829:CYS:SG	2.53	0.48
1:A:808:LEU:O	2:B:728:ARG:NH1	2.44	0.48
1:A:896:ARG:HB3	1:A:898:ARG:CG	2.43	0.48
1:A:1396:ALA:N	1:A:1419:ASP:OD2	2.47	0.48
2:B:215:GLN:HB3	2:B:407:ASP:HB2	1.95	0.48
3:C:252:GLN:HG2	9:K:95:ILE:HG23	1.95	0.48
2:B:365:THR:HB	2:B:367:LEU:HG	1.94	0.48
2:B:561:TRP:HZ3	2:B:595:ARG:HD3	1.78	0.48
2:B:843:GLN:OE1	2:B:993:THR:OG1	2.18	0.48
2:B:904:ARG:HG2	2:B:948:ILE:HG13	1.95	0.48
7:I:84:VAL:HG13	7:I:102:VAL:HB	1.94	0.48
1:A:445:ASN:OD1	1:A:446:ARG:N	2.46	0.48
2:B:460:ALA:HB1	2:B:466:TRP:HE1	1.77	0.48
2:B:731:VAL:CG1	2:B:732:SER:N	2.75	0.48
2:B:778:MET:HE2	2:B:1094:ARG:HB3	1.94	0.48
13:N:3:DT:H2'	13:N:4:DC:C6	2.49	0.48
1:A:463:ILE:C	1:A:463:ILE:CD1	2.82	0.48
2:B:797:TYR:HE2	3:C:62:PHE:HA	1.79	0.48
3:C:252:GLN:NE2	9:K:95:ILE:O	2.47	0.48
4:E:103:LYS:HB2	4:E:105:PHE:CE1	2.47	0.48
1:A:302:THR:HG21	1:A:313:GLN:OE1	2.13	0.48
1:A:780:VAL:HG23	1:A:789:LYS:NZ	2.29	0.48
2:B:770:GLN:NE2	2:B:983:ARG:O	2.46	0.48
4:E:198:ILE:HG13	4:E:212:ARG:HH12	1.79	0.48
6:H:15:VAL:HA	6:H:26:ILE:HD12	1.96	0.48
8:J:57:ILE:HA	8:J:60:PHE:CD2	2.43	0.48
1:A:328:ARG:HD3	1:A:335:ARG:HH21	1.79	0.48
1:A:523:ILE:HG23	1:A:527:THR:HB	1.95	0.48
1:A:551:TYR:CD1	9:K:74:ARG:HD3	2.49	0.48
1:A:675:THR:OG1	1:A:736:ASN:OD1	2.27	0.48
1:A:706:HIS:NE2	1:A:1139:GLU:OE1	2.46	0.48
1:A:357:PRO:HD2	2:B:833:TYR:HE1	1.79	0.48
1:A:873:MET:HA	1:A:1058:VAL:H	1.79	0.48
1:A:1065:GLY:HA2	1:A:1370:LEU:HD21	1.96	0.48
1:A:1148:ILE:HD13	7:I:49:ILE:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:28:ALA:HB1	9:K:44:ASN:OD1	2.14	0.47
4:E:153:HIS:CD2	4:E:184:VAL:HG11	2.49	0.47
8:J:38:ARG:HB2	8:J:38:ARG:HH11	1.79	0.47
1:A:219:PHE:HA	1:A:222:LEU:HG	1.96	0.47
1:A:272:ALA:HB3	1:A:296:LEU:HD13	1.96	0.47
1:A:471:ASN:OD1	1:A:472:LEU:N	2.47	0.47
2:B:954:VAL:HG22	2:B:964:VAL:HG12	1.95	0.47
2:B:1187:ASN:OD1	2:B:1190:ASP:N	2.47	0.47
7:I:10:CYS:O	7:I:12:ASN:ND2	2.47	0.47
2:B:1068:GLY:HA3	2:B:1086:PHE:HE1	1.79	0.47
2:B:1084:GLN:HG2	3:C:201:TRP:CH2	2.49	0.47
12:T:8:DT:H2'	12:T:9:DA:N7	2.29	0.47
1:A:592:ASP:H	1:A:595:THR:HG21	1.78	0.47
1:A:1351:GLU:O	1:A:1355:VAL:HG23	2.15	0.47
2:B:515:HIS:ND1	2:B:517:THR:HG23	2.29	0.47
2:B:875:GLU:OE2	2:B:915:THR:OG1	2.28	0.47
3:C:49:VAL:HG22	3:C:157:CYS:HB3	1.97	0.47
6:H:112:ILE:HG22	6:H:127:GLY:O	2.14	0.47
6:H:113:ALA:HA	6:H:125:LEU:O	2.15	0.47
9:K:7:PHE:HA	9:K:10:PHE:CE2	2.49	0.47
1:A:302:THR:HG23	1:A:306:ASN:HD21	1.78	0.47
1:A:783:THR:HG21	1:A:796:SER:O	2.15	0.47
2:B:612:GLU:HG2	2:B:632:ARG:HH22	1.78	0.47
1:A:21:LEU:HB2	1:A:229:SER:HA	1.96	0.47
1:A:990:VAL:O	1:A:994:GLN:NE2	2.48	0.47
1:A:1119:TYR:HD1	1:A:1326:ARG:HB3	1.79	0.47
2:B:326:ASP:OD1	2:B:326:ASP:N	2.46	0.47
1:A:440:ASP:O	1:A:460:VAL:HG23	2.15	0.47
2:B:952:VAL:HG22	2:B:966:VAL:HG22	1.97	0.47
4:E:108:GLY:N	4:E:131:THR:O	2.39	0.47
5:F:82:THR:O	5:F:136:ARG:NH1	2.41	0.47
6:H:47:PHE:HE1	6:H:94:ASP:HB2	1.79	0.47
1:A:323:LYS:HE3	1:A:325:ILE:HG12	1.96	0.47
1:A:1153:TYR:CE1	7:I:42:LEU:HD13	2.49	0.47
2:B:842:ASN:OD1	2:B:845:SER:N	2.33	0.47
3:C:220:ASP:OD2	3:C:223:ALA:HB2	2.15	0.47
12:T:8:DT:H2'	12:T:9:DA:C5	2.50	0.47
1:A:86:LEU:HB3	1:A:237:THR:O	2.15	0.47
1:A:782:ARG:NH1	2:B:701:ILE:O	2.45	0.47
2:B:399:ASP:HB2	2:B:515:HIS:CD2	2.50	0.47
2:B:950:ASP:HB2	2:B:969:ARG:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1158:PHE:CE2	2:B:1201:LYS:HD2	2.50	0.47
6:H:86:ASP:N	6:H:86:ASP:OD1	2.48	0.47
1:A:40:THR:O	1:A:49:LYS:HE2	2.15	0.47
1:A:313:GLN:HG2	1:A:314:ALA:H	1.79	0.47
2:B:1102:LYS:HB3	2:B:1102:LYS:HE3	1.68	0.47
1:A:665:GLY:N	1:A:668:ASP:OD2	2.37	0.46
1:A:782:ARG:HH21	2:B:699:GLU:C	2.19	0.46
6:H:36:CYS:HA	6:H:126:GLU:O	2.15	0.46
6:H:93:TYR:HD1	6:H:143:LEU:HB3	1.80	0.46
1:A:33:ALA:HB2	1:A:57:ARG:HH12	1.80	0.46
1:A:513:SER:OG	1:A:518:LYS:O	2.32	0.46
1:A:542:GLU:O	1:A:546:VAL:HG23	2.16	0.46
1:A:1070:GLN:HE22	2:B:1137:CYS:HA	1.80	0.46
2:B:579:ARG:HA	2:B:589:VAL:HA	1.97	0.46
2:B:955:THR:OG1	10:L:55:ILE:HA	2.15	0.46
4:E:55:ARG:NH1	4:E:83:CYS:O	2.48	0.46
1:A:62:ASP:O	1:A:63:ARG:HG3	2.15	0.46
1:A:537:ARG:NH2	6:H:25:ARG:HH12	2.13	0.46
1:A:739:ASP:O	1:A:745:GLN:NE2	2.48	0.46
2:B:460:ALA:HB1	2:B:466:TRP:CD1	2.51	0.46
6:H:43:ASN:OD1	6:H:46:LEU:N	2.32	0.46
1:A:344:ARG:HB2	2:B:1118:PRO:HG2	1.96	0.46
1:A:901:LEU:HA	1:A:907:THR:OG1	2.16	0.46
2:B:521:LEU:HD22	2:B:633:VAL:HG12	1.97	0.46
2:B:750:GLY:O	2:B:754:SER:OG	2.18	0.46
2:B:796:LEU:HD23	2:B:799:PRO:HA	1.96	0.46
2:B:1094:ARG:HH22	2:B:1098:MET:HE1	1.75	0.46
12:T:26:DG:C2	12:T:27:DA:C5	3.03	0.46
1:A:813:PHE:HE2	2:B:749:LEU:HD21	1.80	0.46
2:B:213:ILE:HD12	2:B:213:ILE:HA	1.72	0.46
3:C:88:CYS:SG	3:C:92:CYS:HB2	2.55	0.46
2:B:465:ASN:HA	2:B:476:ARG:HB3	1.98	0.46
2:B:680:THR:OG1	2:B:681:TRP:N	2.49	0.46
2:B:1104:HIS:NE2	2:B:1126:GLY:O	2.43	0.46
3:C:114:TYR:CG	3:C:140:ASN:HB2	2.51	0.46
10:L:31:CYS:SG	10:L:48:CYS:HB2	2.56	0.46
1:A:91:PHE:HB2	1:A:297:GLN:HE22	1.80	0.46
1:A:798:GLY:HA2	1:A:815:PHE:HD1	1.81	0.46
2:B:533:CYS:SG	2:B:534:GLY:N	2.88	0.46
2:B:1080:LYS:HG3	3:C:188:HIS:HB3	1.98	0.46
8:J:36:LEU:HD13	8:J:47:ARG:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:SER:HB3	2:B:1159:ARG:HH22	1.80	0.46
1:A:446:ARG:NH2	1:A:448:PRO:HD2	2.30	0.46
1:A:765:VAL:HG12	1:A:804:TYR:CD1	2.51	0.46
1:A:781:ASP:O	1:A:790:ASP:N	2.28	0.46
3:C:34:ARG:HH21	3:C:38:ILE:HD12	1.81	0.46
1:A:85:ASP:OD1	1:A:85:ASP:N	2.45	0.46
1:A:344:ARG:HA	2:B:1129:ARG:HA	1.96	0.46
1:A:452:LYS:HE2	2:B:1141:HIS:CD2	2.48	0.46
1:A:770:VAL:HG21	1:A:818:MET:HE2	1.96	0.46
2:B:586:TRP:NE1	2:B:588:GLY:O	2.47	0.46
2:B:867:GLY:O	2:B:868:MET:HG2	2.16	0.46
2:B:1124:ARG:HH12	11:R:2:U:P	2.39	0.46
3:C:35:ARG:NH1	9:K:39:ASP:OD2	2.49	0.46
4:E:123:LEU:HD23	4:E:123:LEU:N	2.23	0.46
7:I:116:ASN:OD1	7:I:118:ARG:NH2	2.48	0.46
1:A:82:GLY:H	1:A:241:VAL:HG22	1.80	0.46
1:A:113:LEU:HD21	1:A:218:ASP:HB2	1.98	0.46
1:A:814:PHE:O	1:A:818:MET:HG3	2.15	0.46
1:A:836:TYR:CZ	1:A:840:ARG:HD2	2.51	0.46
1:A:1054:LEU:HD13	5:F:84:TYR:CZ	2.50	0.46
3:C:4:GLU:N	3:C:4:GLU:OE1	2.49	0.46
4:E:178:ILE:HB	4:E:212:ARG:HG2	1.98	0.46
6:H:40:LEU:HB3	6:H:123:MET:HG3	1.97	0.46
6:H:80:ARG:HD3	9:K:57:LEU:HD22	1.97	0.46
7:I:34:TYR:CE2	7:I:36:GLU:HB2	2.49	0.46
8:J:57:ILE:O	8:J:61:LEU:HG	2.16	0.46
1:A:131:SER:HB2	1:A:223:GLY:HA2	1.97	0.45
2:B:23:ALA:HB3	2:B:655:LYS:HB3	1.98	0.45
2:B:728:ARG:NH2	2:B:760:ASP:OD2	2.49	0.45
2:B:979:LYS:HB3	2:B:1097:HIS:HB2	1.98	0.45
6:H:7:ASP:HB2	6:H:58:THR:HG23	1.98	0.45
9:K:21:ILE:HG23	9:K:31:VAL:HG21	1.98	0.45
1:A:463:ILE:CD1	1:A:464:PRO:O	2.55	0.45
2:B:705:MET:H	2:B:710:LEU:HD12	1.81	0.45
1:A:465:TYR:CE1	9:K:4:PRO:HD2	2.52	0.45
1:A:837:ILE:O	1:A:841:LEU:HG	2.16	0.45
1:A:24:PRO:HA	1:A:27:VAL:HG12	1.98	0.45
1:A:28:ARG:NE	1:A:238:CYS:SG	2.78	0.45
1:A:243:PRO:HB2	1:A:245:PRO:HD2	1.97	0.45
1:A:444:PHE:HE2	1:A:470:LEU:HD11	1.82	0.45
1:A:1297:GLU:OE1	1:A:1297:GLU:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:29:ASP:O	2:B:33:VAL:HG23	2.16	0.45
3:C:166:GLU:HB2	9:K:10:PHE:CE2	2.52	0.45
1:A:208:LEU:HD23	1:A:235:ILE:HG21	1.99	0.45
1:A:315:LEU:HB2	1:A:321:PRO:HD2	1.98	0.45
1:A:526:ASP:OD2	2:B:835:GLN:NE2	2.50	0.45
1:A:848:ILE:HA	1:A:857:ARG:O	2.17	0.45
2:B:287:ARG:NE	2:B:324:ILE:O	2.42	0.45
2:B:420:LEU:HD21	2:B:468:GLU:HB3	1.98	0.45
2:B:1166:CYS:HB3	2:B:1168:LEU:HD12	1.98	0.45
4:E:120:ALA:HA	4:E:123:LEU:HD21	1.99	0.45
11:R:5:A:H61	12:T:25:DC:N4	2.09	0.45
1:A:455:MET:HE3	1:A:455:MET:HB3	1.88	0.45
1:A:919:ILE:HD12	1:A:983:ILE:HD13	1.99	0.45
2:B:481:GLN:OE1	11:R:6:G:O2'	2.34	0.45
11:R:1:A:H2'	11:R:2:U:C6	2.51	0.45
1:A:1303:GLU:OE2	1:A:1326:ARG:NH2	2.49	0.45
1:A:1395:GLY:HA3	1:A:1426:GLU:OE2	2.17	0.45
2:B:244:LEU:HD21	2:B:250:PHE:HD1	1.82	0.45
2:B:415:GLN:O	2:B:419:THR:OG1	2.32	0.45
1:A:317:LYS:HD2	12:T:28:DT:H4'	1.99	0.45
1:A:362:ASP:OD2	1:A:362:ASP:N	2.44	0.45
1:A:446:ARG:NH1	1:A:478:TYR:O	2.49	0.45
1:A:508:PRO:O	1:A:511:ILE:HG13	2.16	0.45
2:B:520:GLY:HA3	2:B:635:ARG:HH11	1.82	0.45
2:B:857:ARG:CZ	2:B:942:ARG:HH12	2.30	0.45
2:B:978:ASP:HB2	2:B:980:PHE:HE1	1.81	0.45
9:K:45:LEU:HA	9:K:45:LEU:HD22	1.77	0.45
12:T:6:DG:H2''	12:T:7:DA:C8	2.51	0.45
1:A:271:LYS:HE3	1:A:295:LEU:HD21	1.99	0.45
1:A:517:ASN:OD1	1:A:1364:ASN:ND2	2.49	0.45
1:A:1290:LYS:HA	1:A:1300:LYS:HA	1.98	0.45
2:B:760:ASP:OD1	2:B:760:ASP:N	2.49	0.45
2:B:863:GLU:HB3	2:B:872:GLU:HB2	1.99	0.45
1:A:452:LYS:HE2	1:A:510:GLN:HE22	1.82	0.45
1:A:502:SER:O	1:A:506:ALA:HB2	2.17	0.45
2:B:54:PHE:HZ	2:B:417:PHE:HD1	1.65	0.45
1:A:71:GLN:OE1	2:B:1176:ASN:HB2	2.16	0.44
1:A:446:ARG:NH1	1:A:480:ALA:HB2	2.31	0.44
8:J:24:LEU:HD11	8:J:39:LEU:HD21	1.98	0.44
9:K:30:ALA:HB2	9:K:76:GLN:HB2	1.98	0.44
1:A:339:ASN:O	1:A:343:LYS:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:118:ARG:NH2	2:B:194:GLU:OE2	2.45	0.44
2:B:247:GLY:HA2	2:B:418:LYS:NZ	2.32	0.44
2:B:900:ALA:HB3	10:L:61:THR:HB	1.99	0.44
3:C:29:MET:HA	9:K:45:LEU:HD21	1.99	0.44
3:C:88:CYS:HB3	3:C:92:CYS:HB2	1.99	0.44
4:E:81:GLU:HG2	4:E:96:PHE:CE1	2.53	0.44
6:H:57:VAL:HG22	6:H:144:ILE:HG12	1.98	0.44
6:H:80:ARG:NH1	9:K:56:VAL:O	2.51	0.44
3:C:33:LEU:O	3:C:37:MET:HG2	2.16	0.44
3:C:162:GLY:HA3	3:C:170:TRP:CD2	2.52	0.44
10:L:42:ARG:HA	10:L:42:ARG:HD2	1.88	0.44
12:T:27:DA:H4'	12:T:28:DT:OP1	2.17	0.44
1:A:164:ARG:HD2	1:A:165:GLY:N	2.33	0.44
1:A:548:ASN:HD21	9:K:47:ARG:HD2	1.82	0.44
2:B:405:ARG:NH2	2:B:632:ARG:CD	2.80	0.44
2:B:462:ALA:HB1	12:T:26:DG:H4'	1.99	0.44
4:E:109:ILE:HG22	4:E:110:PHE:H	1.82	0.44
13:N:9:DT:H2''	13:N:10:DA:C5	2.51	0.44
1:A:176:LYS:HB3	1:A:181:LEU:HB3	1.98	0.44
1:A:524:VAL:HG22	1:A:525:GLN:HB2	1.99	0.44
1:A:771:GLU:N	1:A:822:GLU:OE1	2.47	0.44
1:A:44:THR:O	1:A:44:THR:OG1	2.34	0.44
1:A:1107:VAL:HG23	1:A:1383:SER:HB3	1.99	0.44
2:B:103:ASN:OD1	2:B:169:ARG:NH1	2.51	0.44
2:B:617:ARG:HA	2:B:624:LEU:HD12	2.00	0.44
3:C:18:VAL:HG12	3:C:20:PHE:HD2	1.83	0.44
3:C:136:ASP:OD1	3:C:140:ASN:N	2.50	0.44
4:E:88:VAL:HG13	4:E:116:ILE:HA	2.00	0.44
1:A:771:GLU:H	1:A:822:GLU:CD	2.21	0.44
2:B:412:LEU:HB3	2:B:466:TRP:CZ3	2.52	0.44
2:B:890:TYR:CZ	2:B:910:VAL:HG21	2.53	0.44
11:R:2:U:H2'	11:R:3:C:H6	1.82	0.44
11:R:6:G:H2'	11:R:7:A:C8	2.52	0.44
2:B:555:ILE:HA	2:B:558:LEU:HD12	1.99	0.44
2:B:969:ARG:HH22	3:C:60:ASP:CG	2.21	0.44
2:B:1001:PHE:CE1	2:B:1073:TYR:HB2	2.53	0.44
3:C:137:LYS:HB3	3:C:137:LYS:HE2	1.69	0.44
5:F:76:LYS:O	5:F:79:ARG:NE	2.43	0.44
1:A:68:GLN:HG2	1:A:69:THR:OG1	2.17	0.44
2:B:766:ARG:HA	2:B:766:ARG:HD3	1.71	0.43
1:A:451:HIS:CD2	1:A:453:MET:HG3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:ILE:HG13	1:A:561:PRO:HD2	2.00	0.43
1:A:1013:ASP:HA	1:A:1016:THR:OG1	2.18	0.43
1:A:1423:GLY:N	1:A:1426:GLU:OE1	2.47	0.43
1:A:1434:ALA:HB3	1:A:1436:ILE:HG22	2.00	0.43
2:B:60:GLN:OE1	2:B:94:LYS:HD3	2.18	0.43
2:B:1150:ARG:HA	2:B:1150:ARG:HD3	1.78	0.43
3:C:115:SER:HB3	3:C:142:VAL:HB	2.00	0.43
6:H:94:ASP:N	6:H:94:ASP:OD1	2.51	0.43
12:T:22:DT:H2'	12:T:23:DC:C6	2.53	0.43
2:B:826:ALA:O	2:B:1011:ILE:HA	2.19	0.43
12:T:1:DC:H2''	12:T:2:DT:H71	2.00	0.43
1:A:453:MET:HE2	1:A:510:GLN:HB3	2.00	0.43
1:A:549:MET:HA	1:A:552:TRP:HD1	1.83	0.43
2:B:426:LYS:HA	2:B:426:LYS:HD3	1.68	0.43
2:B:866:TYR:CD2	2:B:870:ILE:HD11	2.53	0.43
3:C:115:SER:N	3:C:142:VAL:O	2.50	0.43
1:A:763:ALA:O	1:A:803:SER:OG	2.36	0.43
1:A:874:ASP:OD2	1:A:875:ALA:N	2.51	0.43
2:B:188:ASP:O	2:B:192:LEU:HG	2.19	0.43
2:B:830:TYR:CZ	2:B:1000:PRO:HD3	2.53	0.43
2:B:917:PRO:C	2:B:935:ARG:HH22	2.22	0.43
6:H:25:ARG:HA	6:H:41:ASP:HA	2.00	0.43
8:J:45:CYS:O	8:J:48:ARG:HG3	2.18	0.43
12:T:10:DA:H2'	12:T:11:DG:H8	1.83	0.43
1:A:135:PHE:HA	1:A:138:ILE:CG2	2.49	0.43
1:A:573:SER:OG	1:A:575:LYS:HE3	2.18	0.43
1:A:874:ASP:O	1:A:878:ILE:HG13	2.18	0.43
1:A:897:TYR:HA	1:A:1029:ARG:HB3	2.00	0.43
2:B:618:ASP:O	2:B:622:LYS:N	2.51	0.43
2:B:846:ILE:HG12	2:B:974:PRO:HG2	2.01	0.43
2:B:941:LEU:HD13	2:B:942:ARG:N	2.33	0.43
2:B:1192:TYR:CD1	2:B:1218:THR:HG21	2.53	0.43
3:C:241:ASP:OD1	3:C:242:GLN:N	2.49	0.43
4:E:190:LEU:HD23	4:E:190:LEU:HA	1.73	0.43
6:H:56:THR:OG1	6:H:145:ARG:HB3	2.18	0.43
7:I:42:LEU:HD12	7:I:43:VAL:H	1.83	0.43
1:A:31:SER:HB2	1:A:83:HIS:HB3	2.00	0.43
1:A:848:ILE:HB	1:A:1065:GLY:HA3	2.01	0.43
2:B:35:SER:HA	2:B:811:TYR:HE2	1.82	0.43
2:B:367:LEU:HD13	2:B:370:PHE:H	1.84	0.43
2:B:842:ASN:HD21	2:B:996:ARG:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:82:TYR:HB2	3:C:85:ASP:HB2	2.01	0.43
6:H:80:ARG:CZ	6:H:81:PRO:HG2	2.48	0.43
1:A:7:SER:HA	2:B:1175:LEU:HD22	1.99	0.43
1:A:38:PRO:HA	1:A:53:LEU:HD22	1.99	0.43
1:A:271:LYS:HE2	1:A:271:LYS:HB3	1.81	0.43
1:A:1267:MET:O	1:A:1271:ILE:CG2	2.64	0.43
2:B:46:GLN:OE1	2:B:544:CYS:HA	2.19	0.43
2:B:69:LEU:HD12	2:B:69:LEU:HA	1.82	0.43
2:B:299:GLU:HG3	2:B:572:HIS:NE2	2.34	0.43
2:B:345:LYS:O	2:B:348:ARG:NH1	2.52	0.43
2:B:546:SER:HB3	2:B:632:ARG:HB2	2.00	0.43
2:B:547:VAL:HG12	2:B:612:GLU:CD	2.39	0.43
2:B:816:GLU:O	8:J:56:LEU:HD21	2.18	0.43
2:B:1106:ARG:CZ	2:B:1118:PRO:HB3	2.48	0.43
3:C:67:LEU:O	3:C:70:ILE:HG12	2.19	0.43
1:A:129:LYS:HA	1:A:134:ARG:HH12	1.84	0.43
1:A:767:GLN:OE1	1:A:768:GLN:N	2.52	0.43
2:B:195:CYS:SG	2:B:782:LEU:HD22	2.59	0.43
2:B:604:ARG:HG3	2:B:611:PRO:HA	2.01	0.43
2:B:824:ILE:HD11	8:J:44:TYR:HE1	1.83	0.43
2:B:1069:PHE:O	2:B:1070:GLU:HG3	2.18	0.43
2:B:1175:LEU:HD12	2:B:1176:ASN:N	2.33	0.43
3:C:184:ASN:OD1	3:C:188:HIS:N	2.52	0.43
7:I:30:ARG:HA	7:I:30:ARG:NH2	2.34	0.43
1:A:751:SER:HB2	2:B:1015:HIS:CD2	2.54	0.43
1:A:861:GLY:O	4:E:174:GLN:HG3	2.19	0.43
2:B:364:ILE:O	2:B:365:THR:HG23	2.19	0.43
2:B:515:HIS:CE1	2:B:517:THR:HG23	2.54	0.43
2:B:805:THR:O	2:B:1044:ALA:N	2.52	0.43
3:C:172:PRO:O	3:C:235:VAL:CG1	2.62	0.43
7:I:101:PHE:HE1	7:I:112:SER:HB3	1.83	0.43
1:A:119:ASN:OD1	1:A:121:LEU:HB2	2.19	0.42
1:A:531:ILE:HG12	1:A:653:VAL:HG11	2.00	0.42
2:B:401:PHE:HB2	2:B:517:THR:OG1	2.19	0.42
2:B:408:LEU:HD21	2:B:545:ILE:HG13	2.01	0.42
4:E:152:LYS:H	4:E:152:LYS:HG2	1.58	0.42
1:A:62:ASP:HB3	1:A:66:LYS:HE2	2.00	0.42
1:A:336:ILE:HD13	1:A:336:ILE:HA	1.85	0.42
1:A:508:PRO:HG3	1:A:643:ALA:HB2	2.01	0.42
2:B:845:SER:HA	2:B:848:ARG:HB2	2.01	0.42
1:A:504:LEU:HD13	5:F:91:ALA:HB1	1.96	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:810:PRO:HG3	2:B:745:PRO:HB3	2.01	0.42
1:A:909:ASP:HB3	1:A:912:LEU:HG	2.01	0.42
2:B:815:ARG:H	2:B:815:ARG:HG2	1.59	0.42
4:E:151:PRO:HD2	4:E:153:HIS:CE1	2.47	0.42
1:A:416:ARG:HG3	1:A:417:TYR:CD2	2.55	0.42
1:A:564:ALA:N	1:A:576:GLN:HE22	2.18	0.42
2:B:318:VAL:O	2:B:322:PHE:N	2.52	0.42
4:E:136:ASN:OD1	4:E:137:GLU:N	2.52	0.42
6:H:115:TYR:HE2	6:H:124:ARG:HE	1.68	0.42
1:A:483:ASP:HB2	2:B:987:LYS:O	2.19	0.42
1:A:551:TYR:HD1	9:K:74:ARG:HD3	1.84	0.42
1:A:662:PHE:HB3	2:B:829:CYS:SG	2.60	0.42
1:A:666:ILE:HD11	2:B:1027:ILE:HG12	2.01	0.42
1:A:666:ILE:HG21	2:B:1030:LEU:HD22	2.00	0.42
1:A:848:ILE:HD13	1:A:1370:LEU:HD11	2.01	0.42
1:A:981:LEU:HD13	1:A:986:ILE:HG13	2.01	0.42
1:A:1287:TYR:CG	1:A:1305:VAL:HG21	2.54	0.42
2:B:609:ILE:HD12	2:B:609:ILE:HA	1.75	0.42
2:B:757:PRO:CD	2:B:983:ARG:HG2	2.49	0.42
7:I:7:CYS:SG	7:I:9:ASP:N	2.93	0.42
1:A:332:LYS:HD2	1:A:332:LYS:HA	1.68	0.42
1:A:481:ASP:HB3	2:B:836:GLU:O	2.20	0.42
1:A:754:SER:N	1:A:757:ASN:OD1	2.42	0.42
1:A:963:ILE:O	1:A:967:ALA:N	2.53	0.42
1:A:1156:PRO:HA	1:A:1190:PRO:HB3	2.01	0.42
1:A:1323:ASP:OD1	1:A:1325:THR:HG22	2.19	0.42
2:B:409:ALA:O	2:B:413:LEU:HG	2.19	0.42
2:B:579:ARG:HB2	2:B:586:TRP:NE1	2.35	0.42
2:B:798:TYR:O	2:B:821:GLN:NE2	2.52	0.42
3:C:91:HIS:CD2	3:C:158:VAL:HG11	2.55	0.42
4:E:171:LYS:HD3	4:E:173:SER:H	1.85	0.42
5:F:87:LYS:HE3	5:F:88:TYR:CE2	2.54	0.42
6:H:63:LEU:HD12	6:H:90:ALA:HB2	2.02	0.42
1:A:136:ALA:O	1:A:140:THR:OG1	2.24	0.42
1:A:800:VAL:HA	1:A:812:GLU:OE2	2.19	0.42
2:B:580:VAL:HA	2:B:624:LEU:HB3	2.01	0.42
3:C:45:ALA:HB3	3:C:170:TRP:CD1	2.54	0.42
6:H:9:ILE:HA	6:H:56:THR:HA	2.01	0.42
6:H:87:ARG:HA	6:H:87:ARG:NE	2.35	0.42
2:B:175:ARG:HD3	2:B:175:ARG:HA	1.86	0.42
2:B:914:LYS:HG3	2:B:937:ALA:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:10:PHE:CD2	6:H:38:LEU:HD23	2.55	0.42
1:A:977:LYS:HB3	1:A:977:LYS:HE2	1.76	0.42
1:A:1430:LEU:HB3	1:A:1432:GLN:HG3	2.02	0.42
2:B:370:PHE:HZ	2:B:567:GLU:HB3	1.84	0.42
3:C:13:ALA:HA	3:C:18:VAL:HA	2.02	0.42
3:C:252:GLN:HG3	9:K:98:LEU:HD12	2.01	0.42
1:A:500:GLU:OE2	1:A:1438:THR:HG21	2.20	0.42
2:B:25:ILE:HG13	2:B:651:LEU:HD13	2.01	0.42
2:B:485:ARG:NE	2:B:788:ARG:HH22	2.18	0.42
2:B:992:ILE:HD12	2:B:992:ILE:HA	1.96	0.42
2:B:1029:CYS:HA	2:B:1089:PRO:O	2.19	0.42
2:B:1138:MET:HG2	2:B:1146:PHE:HE2	1.85	0.42
4:E:15:ALA:O	4:E:18:THR:HB	2.20	0.42
8:J:41:LEU:HD22	8:J:46:CYS:SG	2.60	0.42
1:A:17:VAL:HG12	1:A:1421:CYS:SG	2.60	0.41
1:A:120:GLU:HA	1:A:123:ARG:HB3	2.02	0.41
1:A:367:PRO:HA	1:A:463:ILE:HD12	2.02	0.41
1:A:897:TYR:HB3	1:A:1027:ALA:HB1	2.01	0.41
2:B:778:MET:HE1	2:B:853:SER:HB3	2.02	0.41
2:B:874:PHE:HD2	2:B:914:LYS:HB3	1.85	0.41
4:E:88:VAL:HG23	4:E:92:THR:OG1	2.20	0.41
7:I:17:ARG:O	7:I:25:LEU:HD12	2.20	0.41
7:I:28:GLU:HB3	7:I:35:VAL:HG22	2.02	0.41
8:J:55:ASP:OD2	8:J:57:ILE:HG22	2.19	0.41
12:T:6:DG:C6	12:T:7:DA:C6	3.08	0.41
1:A:81:PHE:HE1	2:B:1205:GLN:HG2	1.85	0.41
1:A:82:GLY:N	1:A:241:VAL:HG22	2.35	0.41
1:A:442:VAL:HG21	1:A:489:LEU:HD11	2.03	0.41
1:A:586:ILE:HG22	1:A:607:ILE:HG21	2.02	0.41
1:A:757:ASN:ND2	2:B:1018:PRO:O	2.52	0.41
1:A:780:VAL:HG22	2:B:699:GLU:OE2	2.20	0.41
1:A:904:THR:O	1:A:907:THR:HG22	2.20	0.41
1:A:913:LEU:HD12	1:A:913:LEU:HA	1.93	0.41
2:B:121:ASN:HB2	2:B:963:PHE:CZ	2.55	0.41
2:B:1008:PRO:HB3	2:B:1087:PHE:CE1	2.55	0.41
2:B:1163:CYS:HB3	2:B:1166:CYS:HB2	2.01	0.41
12:T:2:DT:H3	13:N:16:DA:N6	2.16	0.41
1:A:35:ILE:HG21	1:A:241:VAL:HG11	2.02	0.41
1:A:333:GLU:HG2	1:A:334:GLY:H	1.84	0.41
1:A:785:PRO:O	2:B:702:LEU:HD12	2.20	0.41
1:A:871:ASP:HB2	4:E:204:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:913:LEU:HD11	1:A:981:LEU:O	2.20	0.41
2:B:918:ILE:HB	2:B:935:ARG:CZ	2.50	0.41
8:J:28:ASP:N	8:J:28:ASP:OD1	2.52	0.41
9:K:50:LEU:HD22	9:K:59:ALA:HB2	2.01	0.41
12:T:6:DG:H2''	12:T:7:DA:H8	1.85	0.41
1:A:63:ARG:NE	1:A:63:ARG:O	2.53	0.41
1:A:218:ASP:OD1	1:A:219:PHE:N	2.53	0.41
1:A:278:THR:HA	1:A:281:HIS:HD1	1.84	0.41
1:A:350:ARG:HH22	12:T:21:DC:H1'	1.84	0.41
1:A:690:VAL:HG11	1:A:794:PRO:HD3	2.02	0.41
1:A:1017:LEU:HB2	4:E:205:SER:C	2.40	0.41
1:A:1134:ILE:O	1:A:1138:ILE:HG12	2.20	0.41
2:B:1070:GLU:OE2	8:J:44:TYR:OH	2.37	0.41
3:C:117:ASP:OD1	3:C:117:ASP:N	2.52	0.41
4:E:178:ILE:N	4:E:213:ILE:O	2.51	0.41
5:F:118:LEU:O	5:F:122:MET:HG3	2.20	0.41
1:A:91:PHE:HE2	1:A:180:LYS:HA	1.86	0.41
1:A:457:ALA:O	1:A:507:VAL:HG23	2.21	0.41
1:A:868:TYR:CE1	1:A:1366:ARG:HG2	2.55	0.41
1:A:929:LEU:HD21	1:A:983:ILE:HG21	2.01	0.41
2:B:255:GLN:O	2:B:272:THR:HG22	2.21	0.41
2:B:726:ALA:HB1	2:B:1051:THR:HB	2.01	0.41
6:H:95:TYR:CE2	6:H:97:MET:HG3	2.56	0.41
11:R:5:A:N6	12:T:25:DC:H42	2.11	0.41
1:A:315:LEU:HD22	1:A:321:PRO:HG2	2.02	0.41
2:B:470:LYS:HA	2:B:470:LYS:HD3	1.87	0.41
2:B:898:LEU:HD12	2:B:952:VAL:HG11	2.02	0.41
2:B:1129:ARG:HB3	12:T:20:DC:H5'	2.02	0.41
5:F:72:LYS:NZ	5:F:73:ALA:O	2.54	0.41
1:A:75:ASN:OD1	2:B:1116:ARG:NH1	2.49	0.41
1:A:226:GLU:O	1:A:230:ARG:NH1	2.46	0.41
1:A:449:SER:HB2	2:B:1133:MET:HB3	2.02	0.41
1:A:320:ARG:N	1:A:320:ARG:HD3	2.36	0.41
1:A:335:ARG:HA	1:A:335:ARG:HD3	1.67	0.41
1:A:384:ASN:O	1:A:388:LEU:HG	2.21	0.41
1:A:451:HIS:HA	1:A:1070:GLN:HB3	2.03	0.41
3:C:11:ARG:NH1	3:C:209:TYR:OH	2.53	0.41
12:T:23:DC:H2''	12:T:24:DT:H5'	2.02	0.41
1:A:420:ARG:O	1:A:424:ILE:HG23	2.20	0.41
1:A:630:ILE:HD12	1:A:630:ILE:H	1.86	0.41
1:A:760:GLN:HG2	1:A:765:VAL:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:809:THR:OG1	1:A:812:GLU:HG3	2.21	0.41
1:A:1066:VAL:O	1:A:1070:GLN:HG3	2.20	0.41
1:A:1271:ILE:C	1:A:1271:ILE:CD1	2.89	0.41
2:B:345:LYS:HB2	2:B:348:ARG:NH1	2.34	0.41
2:B:371:GLU:OE2	2:B:371:GLU:N	2.52	0.41
2:B:711:GLU:N	2:B:712:PRO:HD3	2.35	0.41
2:B:863:GLU:OE2	2:B:864:LYS:NZ	2.47	0.41
3:C:3:GLU:OE2	3:C:3:GLU:N	2.54	0.41
4:E:168:TYR:HB3	4:E:170:LEU:HG	2.01	0.41
6:H:47:PHE:CE1	6:H:95:TYR:HB2	2.55	0.41
8:J:44:TYR:HA	8:J:47:ARG:CB	2.49	0.41
11:R:3:C:H2'	11:R:4:G:C8	2.55	0.41
12:T:8:DT:H2'	12:T:9:DA:C8	2.55	0.41
2:B:601:ARG:HE	2:B:601:ARG:HB2	1.58	0.41
2:B:1122:ARG:HB3	12:T:22:DT:OP2	2.21	0.41
4:E:191:LYS:HD2	4:E:191:LYS:HA	1.98	0.41
6:H:78:SER:OG	6:H:79:TRP:N	2.54	0.41
7:I:50:THR:HG22	7:I:52:ILE:H	1.85	0.41
8:J:3:VAL:HG21	8:J:18:TRP:CG	2.55	0.41
1:A:105:CYS:O	1:A:114:LEU:N	2.55	0.40
1:A:549:MET:HA	1:A:552:TRP:CD1	2.57	0.40
1:A:590:ARG:NE	1:A:621:THR:HG22	2.31	0.40
2:B:310:MET:O	2:B:314:LEU:HD12	2.21	0.40
2:B:405:ARG:NH2	2:B:632:ARG:HD3	2.36	0.40
2:B:416:LEU:HD22	2:B:466:TRP:NE1	2.32	0.40
8:J:44:TYR:O	8:J:48:ARG:N	2.52	0.40
1:A:507:VAL:HG13	1:A:521:MET:HE3	2.02	0.40
1:A:899:VAL:HG23	1:A:929:LEU:HB3	2.02	0.40
1:A:956:LEU:HD21	1:A:1017:LEU:HD12	2.03	0.40
2:B:173:MET:HB3	2:B:203:PHE:CZ	2.56	0.40
4:E:55:ARG:HD2	4:E:84:ASP:HA	2.02	0.40
6:H:93:TYR:CD2	6:H:145:ARG:HB2	2.56	0.40
8:J:12:LYS:HD2	8:J:46:CYS:SG	2.61	0.40
12:T:4:DC:H1'	12:T:5:DC:H5'	2.03	0.40
2:B:205:ILE:HD13	2:B:205:ILE:HA	1.92	0.40
2:B:412:LEU:HD22	2:B:466:TRP:HZ3	1.86	0.40
2:B:540:SER:O	2:B:543:SER:OG	2.40	0.40
2:B:852:ARG:HD3	2:B:973:ILE:HG22	2.02	0.40
2:B:893:LEU:HD23	2:B:893:LEU:HA	1.76	0.40
4:E:12:LEU:O	4:E:15:ALA:HB3	2.21	0.40
5:F:132:LEU:HD23	5:F:132:LEU:HA	1.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:49:LYS:H	10:L:49:LYS:HG2	1.58	0.40
1:A:260:ASP:OD1	1:A:263:THR:N	2.52	0.40
1:A:577:ILE:O	1:A:580:VAL:HG22	2.22	0.40
1:A:846:GLU:CD	1:A:1425:SER:HG	2.25	0.40
1:A:1116:LEU:HD23	1:A:1116:LEU:HA	1.86	0.40
2:B:791:THR:HA	2:B:858:SER:HB2	2.03	0.40
5:F:85:MET:N	5:F:152:ILE:O	2.37	0.40
8:J:10:CYS:SG	8:J:46:CYS:HB2	2.62	0.40
12:T:23:DC:H2'	12:T:24:DT:C6	2.56	0.40
1:A:78:PRO:O	2:B:1205:GLN:NE2	2.50	0.40
1:A:97:ALA:O	1:A:101:LYS:HD3	2.21	0.40
1:A:546:VAL:HG21	1:A:572:TRP:CE3	2.56	0.40
1:A:765:VAL:CG2	1:A:800:VAL:HB	2.51	0.40
1:A:935:GLN:HA	1:A:938:LYS:HB3	2.04	0.40
2:B:29:ASP:OD2	2:B:658:ILE:HG21	2.21	0.40
2:B:884:ARG:HB2	2:B:936:ASP:H	1.86	0.40
3:C:58:LEU:HB2	3:C:63:ILE:HD11	2.04	0.40
7:I:16:PRO:HB3	7:I:27:PHE:HE2	1.85	0.40
8:J:43:ARG:H	8:J:43:ARG:HG2	1.66	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)
13:N:17:DG:C6	13:N:17:DG:O6[2_856]	1.25	0.95

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	1378/1733 (80%)	1285 (93%)	93 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	1088/1224 (89%)	1021 (94%)	67 (6%)	0	100	100
3	C	264/318 (83%)	242 (92%)	22 (8%)	0	100	100
4	E	212/215 (99%)	206 (97%)	6 (3%)	0	100	100
5	F	82/155 (53%)	80 (98%)	2 (2%)	0	100	100
6	H	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
7	I	117/122 (96%)	111 (95%)	6 (5%)	0	100	100
8	J	63/70 (90%)	62 (98%)	1 (2%)	0	100	100
9	K	112/120 (93%)	108 (96%)	4 (4%)	0	100	100
10	L	44/70 (63%)	43 (98%)	1 (2%)	0	100	100
All	All	3489/4173 (84%)	3279 (94%)	210 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	1210/1520 (80%)	1123 (93%)	87 (7%)	14	44
2	B	960/1061 (90%)	898 (94%)	62 (6%)	17	46
3	C	233/274 (85%)	225 (97%)	8 (3%)	37	62
4	E	195/197 (99%)	180 (92%)	15 (8%)	13	42
5	F	74/137 (54%)	70 (95%)	4 (5%)	22	52
6	H	117/128 (91%)	105 (90%)	12 (10%)	7	30
7	I	113/116 (97%)	106 (94%)	7 (6%)	18	48
8	J	60/65 (92%)	54 (90%)	6 (10%)	7	30
9	K	99/102 (97%)	97 (98%)	2 (2%)	55	74
10	L	39/57 (68%)	33 (85%)	6 (15%)	2	17
All	All	3100/3657 (85%)	2891 (93%)	209 (7%)	16	46

All (209) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LYS
1	A	22	PHE
1	A	23	SER
1	A	34	LYS
1	A	36	ARG
1	A	42	ASP
1	A	43	GLU
1	A	60	SER
1	A	63	ARG
1	A	67	CYS
1	A	68	GLN
1	A	70	CYS
1	A	88	LYS
1	A	100	LYS
1	A	107	CYS
1	A	117	GLU
1	A	119	ASN
1	A	131	SER
1	A	133	LYS
1	A	134	ARG
1	A	141	LEU
1	A	143	LYS
1	A	145	LYS
1	A	176	LYS
1	A	219	PHE
1	A	257	ARG
1	A	264	PHE
1	A	268	ASP
1	A	270	LEU
1	A	271	LYS
1	A	280	GLU
1	A	282	ASN
1	A	287	HIS
1	A	313	GLN
1	A	316	GLN
1	A	323	LYS
1	A	333	GLU
1	A	337	ARG
1	A	411	ASP
1	A	416	ARG
1	A	417	TYR
1	A	444	PHE

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Mol	Chain	Res	Type
1	A	446	ARG
1	A	451	HIS
1	A	452	LYS
1	A	468	PHE
1	A	520	CYS
1	A	537	ARG
1	A	538	ASP
1	A	575	LYS
1	A	589	GLN
1	A	603	ASN
1	A	614	PHE
1	A	635	ARG
1	A	646	PHE
1	A	659	HIS
1	A	720	ARG
1	A	746	MET
1	A	764	CYS
1	A	768	GLN
1	A	781	ASP
1	A	806	ARG
1	A	852	TYR
1	A	897	TYR
1	A	898	ARG
1	A	1035	TYR
1	A	1110	ASN
1	A	1132	LYS
1	A	1155	ASP
1	A	1173	HIS
1	A	1188	GLN
1	A	1189	SER
1	A	1205	LYS
1	A	1231	ASP
1	A	1234	GLU
1	A	1264	GLU
1	A	1274	ARG
1	A	1281	ARG
1	A	1285	MET
1	A	1286	LYS
1	A	1289	ARG
1	A	1293	SER
1	A	1330	ASN
1	A	1386	ARG

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Mol	Chain	Res	Type
1	A	1402	PHE
1	A	1407	GLU
1	A	1442	ASP
2	B	50	SER
2	B	64	CYS
2	B	110	HIS
2	B	133	LYS
2	B	183	GLU
2	B	195	CYS
2	B	199	MET
2	B	245	GLU
2	B	249	ARG
2	B	286	PHE
2	B	298	LEU
2	B	322	PHE
2	B	367	LEU
2	B	370	PHE
2	B	400	HIS
2	B	401	PHE
2	B	405	ARG
2	B	417	PHE
2	B	422	LYS
2	B	451	LYS
2	B	459	TYR
2	B	466	TRP
2	B	468	GLU
2	B	471	LYS
2	B	473	MET
2	B	489	SER
2	B	490	SER
2	B	533	CYS
2	B	560	GLU
2	B	579	ARG
2	B	618	ASP
2	B	666	TYR
2	B	678	GLU
2	B	679	TYR
2	B	709	ASP
2	B	728	ARG
2	B	730	ARG
2	B	738	PHE
2	B	797	TYR

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Mol	Chain	Res	Type
2	B	829	CYS
2	B	857	ARG
2	B	886	LYS
2	B	895	ASP
2	B	935	ARG
2	B	969	ARG
2	B	983	ARG
2	B	984	HIS
2	B	987	LYS
2	B	994	TYR
2	B	1020	ARG
2	B	1025	HIS
2	B	1065	GLN
2	B	1086	PHE
2	B	1106	ARG
2	B	1122	ARG
2	B	1130	PHE
2	B	1148	LYS
2	B	1155	SER
2	B	1179	GLN
2	B	1190	ASP
2	B	1210	MET
2	B	1222	ARG
3	C	62	PHE
3	C	149	LYS
3	C	157	CYS
3	C	178	PHE
3	C	193	TYR
3	C	215	GLU
3	C	217	ASP
3	C	221	TYR
4	E	2	ASP
4	E	4	GLU
4	E	17	ARG
4	E	32	GLN
4	E	43	LYS
4	E	47	CYS
4	E	50	MET
4	E	93	MET
4	E	96	PHE
4	E	103	LYS
4	E	110	PHE

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Mol	Chain	Res	Type
4	E	123	LEU
4	E	174	GLN
4	E	180	ARG
4	E	205	SER
5	F	79	ARG
5	F	135	ARG
5	F	137	TYR
5	F	147	SER
6	H	6	PHE
6	H	21	ASN
6	H	41	ASP
6	H	62	SER
6	H	83	GLN
6	H	86	ASP
6	H	94	ASP
6	H	129	TYR
6	H	134	ASN
6	H	135	LEU
6	H	139	ASN
6	H	146	ARG
7	I	7	CYS
7	I	8	ARG
7	I	10	CYS
7	I	19	ASP
7	I	24	ARG
7	I	28	GLU
7	I	81	ARG
8	J	27	GLU
8	J	28	ASP
8	J	45	CYS
8	J	47	ARG
8	J	48	ARG
8	J	53	HIS
9	K	67	PHE
9	K	81	TYR
10	L	27	LEU
10	L	37	LYS
10	L	49	LYS
10	L	50	ASP
10	L	54	ARG
10	L	67	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	GLN
1	A	171	GLN
1	A	311	GLN
1	A	1312	ASN
2	B	110	HIS
2	B	395	GLN
2	B	835	GLN
2	B	984	HIS
2	B	1025	HIS
2	B	1177	HIS
3	C	167	HIS
3	C	231	ASN
4	E	153	HIS
6	H	11	GLN
6	H	52	GLN
6	H	128	ASN
7	I	22	ASN
9	K	112	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	R	9/10 (90%)	2 (22%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	R	5	A
11	R	10	A

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is 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
12	WC7	T	18	12	16,23,24	1.39	3 (18%)	17,33,36	1.39	3 (17%)

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
12	WC7	T	18	12	-	3/7/21/22	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	T	18	WC7	C5-S1	-3.19	1.59	1.66
12	T	18	WC7	C1-C2	3.00	1.40	1.33
12	T	18	WC7	C3-C2	-2.44	1.39	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	T	18	WC7	C6-C3-C4	3.67	113.60	107.10
12	T	18	WC7	C2-C1-N1	2.40	124.41	121.25
12	T	18	WC7	C3'-C2'-C1'	2.02	107.60	102.54

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	T	18	WC7	C3'-C4'-C5'-O5'
12	T	18	WC7	O4'-C4'-C5'-O5'
12	T	18	WC7	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 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
16	WC4	R	11	15,11	23,26,27	7.11	18 (78%)	33,37,40	1.53	4 (12%)

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
16	WC4	R	11	15,11	-	9/9/27/28	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	R	11	WC4	C16-C05	-16.02	1.35	1.54
16	R	11	WC4	O06-C05	14.76	1.66	1.44
16	R	11	WC4	C25-C03	11.16	1.56	1.36
16	R	11	WC4	C18-C04	10.46	1.54	1.36
16	R	11	WC4	C23-C24	8.24	1.55	1.36
16	R	11	WC4	C03-C04	7.11	1.53	1.39
16	R	11	WC4	C22-C21	6.92	1.52	1.36
16	R	11	WC4	C21-C20	6.71	1.58	1.41
16	R	11	WC4	C18-C19	6.55	1.56	1.42
16	R	11	WC4	C23-C22	6.50	1.55	1.38
16	R	11	WC4	O06-C07	-5.63	1.32	1.45
16	R	11	WC4	C24-C19	5.53	1.55	1.41
16	R	11	WC4	C25-C20	5.02	1.53	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	R	11	WC4	C20-C19	4.39	1.52	1.42
16	R	11	WC4	O15-C14	-4.12	1.33	1.43
16	R	11	WC4	O02-C03	4.11	1.43	1.37
16	R	11	WC4	C14-C07	3.12	1.61	1.53
16	R	11	WC4	O17-C16	2.12	1.48	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	R	11	WC4	C14-C16-C05	4.14	106.70	101.93
16	R	11	WC4	O02-C03-C25	-3.87	120.23	125.24
16	R	11	WC4	O02-C03-C04	3.83	119.49	115.83
16	R	11	WC4	C01-O02-C03	-2.51	113.74	117.53

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	R	11	WC4	C03-C04-C05-C16
16	R	11	WC4	C18-C04-C05-C16
16	R	11	WC4	C14-C07-C08-O5'
16	R	11	WC4	O06-C07-C08-O5'
16	R	11	WC4	C25-C03-O02-C01
16	R	11	WC4	C04-C03-O02-C01
16	R	11	WC4	C18-C04-C05-O06
16	R	11	WC4	C07-C08-O5'-P
16	R	11	WC4	C03-C04-C05-O06

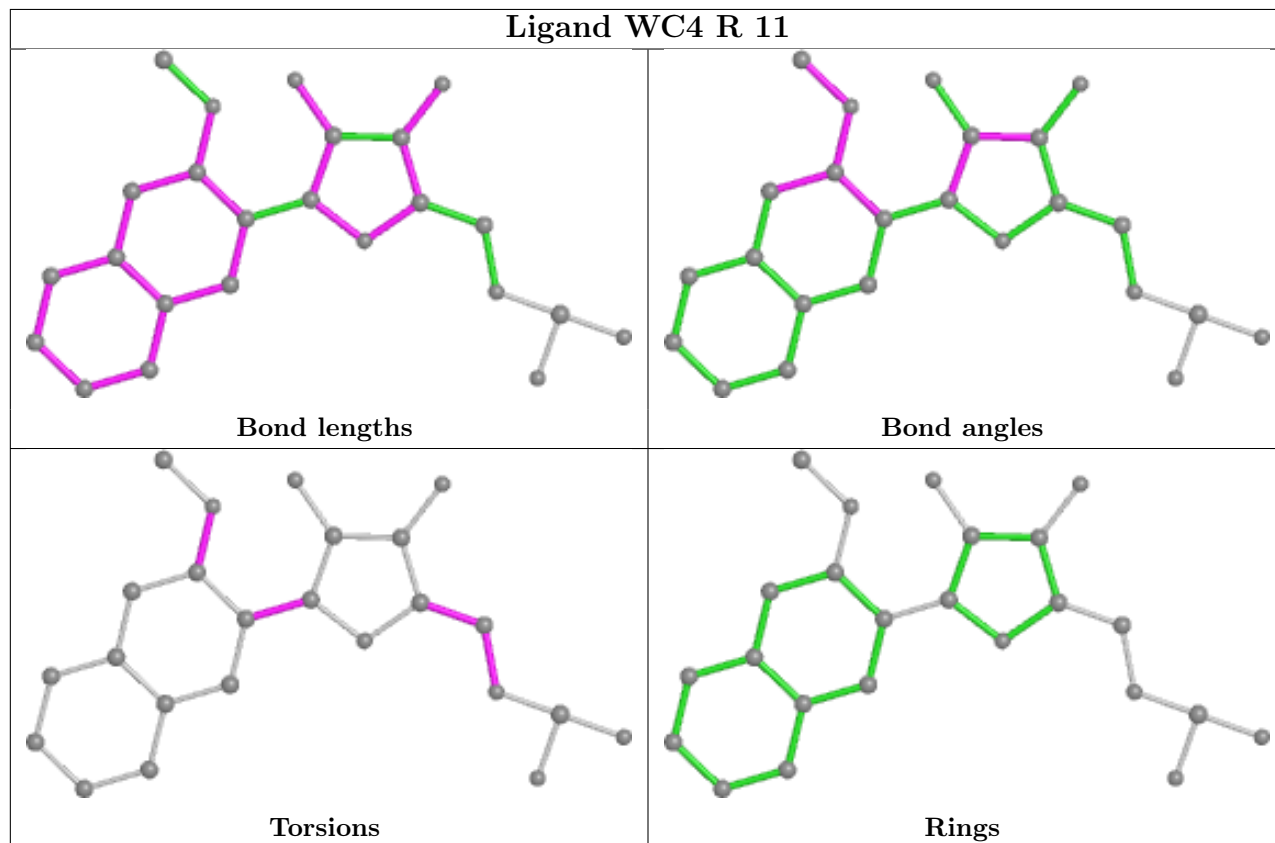
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	R	11	WC4	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](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1390/1733 (80%)	-0.05	24 (1%) 70 60	56, 105, 169, 216	0
2	B	1106/1224 (90%)	-0.04	22 (1%) 65 55	65, 108, 158, 199	0
3	C	266/318 (83%)	-0.17	3 (1%) 80 73	66, 105, 134, 156	0
4	E	214/215 (99%)	-0.03	10 (4%) 31 25	68, 126, 185, 214	0
5	F	84/155 (54%)	-0.25	0 100 100	81, 107, 128, 139	0
6	H	133/146 (91%)	-0.05	2 (1%) 73 64	95, 126, 164, 190	0
7	I	119/122 (97%)	-0.13	0 100 100	83, 117, 144, 172	0
8	J	65/70 (92%)	-0.14	0 100 100	74, 101, 130, 149	0
9	K	114/120 (95%)	-0.17	1 (0%) 84 77	75, 107, 132, 142	0
10	L	46/70 (65%)	0.13	1 (2%) 62 51	90, 143, 170, 183	0
11	R	10/10 (100%)	0.38	0 100 100	101, 121, 165, 172	0
12	T	27/29 (93%)	-0.10	0 100 100	109, 164, 257, 265	0
13	N	15/16 (93%)	-0.09	0 100 100	149, 224, 249, 252	0
All	All	3589/4228 (84%)	-0.07	63 (1%) 68 59	56, 109, 167, 265	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	258	GLY	5.9
4	E	126	SER	5.6
4	E	125	PRO	4.6
4	E	83	CYS	4.5
4	E	123	LEU	4.5
6	H	84	ALA	4.5
10	L	27	LEU	3.7
2	B	132	VAL	3.6
1	A	141	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
9	K	80	GLY	3.4
1	A	199	LEU	3.4
2	B	474	SER	3.4
1	A	1192	LEU	3.3
4	E	91	LYS	3.2
3	C	212	PRO	3.2
4	E	49	SER	3.1
4	E	124	VAL	3.0
2	B	477	ALA	3.0
4	E	90	VAL	2.9
2	B	883	LEU	2.9
2	B	250	PHE	2.9
2	B	257	LYS	2.8
2	B	1221	SER	2.8
2	B	1218	THR	2.8
2	B	465	ASN	2.7
4	E	48	ASP	2.6
2	B	249	ARG	2.6
1	A	116	ASP	2.6
1	A	165	GLY	2.6
1	A	1194	ARG	2.6
2	B	869	SER	2.5
1	A	143	LYS	2.5
1	A	44	THR	2.4
1	A	39	GLU	2.4
1	A	259	GLU	2.4
2	B	25	ILE	2.4
2	B	909	ASP	2.4
2	B	1224	PHE	2.4
1	A	908	LEU	2.4
2	B	643	ASP	2.3
2	B	300	HIS	2.3
1	A	1126	ALA	2.3
1	A	426	LEU	2.3
1	A	425	GLN	2.2
1	A	168	GLY	2.2
2	B	476	ARG	2.2
3	C	211	ASP	2.2
2	B	709	ASP	2.2
3	C	10	ILE	2.2
1	A	660	ASN	2.2
2	B	112	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1166	ASP	2.2
1	A	65	LEU	2.2
1	A	488	ASN	2.2
1	A	388	LEU	2.1
2	B	1222	ARG	2.1
1	A	1108	ALA	2.1
1	A	35	ILE	2.1
2	B	285	ILE	2.0
6	H	24	CYS	2.0
2	B	458	LYS	2.0
1	A	174	ILE	2.0
4	E	84	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
12	WC7	T	18	21/22	0.88	0.21	110,121,135,140	0

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.

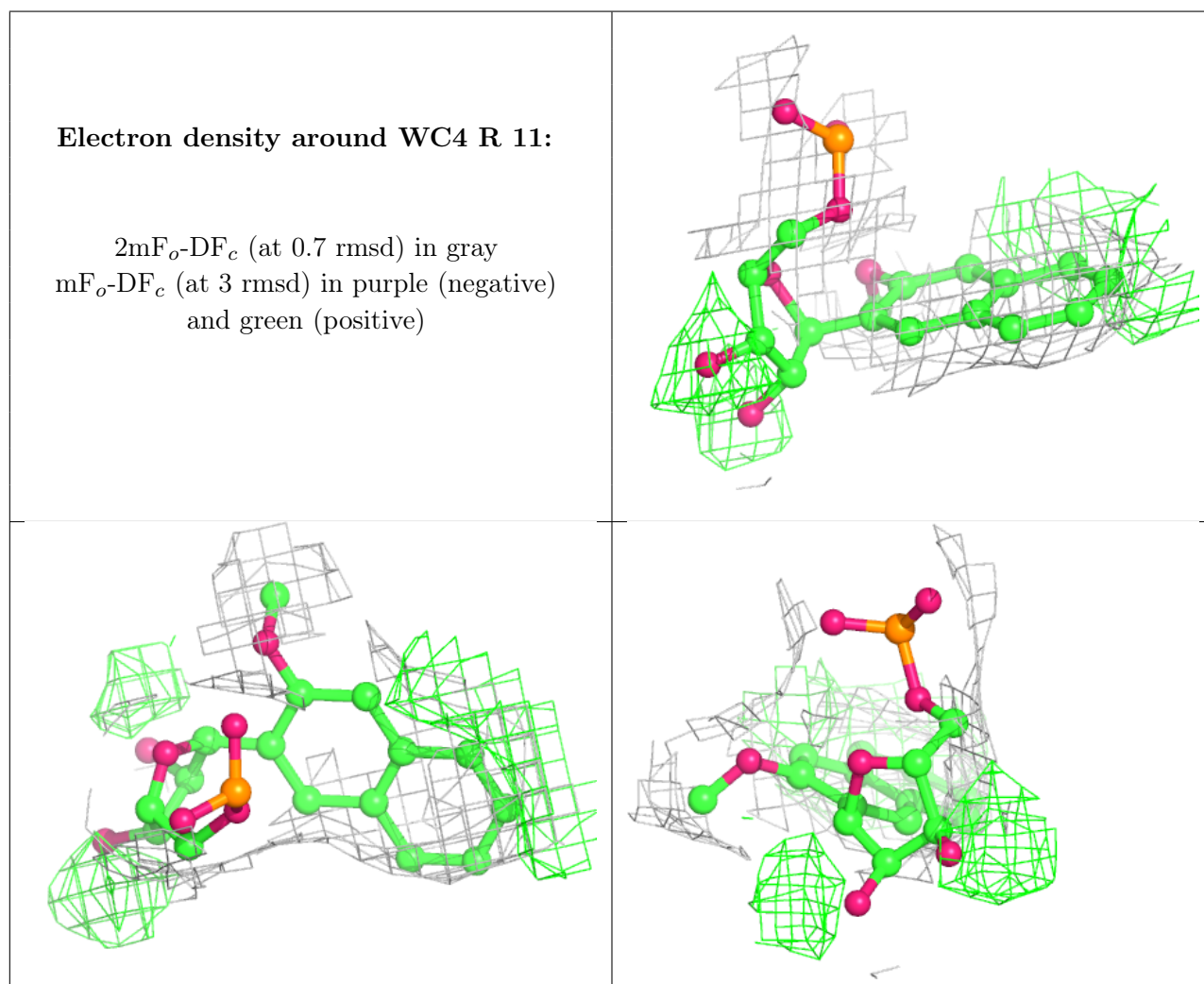
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	ZN	B	1307	1/1	0.79	0.10	179,179,179,179	0
14	ZN	L	105	1/1	0.79	0.08	179,179,179,179	0
16	WC4	R	11	24/25	0.90	0.25	96,109,119,123	0
14	ZN	C	319	1/1	0.92	0.10	91,91,91,91	0
14	ZN	J	101	1/1	0.92	0.21	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
14	ZN	A	1735	1/1	0.93	0.04	134,134,134,134	0
14	ZN	I	204	1/1	0.94	0.08	131,131,131,131	0
14	ZN	I	203	1/1	0.97	0.07	98,98,98,98	0
15	MG	A	2001	1/1	0.98	0.09	88,88,88,88	0
14	ZN	A	1734	1/1	0.98	0.21	206,206,206,206	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.