



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:21 PM UTC

PDB ID : 9N5D / pdb_00009n5d
Title : RNA polymerase II elongation complex with 8-oxoG at +1 site, CMP added
Authors : Oh, J.; Wang, D.
Deposited on : 2025-02-04
Resolution : 3.35 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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

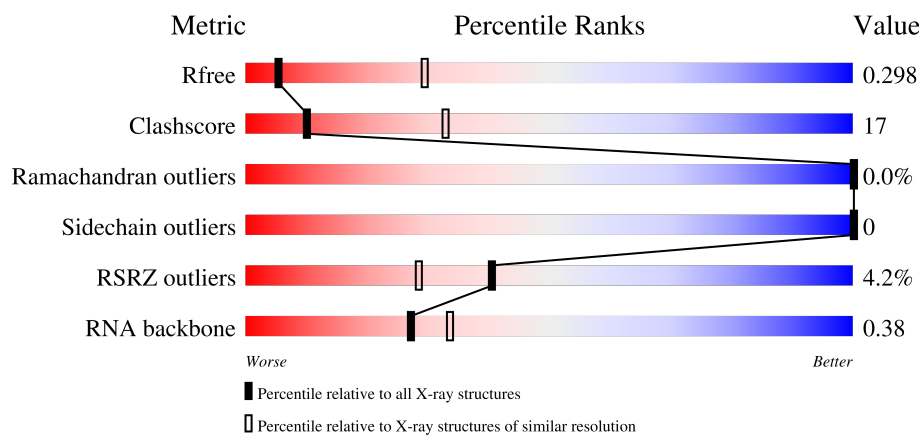
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)
RNA backbone	3983	1110 (3.72-3.00)

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	R	10	10% 90% 10%
2	T	29	31% 59% 10%
3	N	18	11% 72% 17%
4	A	1733	4% 49% 31% 20%

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Mol	Chain	Length	Quality of chain
5	B	1224	
6	C	318	
7	E	215	
8	F	155	
9	H	146	
10	I	122	
11	J	70	
12	K	120	
13	L	70	

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 29066 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 RNA chain called RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	10	Total	C	N	O	P	0	0	0
			219	97	43	69	10			

- Molecule 2 is a DNA chain called Template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	26	Total	C	N	O	P	0	0	0
			521	250	80	165	26			

- Molecule 3 is a DNA chain called Non-template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	15	Total	C	N	O	P	0	0	0
			317	148	71	83	15			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	1385	Total	C	N	O	S	0	0	0
			10831	6833	1895	2043	60			

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1121	Total	C	N	O	S	0	0	0
			8849	5601	1550	1645	53			

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	267	Total	C	N	O	S	0	0	0
			2101	1320	349	419	13			

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	213	Total	C	N	O	S	0	0	0
			1728	1099	301	317	11			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	86	Total	C	N	O	S	0	0	0
			684	437	115	129	3			

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	H	133	Total	C	N	O	S	0	0	0
			1064	670	179	211	4			

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	I	118	Total	C	N	O	S	0	0	0
			946	582	170	184	10			

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB11.

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

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	43	Total	C	N	O	S	0	0	0
			337	208	66	59	4			

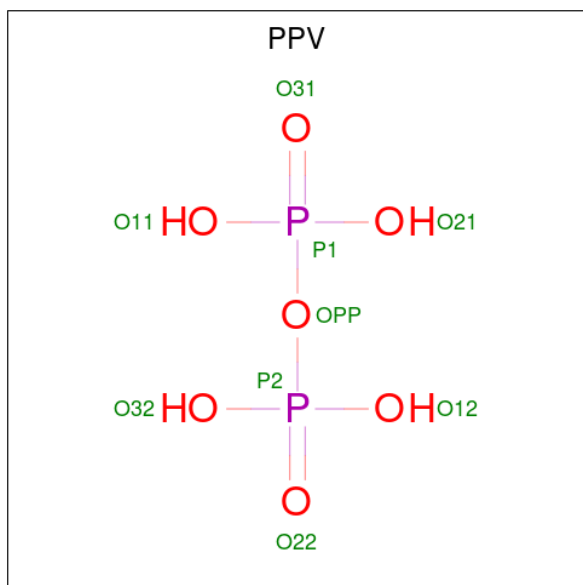
- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn).

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 (CCD ID: MG) (formula: Mg).

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

- Molecule 16 is PYROPHOSPHATE (CCD ID: PPV) (formula: $\text{H}_4\text{O}_7\text{P}_2$) (labeled as "Ligand of Interest" by depositor).

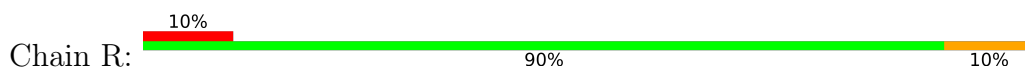


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	A	1	Total	O	P	0	0
			9	7	2		

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.

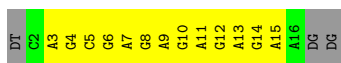
- Molecule 1: RNA



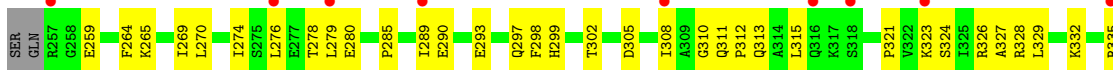
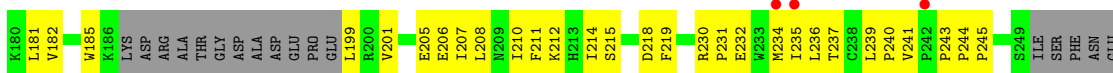
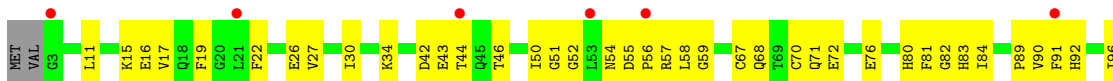
- Molecule 2: Template strand DNA



- Molecule 3: Non-template strand DNA

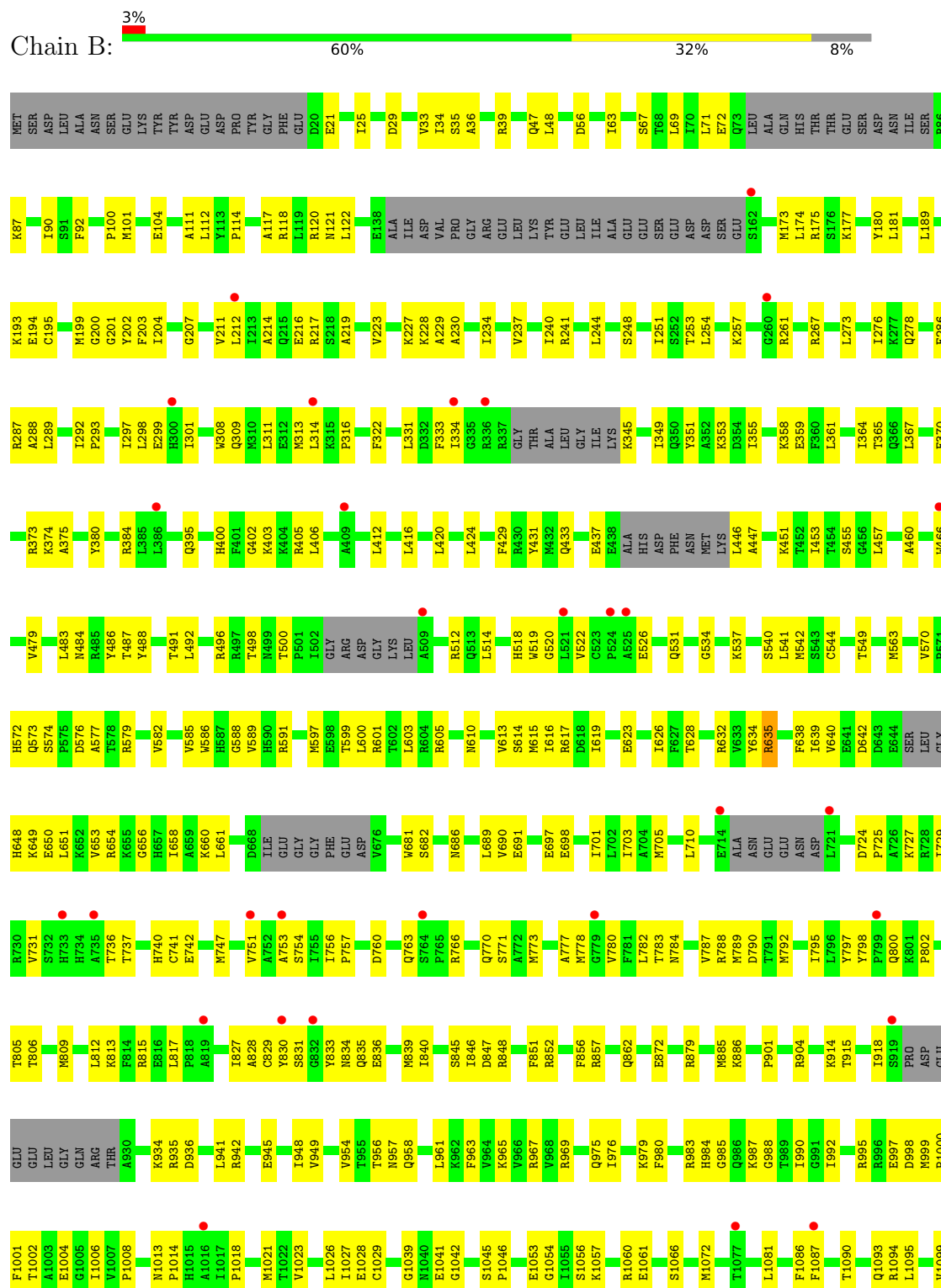


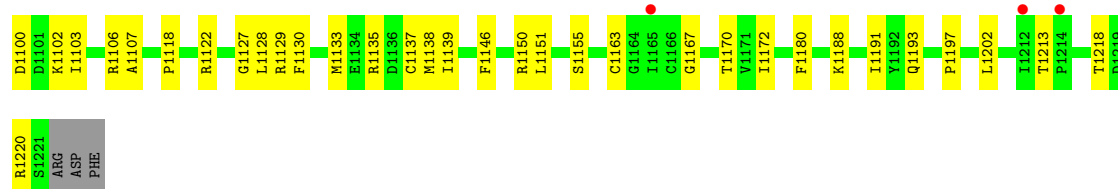
- Molecule 4: DNA-directed RNA polymerase II subunit RPB1



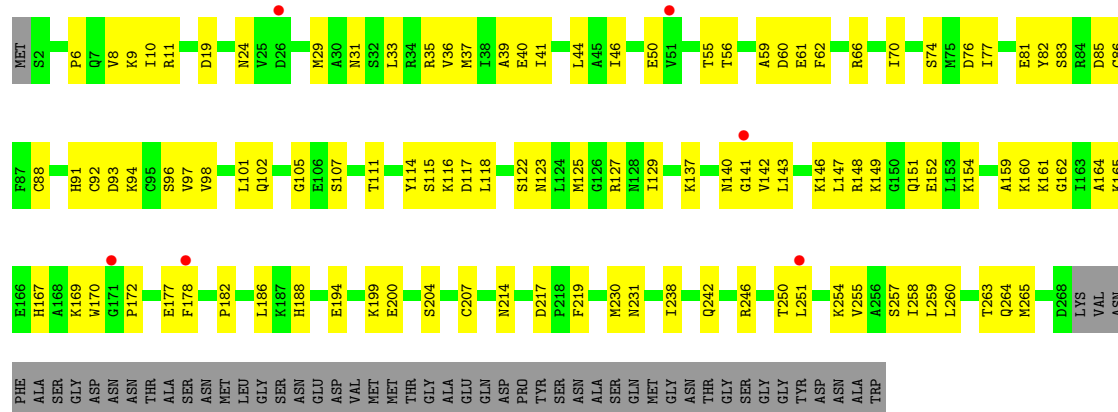
TYR	GLY	GLN	M1364	M1267	L1192	K1112	P910	G820	T709	I607	P514	R434	I336
SER	GLU	LYS	I1365	L1268	L1193	T1113	L914	R821	L710	I607	N517	R337	R337
PRO	ALA	ILE	R1366	I1271	P1114	S1115	E914	E822	R711	Q611	N518	G338	G338
THR	THR	THR	L1195	L1196	L1195	S1116	S915	G823	L722	Q612	P519	N339	N339
PRO	PRO	ILE	L1370	L1371	L1197	T1117	G916	L824	L732	I613	C520	L340	L340
SER	PHE	GLU	I1372	G1275	D1198	V1118	S917	I825	L732	I613	Q525	R344	R344
TYR	GLY	ASP	D1373	V1276	R1199	T1119	E918	D826	L732	V617	Q525	R344	R344
PRO	ALA	GLN	V1374	V1276	T1119	L1120	I919	T827	N736	E618	Q525	F347	F347
THR	GLY	ASP	M1375	E1280	D1207	A1125	L923	A828	L737	P448	L528	R350	R350
PRO	GLY	GLN	T1376	R1281	T1208	L1132	K924	V829	K738	S449	C529	T351	T351
SER	GLU	GLY	T1377	V1282	M1209	L1133	L925	T831	D739	K620	L534	V352	V352
PRO	ALA	VAL	S1383	V1283	V1212	Q1130	Q826	T831	L740	S824	R532	I353	I353
TYR	THR	THR	V1384	M1284	G1213	A1131	V927	R840	K744	I630	K533	S354	S354
SER	PRO	THR	T1385	R1289	E1214	L1133	Y932	K843	Q745	R635	L534	G355	G355
PRO	PRO	THR	R1386	R1289	E1214	L1133	Y932	L845	M746	R635	M455	D356	D356
THR	GLY	THR	H1387	T1295	R1215	I1134	L936	E846	M748	C642	T535	D356	D356
SER	PHE	ASN	T1296	K1217	K1216	I1138	L936	E846	M748	C642	T535	D356	D356
PRO	GLY	GLU	G1296	Q1218	Q1218	I1138	L936	E846	M748	C642	T535	D356	D356
SER	VAL	GLY	E1297	Q1219	Q1219	I1138	L936	E846	M748	C642	T535	D356	D356
TYR	SER	LEU	E1301	F1220	F1220	T1141	D939	T848	K752	Q650	E542	P464	P464
PRO	PRO	VAL	E1301	F1220	F1220	T1141	D939	T848	K752	Q650	E542	P464	P464
THR	GLY	ASN	L1306	L1224	L1224	K1144	K941	V850	I756	N654	N649	K368	K368
SER	PHE	ALA	E1307	F1225	F1225	I1148	L943	N854	Q760	F855	L550	I370	I370
PRO	SER	ASP	T1308	V1226	V1226	A1149	E944	T864	M761	W656	P561	Y376	Y376
SER	PRO	LEU	D1309	I1227	I1227	S1150	E945	Q865	Q767	F662	P563	Y376	Y376
TYR	THR	ASP	A1412	D1231	D1231	E1151	A952	F866	Q768	F662	P563	Y376	Y376
PRO	PRO	LYS	L1313	L1313	L1313	Y1152	N953	T867	S769	F662	P563	Y376	Y376
THR	THR	ASP	S1314	S1314	S1314	Y1154	N953	T867	S769	F662	P563	Y376	Y376
PRO	TYR	GLY	E1417	E1315	E1315	Y1154	N953	T867	S769	F662	P563	Y376	Y376
PRO	SER	LEU	D1419	T1318	T1318	D1155	L956	M873	R774	G667	P568	D386	D386
TYR	THR	PHE	C1421	T1326	T1326	D1157	P957	D874	I775	T669	K569	R387	R387
PRO	PRO	PRO	M1427	R1326	R1326	S1160	N959	A875	A776	A671	L571	L389	L389
THR	ALA	LEU	V1428	I1327	I1327	T1161	I960	A875	A776	A671	L571	L389	L389
SER	TYR	VAL	I1429	Y1328	Y1328	V1162	R961	H877	F777	D672	K575	V392	V392
PRO	SER	ASP	L1430	T1329	T1329	L1080	R962	I878	F779	G673	K575	R393	R393
SER	PRO	SER	G1431	N1330	N1330	L1081	Q968	E879	D781	G673	K575	R393	R393
TYR	GLY	GLY	Q1432	S1331	S1331	ASN	Q968	Q881	D781	G673	K575	R393	R393
SER	SER	THR	M1433	F1332	F1332	PHE	I973	Q881	D781	G673	K575	R393	R393
PRO	PRO	ASN	T1436	I1335	I1335	THR	D974	L883	R782	M676	L578	P396	P396
THR	SER	ALA	F1441	M1336	M1336	ALA	H975	D884	P785	E677	H489	H399	H399
SER	PRO	ALA	I1441	I1340	I1340	LEU	L981	T885	H786	I679	H490	P400	P400
TYR	GLY	GLY	D1445	I1341	I1341	ASP	I386	R896	E795	I683	R590	I406	I406
PRO	SER	PHE	GLU	E1343	E1343	GLU	V987	Y897	F799	K688	P591	R407	R407
THR	PRO	THR	SER	R1343	R1343	GLU	V990	R898	F799	K688	P591	R407	R407
SER	THR	THR	SER	R1345	R1345	ALA	K991	V899	S803	T694	T595	R416	R416
PRO	ALA	ALA	LEU	R1345	R1345	GLU	L901	D900	S803	T694	T595	R416	R416
PRO	TYR	ALA	VAL	E1351	E1351	GLN	Q994	L902	L805	K695	T596	R420	R420
SER	GLY	GLY	LYS	V1352	V1352	THR	I1104	N903	R806	A697	L598	R420	R420
TYR	THR	ALA	TYR	V1355	V1355	PHE	V1107	T907	F814	Q698	K601	D423	D423
PRO	PRO	ASP	PRO	I1356	I1356	ASP	A1108	L908	F815	L702	D602	I424	I424
THR	SER	THR	GLU	I1356	I1356	Q1187	M1111	D909	H816	L702	N603	K431	K431

- Molecule 5: DNA-directed RNA polymerase II subunit RPB2

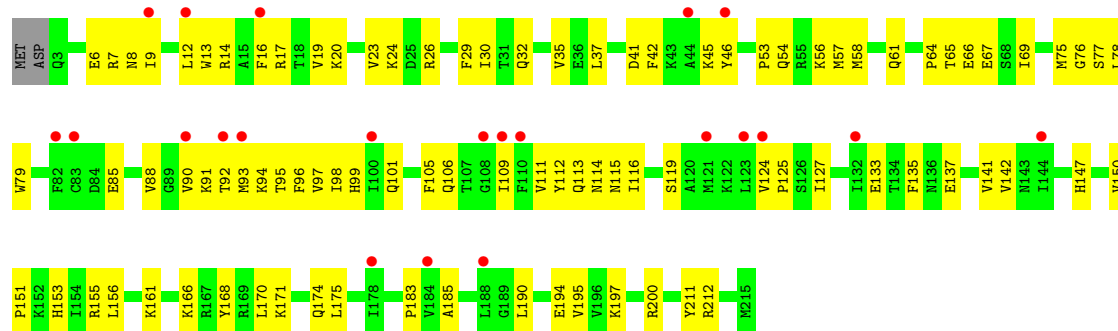




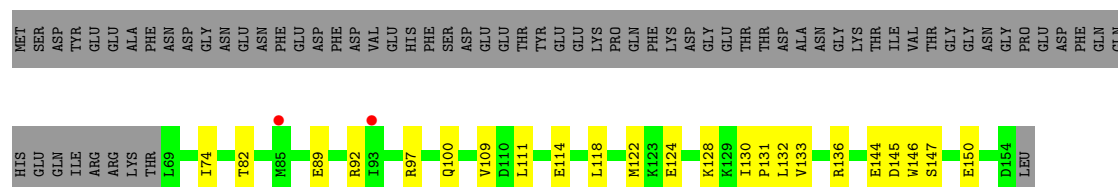
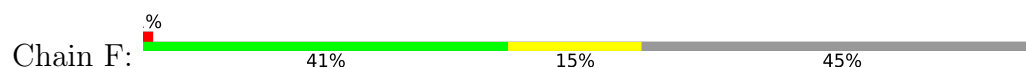
• Molecule 6: DNA-directed RNA polymerase II subunit RPB3



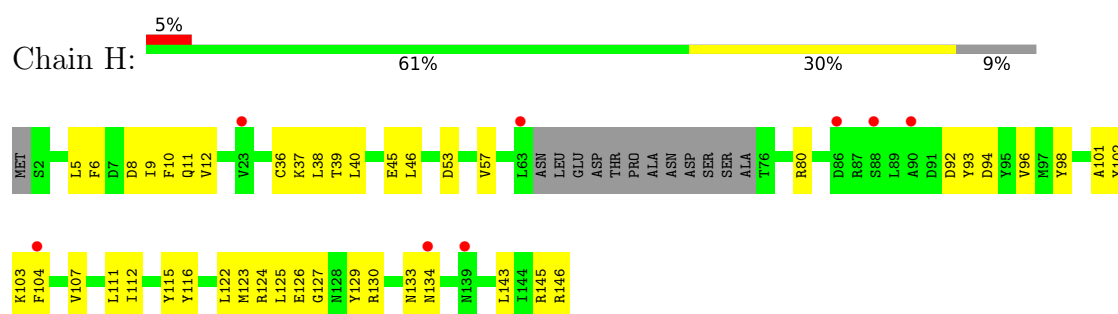
• Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1



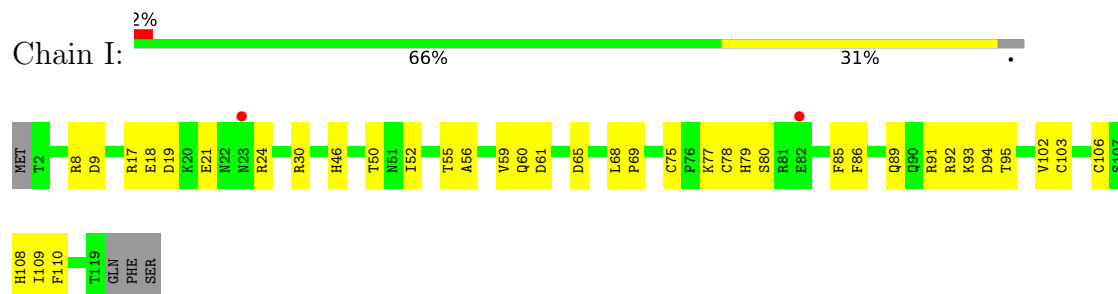
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC2



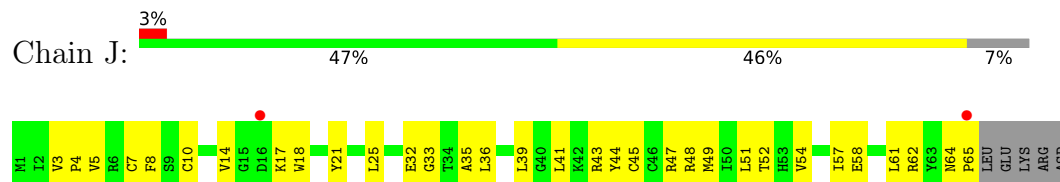
• Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC3



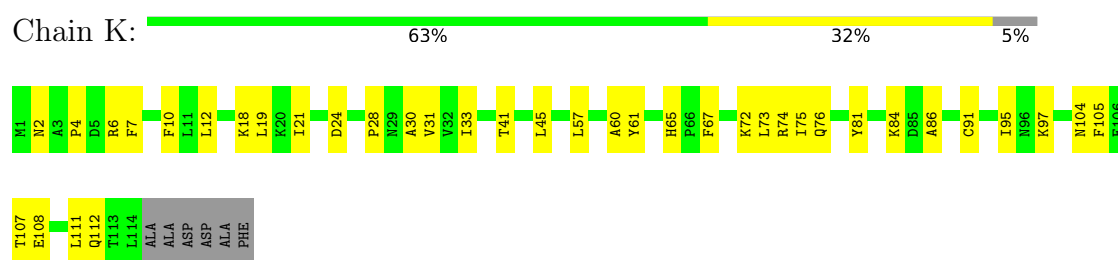
- Molecule 10: DNA-directed RNA polymerase II subunit RPB9



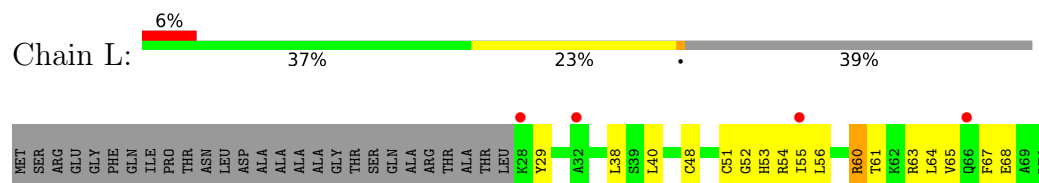
- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 12: DNA-directed RNA polymerase II subunit RPB11



- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC4



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	165.90Å 222.27Å 193.15Å 90.00° 100.27° 90.00°	Depositor
Resolution (Å)	49.31 – 3.35 49.31 – 3.35	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.31-3.35) 98.8 (49.31-3.35)	Depositor EDS
R_{merge}	0.51	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.265 , 0.300 0.264 , 0.298	Depositor DCC
R_{free} test set	2000 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å ²)	91.1	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 75.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	29066	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, 8OG, PPV

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	R	0.14	0/245	0.32	0/379
2	T	0.23	0/551	0.49	0/843
3	N	0.21	0/359	0.39	0/553
4	A	0.15	0/11023	0.39	0/14912
5	B	0.14	0/9020	0.35	0/12172
6	C	0.14	0/2139	0.34	0/2899
7	E	0.15	0/1764	0.39	0/2376
8	F	0.13	0/696	0.36	0/943
9	H	0.14	0/1082	0.42	0/1466
10	I	0.16	0/964	0.40	0/1301
11	J	0.17	0/541	0.40	0/727
12	K	0.14	0/937	0.36	0/1265
13	L	0.16	0/339	0.41	0/450
All	All	0.15	0/29660	0.38	0/40286

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
4	A	0	1
5	B	0	2
13	L	0	1
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	311	GLN	Peptide
5	B	267	ARG	Sidechain
5	B	635	ARG	Sidechain
13	L	60	ARG	Sidechain

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	R	219	0	110	1	0
2	T	521	0	297	19	0
3	N	317	0	166	14	0
4	A	10831	0	10873	419	1
5	B	8849	0	8808	311	0
6	C	2101	0	2058	85	0
7	E	1728	0	1744	79	0
8	F	684	0	692	18	0
9	H	1064	0	1029	40	0
10	I	946	0	888	36	1
11	J	532	0	544	38	0
12	K	919	0	929	35	0
13	L	337	0	354	15	0
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	A	9	0	0	0	0
All	All	29066	0	28492	991	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 17.

All (991) 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)
7:E:96:PHE:HA	7:E:99:HIS:HD2	1.26	1.00
6:C:66:ARG:NH2	11:J:3:VAL:O	2.03	0.91
7:E:96:PHE:HA	7:E:99:HIS:CD2	2.08	0.88
4:A:567:LYS:HB2	9:H:96:VAL:HB	1.56	0.88
11:J:36:LEU:HD13	11:J:47:ARG:HD3	1.55	0.86
4:A:50:ILE:HG22	4:A:52:GLY:H	1.39	0.86
8:F:74:ILE:HD13	8:F:144:GLU:HG2	1.59	0.84
4:A:269:ILE:HG12	4:A:299:HIS:HB3	1.57	0.84
4:A:179:LEU:HD23	4:A:297:GLN:HG2	1.60	0.83
6:C:39:ALA:HA	6:C:164:ALA:HB3	1.60	0.83
4:A:1206:ASP:HB2	4:A:1274:ARG:HH12	1.43	0.83
4:A:1144:LYS:HG2	4:A:1268:LEU:HB3	1.61	0.81
9:H:36:CYS:HA	9:H:126:GLU:O	1.80	0.81
9:H:92:ASP:OD1	9:H:145:ARG:NH1	2.14	0.81
7:E:64:PRO:HD3	7:E:76:GLY:HA2	1.61	0.80
6:C:94:LYS:HA	6:C:127:ARG:HH22	1.46	0.80
9:H:94:ASP:HB3	9:H:146:ARG:HH21	1.46	0.80
9:H:5:LEU:HD12	9:H:134:ASN:H	1.46	0.79
4:A:449:SER:HB2	5:B:1133:MET:HG2	1.66	0.78
4:A:350:ARG:HH22	4:A:447:GLN:HG2	1.48	0.78
5:B:1060:ARG:NH1	6:C:199:LYS:O	2.13	0.78
10:I:91:ARG:NH1	10:I:95:THR:HG21	1.98	0.78
5:B:212:LEU:HD21	5:B:466:TRP:HZ2	1.48	0.78
4:A:1224:LEU:HD21	4:A:1240:CYS:HB3	1.65	0.77
4:A:1187:GLN:N	4:A:1187:GLN:OE1	2.18	0.77
4:A:117:GLU:O	4:A:123:ARG:NE	2.18	0.77
11:J:33:GLY:HA2	11:J:36:LEU:HD12	1.65	0.76
7:E:185:ALA:HA	7:E:190:LEU:HD23	1.68	0.76
4:A:795:GLU:HG2	5:B:731:VAL:HG11	1.67	0.75
4:A:1120:LEU:HD23	4:A:1125:ALA:HA	1.68	0.75
4:A:1165:GLU:OE1	4:A:1194:ARG:NH2	2.20	0.74
4:A:1282:VAL:HG12	4:A:1306:LEU:HD22	1.67	0.74
11:J:45:CYS:O	11:J:48:ARG:NH1	2.21	0.74
5:B:1054:GLY:HA2	5:B:1057:LYS:HD2	1.70	0.73
5:B:496:ARG:NH2	5:B:540:SER:O	2.21	0.73
4:A:613:ILE:HG21	9:H:102:TYR:HB3	1.71	0.73
5:B:1056:SER:HB3	5:B:1066:SER:HB2	1.69	0.73
6:C:165:LYS:O	12:K:6:ARG:NH1	2.21	0.73
6:C:102:GLN:HB3	6:C:154:LYS:HG3	1.70	0.73
4:A:1118:VAL:HB	4:A:1306:LEU:HB2	1.71	0.72
4:A:167:CYS:SG	4:A:169:ASN:ND2	2.62	0.72
4:A:42:ASP:HA	4:A:50:ILE:HD11	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:821:ARG:HH21	5:B:534:GLY:HA2	1.54	0.72
7:E:16:PHE:HZ	7:E:37:LEU:HD11	1.54	0.72
4:A:151:ASP:OD2	4:A:161:LEU:N	2.23	0.72
4:A:903:ASN:O	4:A:907:THR:OG1	2.08	0.71
6:C:56:THR:HG22	6:C:147:LEU:HD21	1.72	0.71
12:K:28:PRO:O	12:K:76:GLN:NE2	2.20	0.71
4:A:806:ARG:NH1	5:B:725:PRO:O	2.24	0.71
6:C:29:MET:HE1	12:K:97:LYS:HB2	1.71	0.71
5:B:69:LEU:HB2	5:B:90:ILE:HB	1.70	0.71
4:A:671:ALA:HB3	4:A:676:MET:HE2	1.72	0.71
5:B:358:LYS:HG2	5:B:359:GLU:HG2	1.73	0.70
6:C:33:LEU:HG	6:C:37:MET:HE2	1.73	0.70
5:B:173:MET:HB2	5:B:203:PHE:HE1	1.56	0.70
7:E:111:VAL:HG12	7:E:137:GLU:HG2	1.71	0.70
4:A:68:GLN:NE2	4:A:70:CYS:SG	2.65	0.70
5:B:212:LEU:HD21	5:B:466:TRP:CZ2	2.26	0.70
4:A:1129:GLU:HA	4:A:1132:LYS:HD2	1.74	0.70
4:A:1342:GLU:OE1	7:E:200:ARG:NH2	2.24	0.70
4:A:975:HIS:O	4:A:1036:ARG:NH1	2.25	0.69
4:A:55:ASP:HA	4:A:58:LEU:HB2	1.74	0.69
6:C:77:ILE:HG13	6:C:161:LYS:HD2	1.73	0.69
4:A:540:PHE:HB3	4:A:571:LEU:HD22	1.75	0.69
4:A:1364:ASN:OD1	4:A:1366:ARG:NH1	2.23	0.69
5:B:520:GLY:HA3	5:B:635:ARG:NH1	2.07	0.69
5:B:56:ASP:OD2	5:B:177:LYS:NZ	2.22	0.69
4:A:243:PRO:HB2	4:A:245:PRO:HD2	1.75	0.69
7:E:94:LYS:O	7:E:98:ILE:HD12	1.93	0.68
4:A:875:ALA:HB2	4:A:1366:ARG:HD2	1.74	0.68
5:B:815:ARG:NH2	5:B:1041:GLU:OE2	2.27	0.68
6:C:147:LEU:HD22	6:C:151:GLN:HB3	1.74	0.68
4:A:1264:GLU:O	4:A:1268:LEU:HD12	1.94	0.67
7:E:88:VAL:HG23	7:E:92:THR:HB	1.76	0.67
5:B:1029:CYS:SG	5:B:1090:THR:OG1	2.49	0.67
10:I:92:ARG:HG3	10:I:94:ASP:OD1	1.93	0.67
6:C:82:TYR:HB2	6:C:85:ASP:HB2	1.76	0.67
5:B:918:ILE:HD13	5:B:935:ARG:HH21	1.60	0.67
4:A:443:LEU:HD21	4:A:455:MET:HB3	1.75	0.67
6:C:93:ASP:O	6:C:127:ARG:NH2	2.27	0.67
4:A:30:ILE:HD12	5:B:1170:THR:HG21	1.77	0.67
9:H:103:LYS:HB3	9:H:115:TYR:HD2	1.61	0.66
4:A:356:ASP:HB3	4:A:359:LEU:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:6:DT:H2"	2:T:7:DC:C4	2.31	0.66
5:B:754:SER:HB2	5:B:812:LEU:HD11	1.76	0.66
5:B:802:PRO:HG2	5:B:805:THR:HG22	1.76	0.66
2:T:11:DC:H2"	2:T:12:DT:H71	1.77	0.66
4:A:329:LEU:HD11	4:A:1406:VAL:HB	1.77	0.66
11:J:7:CYS:HA	11:J:49:MET:HE2	1.78	0.66
5:B:364:ILE:HG12	5:B:585:VAL:HG13	1.78	0.65
4:A:1107:VAL:HG22	4:A:1383:SER:HB3	1.78	0.65
5:B:969:ARG:HH11	6:C:59:ALA:HB1	1.61	0.65
4:A:881:GLN:HA	4:A:961:ARG:HH22	1.62	0.65
4:A:230:ARG:NH1	4:A:232:GLU:OE1	2.29	0.65
10:I:75:CYS:HB2	10:I:110:PHE:CE1	2.32	0.65
5:B:309:GLN:HE22	10:I:50:THR:HG21	1.61	0.65
4:A:535:THR:O	4:A:575:LYS:NZ	2.30	0.64
9:H:80:ARG:HG2	12:K:57:LEU:HD22	1.79	0.64
10:I:50:THR:HG22	10:I:52:ILE:H	1.62	0.64
5:B:483:LEU:HD21	5:B:491:THR:HG23	1.79	0.64
5:B:384:ARG:NH2	5:B:623:GLU:OE2	2.31	0.64
5:B:431:TYR:HE2	5:B:446:LEU:HB3	1.63	0.64
6:C:31:ASN:O	6:C:35:ARG:HG3	1.96	0.64
5:B:412:LEU:HD23	5:B:466:TRP:HE1	1.63	0.64
5:B:979:LYS:HD3	5:B:1095:LEU:HD12	1.80	0.64
4:A:1138:ILE:HG23	4:A:1282:VAL:HG21	1.80	0.63
4:A:1385:THR:OG1	4:A:1387:HIS:O	2.16	0.63
6:C:46:ILE:HA	6:C:159:ALA:HA	1.80	0.63
12:K:24:ASP:OD2	12:K:74:ARG:NH1	2.26	0.63
4:A:22:PHE:HD1	5:B:1213:THR:HG22	1.64	0.63
5:B:998:ASP:OD1	6:C:35:ARG:NH2	2.32	0.63
13:L:51:CYS:SG	13:L:53:HIS:N	2.71	0.63
4:A:450:LEU:HD13	4:A:1077:THR:HG21	1.79	0.63
5:B:753:ALA:HA	5:B:756:ILE:HD12	1.80	0.62
6:C:74:SER:HB2	6:C:238:ILE:HD11	1.80	0.62
7:E:113:GLN:HA	7:E:137:GLU:HG3	1.81	0.62
9:H:94:ASP:HB3	9:H:146:ARG:NH2	2.13	0.62
4:A:1166:ASP:HA	4:A:1169:ILE:HD12	1.82	0.62
5:B:1008:PRO:HB3	5:B:1087:PHE:HE1	1.64	0.62
7:E:37:LEU:HD13	7:E:42:PHE:HB2	1.81	0.62
4:A:848:ILE:HG22	4:A:1064:VAL:HG23	1.82	0.62
4:A:1329:THR:HB	4:A:1335:ILE:HG12	1.81	0.62
5:B:751:VAL:HG23	5:B:812:LEU:HD22	1.82	0.62
5:B:299:GLU:OE2	5:B:572:HIS:ND1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:572:HIS:HD1	5:B:572:HIS:H	1.47	0.62
4:A:679:ILE:HG13	4:A:732:LEU:HD23	1.80	0.62
7:E:54:GLN:HB2	7:E:57:MET:HG2	1.81	0.62
5:B:402:GLY:O	5:B:405:ARG:NH1	2.32	0.61
13:L:48:CYS:HB3	13:L:51:CYS:SG	2.40	0.61
5:B:847:ASP:OD2	12:K:6:ARG:NH2	2.32	0.61
4:A:1262:LYS:HE3	4:A:1262:LYS:HA	1.82	0.61
9:H:101:ALA:HA	9:H:116:TYR:HA	1.82	0.61
4:A:579:SER:OG	4:A:612:ILE:HG22	2.01	0.61
9:H:40:LEU:HD13	9:H:123:MET:HB2	1.83	0.61
4:A:206:GLU:O	4:A:210:ILE:HG13	2.01	0.61
5:B:487:THR:OG1	5:B:777:ALA:O	2.18	0.61
5:B:601:ARG:O	5:B:605:ARG:HD2	1.99	0.61
12:K:21:ILE:HD13	12:K:84:LYS:HE3	1.83	0.61
8:F:92:ARG:HG3	8:F:92:ARG:HH11	1.66	0.60
4:A:825:ILE:HD12	5:B:512:ARG:HD3	1.82	0.60
7:E:114:ASN:OD1	7:E:115:ASN:N	2.34	0.60
4:A:696:GLU:HG2	4:A:702:LEU:HG	1.84	0.60
4:A:756:ILE:O	4:A:760:GLN:HG3	2.01	0.60
4:A:932:GLU:O	4:A:936:LEU:HG	2.01	0.60
5:B:118:ARG:NH2	5:B:194:GLU:OE1	2.34	0.60
5:B:617:ARG:NH2	10:I:61:ASP:OD2	2.33	0.60
5:B:365:THR:HG22	5:B:367:LEU:H	1.65	0.60
5:B:834:ASN:O	5:B:1013:ASN:HB2	2.01	0.60
2:T:21:DC:H1'	4:A:447:GLN:HG3	1.83	0.60
4:A:113:LEU:HD23	4:A:218:ASP:CG	2.27	0.60
4:A:1116:LEU:HB2	4:A:1308:THR:OG1	2.01	0.60
5:B:122:LEU:HD22	5:B:958:GLN:HG3	1.84	0.60
4:A:351:THR:HB	4:A:468:PHE:CD2	2.37	0.60
4:A:1430:LEU:HB3	4:A:1432:GLN:HG3	1.84	0.59
5:B:642:ASP:HA	5:B:649:LYS:HA	1.83	0.59
4:A:72:GLU:HB3	4:A:76:GLU:HB3	1.84	0.59
4:A:535:THR:HG21	4:A:617:VAL:HG23	1.84	0.59
4:A:1231:ASP:HA	4:A:1236:LEU:HD21	1.84	0.59
2:T:25:DC:H5'	5:B:792:MET:HE2	1.84	0.59
5:B:639:ILE:HD11	5:B:691:GLU:HB2	1.85	0.59
7:E:147:HIS:HB3	7:E:150:VAL:HG23	1.84	0.59
11:J:3:VAL:HG21	11:J:18:TRP:CG	2.37	0.59
2:T:8:DT:O2	3:N:12:DG:N2	2.34	0.59
4:A:592:ASP:O	4:A:595:THR:OG1	2.20	0.59
4:A:1327:ILE:O	7:E:147:HIS:NE2	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:5:LEU:O	9:H:133:ASN:ND2	2.36	0.59
5:B:416:LEU:HD23	5:B:457:LEU:HD23	1.84	0.59
2:T:20:DC:H2'	2:T:21:DC:C6	2.38	0.59
4:A:550:LEU:HD21	4:A:561:PRO:HD2	1.85	0.59
6:C:29:MET:HG3	12:K:45:LEU:HD11	1.84	0.59
3:N:12:DG:H1'	3:N:13:DA:C8	2.38	0.59
4:A:666:ILE:HG23	5:B:1026:LEU:HB3	1.84	0.59
4:A:1284:MET:HG2	4:A:1306:LEU:HD21	1.84	0.59
4:A:463:ILE:HD13	4:A:469:ARG:HG3	1.85	0.58
5:B:862:GLN:HG2	5:B:963:PHE:HD1	1.67	0.58
5:B:995:ARG:NH1	5:B:997:GLU:OE2	2.36	0.58
7:E:46:TYR:CZ	7:E:53:PRO:HB2	2.38	0.58
4:A:821:ARG:O	4:A:825:ILE:HG12	2.03	0.58
5:B:195:CYS:SG	5:B:783:THR:OG1	2.59	0.58
4:A:744:LYS:HE3	4:A:748:MET:HE2	1.85	0.58
5:B:276:ILE:HD11	5:B:355:ILE:HD13	1.86	0.58
4:A:1214:GLU:O	4:A:1218:GLN:HG2	2.03	0.58
5:B:460:ALA:HB1	5:B:466:TRP:CE3	2.39	0.58
7:E:64:PRO:HB3	7:E:75:MET:HG2	1.84	0.58
5:B:298:LEU:HD22	5:B:314:LEU:HD13	1.86	0.58
4:A:464:PRO:O	12:K:2:ASN:HB3	2.03	0.57
5:B:857:ARG:NH1	5:B:945:GLU:OE2	2.37	0.57
4:A:42:ASP:OD1	4:A:46:THR:OG1	2.20	0.57
4:A:1431:GLY:HA3	5:B:1197:PRO:HD3	1.87	0.57
5:B:104:GLU:HG3	13:L:54:ARG:CZ	2.34	0.57
5:B:904:ARG:HG2	5:B:948:ILE:HG12	1.86	0.57
2:T:15:DC:H2'	2:T:16:DT:C6	2.40	0.57
4:A:391:LEU:HD11	4:A:437:MET:HE1	1.85	0.57
5:B:1023:VAL:O	5:B:1027:ILE:HG12	2.05	0.57
4:A:483:ASP:HB2	5:B:987:LYS:HD3	1.85	0.57
4:A:897:TYR:HD2	4:A:936:LEU:HD13	1.68	0.57
4:A:534:LEU:HA	4:A:539:THR:HG21	1.86	0.57
4:A:22:PHE:CD1	5:B:1213:THR:HG22	2.39	0.56
4:A:310:GLY:C	4:A:312:PRO:HD3	2.30	0.56
4:A:882:SER:O	4:A:1025:ARG:NH1	2.38	0.56
4:A:1352:VAL:O	4:A:1356:ILE:HG12	2.06	0.56
5:B:1135:ARG:O	5:B:1139:ILE:HG13	2.05	0.56
7:E:41:ASP:O	7:E:45:LYS:HG3	2.04	0.56
4:A:386:ASP:O	4:A:389:THR:OG1	2.21	0.56
5:B:980:PHE:CE2	5:B:1094:ARG:HG3	2.41	0.56
6:C:116:LYS:HD3	6:C:140:ASN:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:13:DA:H2''	3:N:14:DG:C8	2.40	0.56
5:B:29:ASP:HB3	5:B:658:ILE:HG12	1.88	0.56
5:B:496:ARG:HH12	5:B:541:LEU:HA	1.71	0.56
5:B:792:MET:SD	5:B:857:ARG:NH2	2.78	0.56
4:A:469:ARG:HH22	5:B:833:TYR:HE1	1.54	0.56
5:B:237:VAL:HG22	5:B:257:LYS:HG2	1.87	0.56
4:A:15:LYS:HB3	5:B:1220:ARG:HG3	1.88	0.56
4:A:59:GLY:HA2	4:A:67:CYS:HA	1.88	0.55
5:B:460:ALA:HB1	5:B:466:TRP:HE3	1.72	0.55
4:A:376:TYR:HD2	4:A:434:ARG:HH11	1.53	0.55
5:B:957:ASN:OD1	5:B:961:LEU:N	2.39	0.55
4:A:107:CYS:HA	4:A:171:GLN:HG3	1.87	0.55
5:B:658:ILE:HA	5:B:661:LEU:HD12	1.89	0.55
10:I:75:CYS:HB3	10:I:78:CYS:SG	2.47	0.55
5:B:512:ARG:NH2	5:B:531:GLN:O	2.26	0.55
7:E:133:GLU:HB3	7:E:135:PHE:HE1	1.71	0.55
2:T:16:DT:H2'	2:T:17:DG:C8	2.42	0.55
6:C:258:ILE:HG23	12:K:19:LEU:HD11	1.87	0.55
6:C:36:VAL:HG23	12:K:41:THR:HG21	1.89	0.55
7:E:91:LYS:O	7:E:95:THR:HG23	2.07	0.55
4:A:528:LEU:O	4:A:531:ILE:HG22	2.07	0.55
6:C:8:VAL:HG21	12:K:105:PHE:HA	1.89	0.55
6:C:177:GLU:O	6:C:230:MET:HA	2.07	0.55
7:E:66:GLU:O	7:E:69:ILE:HG12	2.07	0.55
5:B:577:ALA:HB1	5:B:589:VAL:CG1	2.37	0.54
5:B:848:ARG:NH1	11:J:8:PHE:O	2.41	0.54
7:E:156:LEU:HD21	7:E:197:LYS:HB2	1.88	0.54
8:F:118:LEU:O	8:F:122:MET:HG3	2.07	0.54
4:A:587:HIS:HA	4:A:607:ILE:O	2.07	0.54
6:C:50:GLU:HB2	13:L:64:LEU:HD21	1.88	0.54
3:N:5:DC:N4	3:N:6:DG:O6	2.40	0.54
4:A:471:ASN:O	4:A:474:VAL:HG12	2.08	0.54
4:A:542:GLU:OE2	4:A:569:LYS:NZ	2.38	0.54
4:A:1340:GLY:HA2	7:E:183:PRO:HD2	1.89	0.54
5:B:784:ASN:CG	5:B:788:ARG:HD2	2.32	0.54
4:A:302:THR:HA	4:A:305:ASP:O	2.06	0.54
5:B:976:ILE:HD11	5:B:992:ILE:HA	1.89	0.54
4:A:1148:ILE:HD12	4:A:1196:GLU:HG2	1.89	0.54
4:A:350:ARG:HB2	5:B:1128:LEU:HD21	1.89	0.54
4:A:351:THR:HG23	5:B:1103:ILE:HD12	1.88	0.54
4:A:420:ARG:HG2	4:A:423:ASP:OD1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:653:VAL:C	5:B:654:ARG:HD2	2.32	0.54
6:C:10:ILE:HD12	12:K:108:GLU:HB3	1.89	0.54
12:K:30:ALA:HA	12:K:75:ILE:O	2.08	0.54
4:A:144:THR:HG22	4:A:146:MET:HE1	1.90	0.54
4:A:513:SER:HB3	4:A:520:CYS:SG	2.48	0.54
4:A:786:HIS:HE1	5:B:742:GLU:HG3	1.73	0.54
5:B:240:ILE:HG22	5:B:254:LEU:HB3	1.90	0.54
5:B:1100:ASP:HA	5:B:1103:ILE:HG12	1.90	0.53
10:I:102:VAL:HG22	10:I:109:ILE:HG13	1.89	0.53
6:C:246:ARG:O	6:C:250:THR:OG1	2.26	0.53
12:K:7:PHE:HA	12:K:10:PHE:CE1	2.43	0.53
4:A:848:ILE:HB	4:A:1065:GLY:HA3	1.91	0.53
6:C:55:THR:OG1	6:C:152:GLU:N	2.33	0.53
6:C:182:PRO:HB2	6:C:207:CYS:SG	2.49	0.53
4:A:219:PHE:CZ	4:A:231:PRO:HD2	2.43	0.53
4:A:761:MET:HG3	5:B:1021:MET:HG2	1.90	0.53
5:B:610:ASN:HB3	5:B:613:VAL:HG23	1.90	0.53
4:A:472:LEU:HD11	5:B:835:GLN:NE2	2.23	0.53
4:A:1104:ILE:HG12	4:A:1332:PHE:CZ	2.43	0.53
10:I:91:ARG:HH12	10:I:95:THR:HG21	1.71	0.53
4:A:84:ILE:HG23	4:A:239:LEU:HB3	1.91	0.53
4:A:596:THR:HG22	4:A:598:LEU:H	1.74	0.53
4:A:58:LEU:HD11	4:A:80:HIS:O	2.08	0.53
4:A:308:ILE:HG22	4:A:310:GLY:H	1.74	0.53
5:B:840:ILE:HG12	5:B:992:ILE:HG22	1.90	0.53
6:C:116:LYS:NZ	6:C:117:ASP:OD1	2.42	0.53
4:A:1129:GLU:O	4:A:1133:LEU:HG	2.09	0.53
4:A:571:LEU:HD12	9:H:46:LEU:HD11	1.90	0.52
4:A:848:ILE:HG21	4:A:1370:LEU:HD11	1.90	0.52
4:A:900:ASP:O	4:A:907:THR:OG1	2.22	0.52
5:B:101:MET:HG2	5:B:111:ALA:HA	1.90	0.52
9:H:102:TYR:CZ	9:H:115:TYR:HB3	2.45	0.52
4:A:864:ILE:HG22	4:A:865:GLN:HG2	1.91	0.52
4:A:924:LYS:O	4:A:927:VAL:HG22	2.09	0.52
5:B:570:VAL:HG23	5:B:573:GLN:HB2	1.91	0.52
7:E:67:GLU:OE1	7:E:67:GLU:N	2.28	0.52
11:J:3:VAL:HG11	11:J:18:TRP:HB2	1.90	0.52
11:J:10:CYS:SG	11:J:43:ARG:NH2	2.76	0.52
4:A:456:MET:HE3	4:A:507:VAL:HG22	1.92	0.52
4:A:767:GLN:HB2	4:A:799:PHE:HD1	1.73	0.52
5:B:1000:PRO:HB2	5:B:1072:MET:HE3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:93:TYR:HD2	9:H:145:ARG:HB2	1.75	0.52
12:K:91:CYS:O	12:K:95:ILE:HG13	2.09	0.52
5:B:234:ILE:HD12	5:B:257:LYS:HB3	1.92	0.52
5:B:576:ASP:HB2	5:B:591:ARG:HH12	1.74	0.52
7:E:93:MET:O	7:E:97:VAL:HG13	2.10	0.52
4:A:567:LYS:HB3	4:A:568:PRO:HD3	1.90	0.52
5:B:120:ARG:HH21	5:B:956:THR:HG23	1.74	0.52
6:C:242:GLN:O	6:C:246:ARG:HD2	2.10	0.52
11:J:14:VAL:HA	11:J:17:LYS:HD3	1.91	0.52
3:N:14:DG:H2"	3:N:15:DA:C8	2.44	0.52
4:A:276:LEU:O	4:A:280:GLU:HG2	2.09	0.52
4:A:932:GLU:OE1	4:A:1028:THR:OG1	2.26	0.52
4:A:1289:ARG:O	4:A:1301:GLU:N	2.36	0.52
4:A:208:LEU:HD12	4:A:235:ILE:HD11	1.91	0.52
4:A:380:VAL:HG12	4:A:388:LEU:HD12	1.92	0.52
4:A:465:TYR:CD2	5:B:976:ILE:HD12	2.44	0.52
6:C:9:LYS:NZ	6:C:10:ILE:O	2.41	0.52
6:C:254:LYS:O	6:C:258:ILE:HG12	2.10	0.52
4:A:443:LEU:O	4:A:489:LEU:HA	2.09	0.52
4:A:881:GLN:HE22	4:A:959:ASN:HA	1.75	0.52
5:B:872:GLU:OE1	5:B:914:LYS:NZ	2.24	0.52
10:I:86:PHE:HE2	10:I:89:GLN:HG2	1.74	0.52
5:B:244:LEU:HB2	5:B:248:SER:HB2	1.91	0.52
5:B:724:ASP:HB3	5:B:727:LYS:HG3	1.92	0.52
4:A:305:ASP:O	4:A:308:ILE:HD11	2.09	0.52
4:A:694:THR:O	4:A:698:GLN:HG3	2.10	0.52
4:A:1063:MET:HE3	4:A:1436:ILE:HG23	1.92	0.52
4:A:1318:THR:HG22	7:E:142:VAL:HG22	1.92	0.52
5:B:227:LYS:H	5:B:395:GLN:CD	2.17	0.52
4:A:111:GLY:HA3	4:A:214:ILE:HD13	1.91	0.51
4:A:146:MET:SD	4:A:146:MET:N	2.84	0.51
4:A:868:TYR:CD2	4:A:1058:VAL:HG11	2.44	0.51
5:B:217:ARG:O	5:B:405:ARG:N	2.31	0.51
5:B:780:VAL:HG23	5:B:817:LEU:HG	1.90	0.51
5:B:827:ILE:HD12	5:B:1086:PHE:HD2	1.74	0.51
6:C:88:CYS:HB3	6:C:92:CYS:HB3	1.92	0.51
13:L:60:ARG:NH1	13:L:65:VAL:HG12	2.24	0.51
5:B:614:SER:HB3	5:B:632:ARG:NH2	2.25	0.51
5:B:648:HIS:CE1	5:B:650:GLU:HB2	2.45	0.51
5:B:983:ARG:HG2	5:B:1093:GLN:HE21	1.75	0.51
6:C:114:TYR:CG	6:C:140:ASN:HB3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:61:TYR:HA	12:K:72:LYS:O	2.11	0.51
2:T:7:DC:H1'	2:T:8:DT:C6	2.46	0.51
2:T:21:DC:OP1	5:B:1129:ARG:NE	2.44	0.51
4:A:672:ASP:H	4:A:736:ASN:ND2	2.09	0.51
4:A:877:HIS:ND1	4:A:1056:SER:HA	2.26	0.51
5:B:349:ILE:O	5:B:353:LYS:HG3	2.10	0.51
5:B:698:GLU:HA	5:B:701:ILE:HG12	1.91	0.51
5:B:830:TYR:CZ	5:B:1000:PRO:HD3	2.45	0.51
7:E:166:LYS:O	7:E:166:LYS:NZ	2.34	0.51
9:H:93:TYR:CD1	9:H:143:LEU:HB3	2.46	0.51
4:A:463:ILE:CD1	4:A:469:ARG:HG3	2.39	0.51
4:A:1094:VAL:HA	4:A:1113:THR:HG21	1.92	0.51
5:B:601:ARG:HA	5:B:615:MET:HE1	1.92	0.51
2:T:11:DC:H2''	2:T:12:DT:C7	2.40	0.51
4:A:92:HIS:HB2	4:A:236:LEU:HD11	1.92	0.51
5:B:519:TRP:CZ2	5:B:705:MET:HE1	2.46	0.51
6:C:83:SER:OG	6:C:160:LYS:HG2	2.11	0.51
8:F:124:GLU:HB3	8:F:130:ILE:HG13	1.93	0.51
4:A:635:ARG:NH1	4:A:877:HIS:HD2	2.09	0.51
4:A:1212:VAL:O	4:A:1216:ILE:HG13	2.11	0.51
4:A:1225:PHE:O	4:A:1240:CYS:HA	2.11	0.51
5:B:35:SER:O	5:B:39:ARG:HG3	2.10	0.51
7:E:90:VAL:O	7:E:94:LYS:HG3	2.11	0.51
11:J:14:VAL:HG12	11:J:41:LEU:HD21	1.92	0.51
4:A:630:ILE:HD12	4:A:630:ILE:H	1.76	0.51
4:A:670:ILE:HG12	4:A:805:LEU:HD11	1.92	0.51
4:A:679:ILE:O	4:A:683:ILE:HG12	2.10	0.51
4:A:846:GLU:HA	4:A:1066:VAL:HG22	1.90	0.51
4:A:886:ILE:HD12	4:A:943:LEU:HB3	1.93	0.51
4:A:1267:MET:O	4:A:1271:ILE:HB	2.11	0.51
4:A:390:GLN:O	4:A:394:ASN:N	2.40	0.51
4:A:968:GLN:HA	4:A:973:ILE:HD13	1.93	0.51
5:B:273:LEU:HB2	5:B:276:ILE:HB	1.93	0.51
5:B:1039:GLY:HA2	11:J:51:LEU:HD21	1.93	0.51
5:B:1041:GLU:HG2	5:B:1042:GLY:N	2.26	0.51
4:A:356:ASP:OD2	4:A:469:ARG:NH2	2.29	0.51
4:A:566:ILE:HD11	9:H:98:TYR:HB2	1.92	0.51
4:A:1148:ILE:N	4:A:1196:GLU:O	2.44	0.51
4:A:1329:THR:HG22	4:A:1331:SER:N	2.26	0.51
5:B:214:ALA:HB1	5:B:406:LEU:HD22	1.92	0.51
13:L:38:LEU:HB3	13:L:40:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:879:GLU:OE1	4:A:962:ARG:NH2	2.44	0.50
5:B:114:PRO:O	5:B:118:ARG:HG3	2.11	0.50
5:B:114:PRO:HG3	5:B:181:LEU:HD11	1.93	0.50
5:B:331:LEU:HB2	5:B:349:ILE:HG23	1.91	0.50
5:B:635:ARG:NH2	5:B:742:GLU:CD	2.70	0.50
7:E:13:TRP:HA	7:E:16:PHE:CD2	2.46	0.50
7:E:46:TYR:CE1	7:E:58:MET:HG2	2.46	0.50
7:E:161:LYS:HD2	7:E:195:VAL:HG23	1.93	0.50
4:A:108:MET:N	4:A:171:GLN:HE21	2.09	0.50
4:A:151:ASP:OD2	4:A:162:VAL:N	2.44	0.50
4:A:1412:ALA:HA	4:A:1417:GLU:HG3	1.94	0.50
5:B:770:GLN:HA	5:B:773:MET:HG3	1.94	0.50
13:L:68:GLU:CD	13:L:68:GLU:H	2.19	0.50
4:A:214:ILE:HB	4:A:219:PHE:CE1	2.47	0.50
4:A:354:SER:O	4:A:469:ARG:HA	2.11	0.50
4:A:455:MET:HB2	5:B:1137:CYS:SG	2.52	0.50
4:A:474:VAL:HG22	4:A:478:TYR:HE2	1.77	0.50
4:A:678:GLU:O	4:A:681:GLU:HG3	2.11	0.50
4:A:1420:ASP:O	5:B:1220:ARG:NH2	2.25	0.50
5:B:640:VAL:HG22	5:B:651:LEU:HG	1.94	0.50
10:I:17:ARG:NH1	10:I:18:GLU:H	2.08	0.50
12:K:57:LEU:N	12:K:76:GLN:O	2.39	0.50
4:A:82:GLY:HA3	4:A:241:VAL:HG22	1.92	0.50
4:A:353:ILE:HD12	4:A:470:LEU:HD21	1.94	0.50
4:A:1399:ARG:NH2	4:A:1417:GLU:OE1	2.24	0.50
5:B:36:ALA:HA	5:B:39:ARG:HD3	1.94	0.50
5:B:400:HIS:HB3	5:B:403:LYS:HG2	1.94	0.50
5:B:806:THR:HG23	5:B:1045:SER:HA	1.94	0.50
7:E:96:PHE:O	7:E:99:HIS:CD2	2.64	0.50
3:N:3:DA:H2"	3:N:4:DG:C8	2.47	0.50
4:A:420:ARG:O	4:A:424:ILE:HG23	2.11	0.50
4:A:709:THR:HG22	4:A:711:ARG:H	1.75	0.50
4:A:1213:GLY:HA2	4:A:1216:ILE:HD12	1.94	0.50
7:E:78:LEU:HD21	7:E:109:ILE:HD13	1.94	0.50
4:A:98:LYS:O	4:A:102:VAL:HG12	2.11	0.50
4:A:457:ALA:HB3	4:A:506:ALA:HA	1.93	0.50
4:A:960:ILE:HB	4:A:1025:ARG:HD3	1.93	0.50
5:B:681:TRP:CH2	5:B:690:VAL:HG11	2.47	0.50
6:C:41:ILE:HB	6:C:172:PRO:HG3	1.92	0.50
4:A:289:ILE:O	4:A:293:GLU:HG3	2.12	0.50
4:A:350:ARG:NH2	4:A:447:GLN:HG2	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:582:VAL:HG22	5:B:626:ILE:HB	1.93	0.50
5:B:635:ARG:NH2	5:B:742:GLU:OE2	2.44	0.50
5:B:846:ILE:O	5:B:852:ARG:NH2	2.41	0.50
7:E:16:PHE:CZ	7:E:37:LEU:HD11	2.41	0.50
4:A:896:ARG:HB3	4:A:897:TYR:HD1	1.75	0.50
5:B:121:ASN:HA	5:B:207:GLY:HA3	1.94	0.50
5:B:806:THR:HG23	5:B:1046:PRO:HD3	1.94	0.50
10:I:92:ARG:HD2	10:I:93:LYS:H	1.77	0.50
4:A:335:ARG:HD2	5:B:1202:LEU:HD22	1.94	0.49
4:A:668:ASP:O	4:A:741:ASN:ND2	2.45	0.49
4:A:1199:ARG:NH1	4:A:1234:GLU:HA	2.27	0.49
5:B:1099:VAL:O	5:B:1102:LYS:N	2.45	0.49
4:A:323:LYS:HD3	4:A:328:ARG:HG3	1.93	0.49
4:A:981:LEU:HG	4:A:1039:LYS:HA	1.94	0.49
4:A:1167:GLU:O	4:A:1170:ILE:HG12	2.12	0.49
5:B:1138:MET:HE2	5:B:1146:PHE:CD1	2.47	0.49
3:N:13:DA:H2"	3:N:14:DG:H8	1.76	0.49
4:A:70:CYS:SG	4:A:80:HIS:NE2	2.85	0.49
4:A:981:LEU:HD13	4:A:986:ILE:HG12	1.94	0.49
4:A:1225:PHE:HE2	4:A:1227:ILE:HD11	1.78	0.49
5:B:174:LEU:HD11	5:B:204:ILE:HD12	1.94	0.49
7:E:19:VAL:O	7:E:23:VAL:HG22	2.12	0.49
4:A:1295:THR:HB	4:A:1297:GLU:OE1	2.13	0.49
5:B:406:LEU:HD21	5:B:498:THR:HB	1.95	0.49
7:E:77:SER:HB2	7:E:105:PHE:CD1	2.47	0.49
5:B:287:ARG:HG2	5:B:292:ILE:HA	1.93	0.49
6:C:62:PHE:O	6:C:66:ARG:HG3	2.12	0.49
4:A:80:HIS:HE1	5:B:1172:ILE:HG13	1.78	0.49
4:A:153:PRO:HA	4:A:161:LEU:HB2	1.95	0.49
4:A:208:LEU:O	4:A:212:LYS:HB2	2.12	0.49
4:A:367:PRO:HD2	4:A:370:ILE:HD12	1.95	0.49
4:A:1130:GLN:O	4:A:1134:ILE:HG12	2.13	0.49
5:B:63:ILE:O	5:B:67:SER:OG	2.27	0.49
5:B:638:PHE:HB2	5:B:741:CYS:O	2.12	0.49
7:E:42:PHE:CE1	7:E:46:TYR:HD2	2.31	0.49
2:T:20:DC:OP2	4:A:337:ARG:NH1	2.45	0.49
4:A:779:PHE:CE2	4:A:785:PRO:HD3	2.48	0.49
5:B:100:PRO:O	5:B:180:TYR:OH	2.26	0.49
5:B:597:MET:HE2	5:B:617:ARG:HB2	1.93	0.49
5:B:635:ARG:NH2	5:B:742:GLU:OE1	2.44	0.49
4:A:82:GLY:CA	4:A:241:VAL:HG22	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:392:VAL:HG13	4:A:415:LEU:HD11	1.95	0.49
4:A:590:ARG:NH1	4:A:592:ASP:OD2	2.39	0.49
4:A:1104:ILE:HG12	4:A:1332:PHE:HZ	1.77	0.49
4:A:803:SER:HB3	4:A:806:ARG:HG3	1.94	0.49
7:E:46:TYR:HE1	7:E:54:GLN:O	1.95	0.49
7:E:197:LYS:HG3	7:E:211:TYR:CE2	2.48	0.49
9:H:8:ASP:HB3	9:H:10:PHE:CE1	2.48	0.49
10:I:80:SER:OG	10:I:103:CYS:SG	2.71	0.49
12:K:107:THR:O	12:K:111:LEU:HG	2.13	0.49
4:A:43:GLU:HG2	4:A:44:THR:HG23	1.94	0.49
4:A:768:GLN:HG2	4:A:816:HIS:HA	1.94	0.49
7:E:171:LYS:HB2	7:E:174:GLN:HG3	1.95	0.49
4:A:182:VAL:HG12	4:A:201:VAL:HG22	1.95	0.48
5:B:370:PHE:CD2	5:B:373:ARG:HD3	2.48	0.48
5:B:976:ILE:HA	5:B:990:ILE:HB	1.94	0.48
7:E:90:VAL:HG22	7:E:119:SER:HB2	1.95	0.48
4:A:19:PHE:O	4:A:1416:ALA:HA	2.13	0.48
6:C:143:LEU:HD21	6:C:146:LYS:HE2	1.94	0.48
9:H:39:THR:HB	9:H:124:ARG:HG2	1.93	0.48
13:L:61:THR:HG22	13:L:63:ARG:H	1.78	0.48
4:A:265:LYS:O	4:A:269:ILE:HG13	2.14	0.48
4:A:939:ASP:O	4:A:943:LEU:HG	2.13	0.48
4:A:941:LYS:O	4:A:945:GLU:HG3	2.12	0.48
5:B:757:PRO:HG3	5:B:983:ARG:CZ	2.43	0.48
6:C:167:HIS:ND1	6:C:169:LYS:HG2	2.28	0.48
4:A:96:ILE:HG21	4:A:176:LYS:HE3	1.95	0.48
4:A:469:ARG:NH2	5:B:833:TYR:HE1	2.11	0.48
4:A:1264:GLU:HA	4:A:1267:MET:HE2	1.96	0.48
4:A:1398:MET:O	4:A:1401:SER:OG	2.30	0.48
5:B:199:MET:SD	5:B:199:MET:N	2.84	0.48
5:B:780:VAL:HA	5:B:795:ILE:HG12	1.96	0.48
6:C:105:GLY:O	6:C:149:LYS:HA	2.14	0.48
2:T:8:DT:H1'	2:T:9:DC:H5'	1.94	0.48
4:A:91:PHE:CZ	4:A:207:ILE:HD12	2.48	0.48
4:A:170:THR:HG23	4:A:185:TRP:HE1	1.78	0.48
5:B:806:THR:H	5:B:809:MET:HE3	1.78	0.48
11:J:36:LEU:HD11	11:J:51:LEU:CD1	2.43	0.48
1:R:9:G:O2'	4:A:485:ASP:OD1	2.28	0.48
4:A:362:ASP:N	4:A:362:ASP:OD1	2.44	0.48
5:B:25:ILE:HD11	5:B:651:LEU:HD22	1.95	0.48
6:C:40:GLU:OE1	6:C:254:LYS:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:168:TYR:HB3	7:E:170:LEU:HG	1.95	0.48
4:A:767:GLN:HA	4:A:799:PHE:HA	1.96	0.48
4:A:868:TYR:HD2	4:A:1058:VAL:HG11	1.79	0.48
5:B:828:ALA:O	5:B:834:ASN:ND2	2.47	0.48
6:C:115:SER:OG	6:C:141:GLY:HA3	2.14	0.48
5:B:703:ILE:HG21	5:B:742:GLU:HG2	1.95	0.48
4:A:913:LEU:HG	4:A:915:SER:H	1.78	0.48
5:B:202:TYR:HB3	5:B:211:VAL:HG22	1.95	0.48
5:B:656:GLY:O	5:B:660:LYS:HG3	2.14	0.48
6:C:11:ARG:NH2	6:C:19:ASP:OD1	2.47	0.48
7:E:8:ASN:O	7:E:12:LEU:HD23	2.14	0.48
7:E:32:GLN:O	7:E:35:VAL:HG12	2.14	0.48
4:A:1111:MET:HB2	4:A:1114:PRO:HG3	1.96	0.47
4:A:1115:SER:HA	4:A:1308:THR:O	2.14	0.47
5:B:72:GLU:HA	5:B:87:LYS:HA	1.96	0.47
8:F:147:SER:OG	8:F:150:GLU:HG3	2.14	0.47
4:A:827:THR:O	4:A:831:THR:HG23	2.14	0.47
4:A:1150:SER:OG	10:I:46:HIS:HB3	2.14	0.47
5:B:420:LEU:HD13	5:B:453:ILE:HA	1.95	0.47
5:B:915:THR:HB	5:B:934:LYS:HB3	1.96	0.47
4:A:58:LEU:HD12	4:A:244:PRO:HD2	1.96	0.47
4:A:91:PHE:HZ	4:A:207:ILE:HD12	1.80	0.47
9:H:101:ALA:HB2	9:H:116:TYR:CE1	2.50	0.47
12:K:21:ILE:HG13	12:K:33:ILE:HG23	1.94	0.47
4:A:99:ILE:HD13	4:A:234:MET:HE3	1.95	0.47
4:A:123:ARG:HA	4:A:126:LEU:HD12	1.95	0.47
4:A:774:ARG:H	4:A:774:ARG:HG3	1.53	0.47
4:A:956:LEU:HD22	4:A:957:PRO:HD2	1.95	0.47
4:A:1114:PRO:HA	4:A:1330:ASN:HD21	1.79	0.47
5:B:879:ARG:HA	5:B:885:MET:SD	2.54	0.47
7:E:13:TRP:HA	7:E:16:PHE:CE2	2.50	0.47
11:J:48:ARG:HG3	11:J:49:MET:N	2.29	0.47
4:A:340:LEU:HD13	4:A:1429:ILE:HG13	1.96	0.47
4:A:396:PRO:HG3	4:A:416:ARG:HG3	1.95	0.47
5:B:653:VAL:HG22	5:B:689:LEU:HB3	1.96	0.47
6:C:146:LYS:HB2	11:J:57:ILE:HG12	1.96	0.47
8:F:97:ARG:O	8:F:100:GLN:HG2	2.15	0.47
4:A:845:LEU:HD22	4:A:1374:VAL:HG21	1.96	0.47
4:A:1151:GLU:HB3	4:A:1153:TYR:HE1	1.78	0.47
5:B:104:GLU:CD	5:B:120:ARG:HH22	2.23	0.47
9:H:10:PHE:CE1	9:H:57:VAL:HB	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:313:GLN:HG2	4:A:321:PRO:HB3	1.95	0.47
4:A:324:SER:HB2	4:A:327:ALA:H	1.78	0.47
4:A:517:ASN:HD22	4:A:1364:ASN:ND2	2.12	0.47
4:A:744:LYS:O	4:A:748:MET:HG3	2.15	0.47
4:A:840:ARG:HB3	4:A:1384:VAL:HG12	1.96	0.47
5:B:322:PHE:CZ	10:I:30:ARG:HB2	2.49	0.47
5:B:1001:PHE:HE2	6:C:178:PHE:HB3	1.80	0.47
10:I:78:CYS:HB3	10:I:106:CYS:HB3	1.66	0.47
4:A:17:VAL:HG23	4:A:1421:CYS:SG	2.55	0.47
5:B:349:ILE:HD12	5:B:349:ILE:H	1.79	0.47
5:B:682:SER:O	5:B:686:ASN:ND2	2.47	0.47
7:E:20:LYS:HZ2	7:E:35:VAL:HA	1.79	0.47
11:J:36:LEU:HD11	11:J:51:LEU:HD11	1.96	0.47
4:A:153:PRO:HG3	4:A:161:LEU:HD12	1.97	0.47
4:A:315:LEU:HA	4:A:321:PRO:HA	1.97	0.47
4:A:635:ARG:HA	4:A:635:ARG:NE	2.28	0.47
5:B:289:LEU:HD13	5:B:375:ALA:HB2	1.97	0.47
8:F:124:GLU:HB3	8:F:130:ILE:CG1	2.45	0.47
9:H:112:ILE:HG22	9:H:127:GLY:O	2.15	0.47
4:A:1035:TYR:HD1	4:A:1037:LEU:HD13	1.80	0.47
5:B:526:GLU:HG3	5:B:771:SER:HB3	1.96	0.47
5:B:757:PRO:HD3	5:B:983:ARG:HB3	1.96	0.47
5:B:1039:GLY:O	11:J:32:GLU:HB2	2.14	0.47
5:B:1180:PHE:HB2	5:B:1191:ILE:HD13	1.96	0.47
6:C:254:LYS:O	6:C:257:SER:OG	2.28	0.47
7:E:101:GLN:HB2	7:E:127:ILE:HD13	1.97	0.47
4:A:80:HIS:CE1	5:B:1172:ILE:HG13	2.50	0.46
4:A:147:VAL:HG23	4:A:169:ASN:C	2.41	0.46
4:A:406:ILE:HB	4:A:431:LYS:HB2	1.96	0.46
5:B:640:VAL:HG11	5:B:710:LEU:HD22	1.97	0.46
5:B:954:VAL:HG21	13:L:29:TYR:HE2	1.80	0.46
6:C:148:ARG:HH22	11:J:64:ASN:HA	1.80	0.46
7:E:124:VAL:N	7:E:125:PRO:HD2	2.30	0.46
13:L:38:LEU:HD11	13:L:48:CYS:HB2	1.96	0.46
4:A:298:PHE:HE2	4:A:312:PRO:HB2	1.81	0.46
4:A:678:GLU:HG2	4:A:732:LEU:HD21	1.97	0.46
4:A:1427:ASN:HA	4:A:1430:LEU:HB2	1.96	0.46
3:N:14:DG:H2"	3:N:15:DA:H8	1.80	0.46
4:A:814:PHE:HB2	5:B:519:TRP:HZ3	1.81	0.46
4:A:1155:ASP:OD2	4:A:1241:ARG:NH2	2.47	0.46
4:A:1161:THR:OG1	4:A:1239:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:177:GLU:HB2	6:C:231:ASN:HB3	1.97	0.46
6:C:219:PHE:HD2	9:H:45:GLU:HG2	1.81	0.46
7:E:20:LYS:O	7:E:24:LYS:HG2	2.16	0.46
7:E:155:ARG:NH1	7:E:194:GLU:OE2	2.44	0.46
4:A:579:SER:HB3	4:A:611:GLN:HA	1.96	0.46
4:A:1197:LEU:HD11	4:A:1238:ILE:HG13	1.96	0.46
5:B:313:MET:HE2	5:B:313:MET:HB3	1.76	0.46
5:B:848:ARG:HD2	11:J:8:PHE:HA	1.97	0.46
7:E:94:LYS:HA	7:E:97:VAL:HG22	1.96	0.46
4:A:172:PRO:HB3	4:A:185:TRP:HB2	1.98	0.46
4:A:1161:THR:HG21	4:A:1166:ASP:HB2	1.98	0.46
5:B:600:LEU:HB3	5:B:615:MET:SD	2.55	0.46
5:B:995:ARG:HB3	5:B:997:GLU:OE1	2.16	0.46
5:B:1041:GLU:HG2	5:B:1042:GLY:H	1.80	0.46
6:C:81:GLU:HG2	6:C:86:CYS:HB2	1.97	0.46
6:C:214:ASN:HB3	6:C:217:ASP:OD2	2.16	0.46
4:A:1117:THR:CG2	4:A:1328:TYR:HB3	2.46	0.46
5:B:193:LYS:HZ3	11:J:65:PRO:HG2	1.81	0.46
5:B:351:TYR:CZ	5:B:355:ILE:HD11	2.50	0.46
5:B:420:LEU:HB3	5:B:453:ILE:HG12	1.98	0.46
5:B:773:MET:HE2	5:B:985:GLY:HA2	1.98	0.46
5:B:1006:ILE:HG12	11:J:45:CYS:SG	2.56	0.46
5:B:1014:PRO:O	5:B:1018:PRO:HD3	2.15	0.46
5:B:1053:GLU:O	5:B:1057:LYS:HG3	2.14	0.46
7:E:91:LYS:HA	7:E:94:LYS:NZ	2.30	0.46
4:A:518:LYS:HD2	4:A:519:PRO:O	2.15	0.46
6:C:251:LEU:O	6:C:255:VAL:HG23	2.15	0.46
4:A:591:PHE:HA	4:A:595:THR:HG21	1.97	0.46
4:A:880:LYS:HD3	4:A:953:ASN:HB3	1.98	0.46
4:A:1165:GLU:OE2	4:A:1235:LYS:NZ	2.33	0.46
5:B:736:THR:OG1	5:B:737:THR:N	2.49	0.46
5:B:813:LYS:HA	5:B:813:LYS:HD3	1.67	0.46
10:I:8:ARG:HG3	10:I:9:ASP:H	1.81	0.46
13:L:56:LEU:HD23	13:L:56:LEU:HA	1.83	0.46
4:A:351:THR:HG22	4:A:352:VAL:O	2.16	0.46
4:A:443:LEU:HD12	4:A:501:LEU:HD11	1.98	0.46
4:A:514:PRO:HB2	4:A:1067:LEU:HD21	1.97	0.46
4:A:650:GLN:O	4:A:654:ASN:ND2	2.49	0.46
5:B:831:SER:OG	5:B:833:TYR:HD2	1.99	0.46
5:B:1060:ARG:HD2	5:B:1060:ARG:HA	1.70	0.46
9:H:6:PHE:CZ	9:H:8:ASP:HB2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:103:CYS:HB3	10:I:106:CYS:SG	2.56	0.46
4:A:1113:THR:O	4:A:1330:ASN:ND2	2.48	0.46
4:A:1386:ARG:HD2	4:A:1404:GLU:HG3	1.97	0.46
5:B:345:LYS:O	5:B:349:ILE:HD12	2.16	0.46
4:A:1373:ASP:O	4:A:1377:THR:HG23	2.17	0.45
5:B:293:PRO:O	5:B:297:ILE:HG13	2.17	0.45
5:B:333:PHE:O	5:B:334:ILE:HD13	2.16	0.45
5:B:851:PHE:HB3	5:B:1094:ARG:HD2	1.97	0.45
7:E:96:PHE:CD2	7:E:99:HIS:NE2	2.64	0.45
2:T:6:DT:H2''	2:T:7:DC:C5	2.51	0.45
3:N:9:DA:H2''	3:N:10:DG:N7	2.32	0.45
4:A:72:GLU:HB3	4:A:76:GLU:CB	2.46	0.45
4:A:344:ARG:HD3	5:B:1127:GLY:O	2.16	0.45
6:C:101:LEU:HB2	6:C:118:LEU:HD23	1.99	0.45
7:E:56:LYS:NZ	7:E:85:GLU:OE1	2.47	0.45
9:H:127:GLY:HA3	9:H:130:ARG:HH12	1.80	0.45
3:N:9:DA:H2''	3:N:10:DG:C8	2.51	0.45
4:A:19:PHE:HA	5:B:1213:THR:O	2.15	0.45
5:B:47:GLN:NE2	5:B:201:GLY:O	2.49	0.45
12:K:18:LYS:HG3	12:K:19:LEU:HD12	1.97	0.45
4:A:873:MET:C	4:A:1058:VAL:HG13	2.41	0.45
4:A:999:VAL:HG12	4:A:1000:LEU:HD12	1.99	0.45
5:B:223:VAL:HG11	5:B:380:TYR:HE2	1.82	0.45
5:B:466:TRP:HE1	5:B:479:VAL:HG11	1.81	0.45
6:C:94:LYS:HA	6:C:127:ARG:NH2	2.23	0.45
7:E:14:ARG:NH2	7:E:141:VAL:HG12	2.31	0.45
9:H:93:TYR:CD2	9:H:145:ARG:HB2	2.51	0.45
4:A:279:LEU:HD22	4:A:285:PRO:HD3	1.97	0.45
4:A:563:PRO:HG2	4:A:566:ILE:HG12	1.99	0.45
5:B:941:LEU:HD23	5:B:942:ARG:N	2.31	0.45
5:B:1057:LYS:O	5:B:1061:GLU:HG3	2.17	0.45
10:I:77:LYS:HD3	10:I:108:HIS:CG	2.51	0.45
10:I:106:CYS:SG	10:I:108:HIS:HB3	2.55	0.45
4:A:452:LYS:HG3	4:A:453:MET:SD	2.56	0.45
4:A:1220:PHE:CE1	4:A:1224:LEU:HD22	2.51	0.45
4:A:1281:ARG:NH2	4:A:1309:ASP:OD1	2.48	0.45
5:B:574:SER:HA	5:B:591:ARG:HH21	1.80	0.45
7:E:85:GLU:H	7:E:85:GLU:CD	2.25	0.45
9:H:107:VAL:HB	9:H:111:LEU:HD22	1.97	0.45
4:A:55:ASP:HA	4:A:58:LEU:CB	2.44	0.45
4:A:208:LEU:HD12	4:A:235:ILE:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:598:LEU:O	9:H:122:LEU:HD12	2.17	0.45
7:E:91:LYS:HA	7:E:94:LYS:HZ2	1.81	0.45
11:J:35:ALA:O	11:J:39:LEU:HD23	2.17	0.45
12:K:12:LEU:HD21	12:K:18:LYS:HE2	1.98	0.45
4:A:26:GLU:O	4:A:30:ILE:HG12	2.17	0.45
4:A:108:MET:HE3	4:A:185:TRP:CH2	2.52	0.45
4:A:115:LEU:C	4:A:122:MET:HG2	2.42	0.45
4:A:782:ARG:NH1	4:A:785:PRO:O	2.49	0.45
7:E:29:PHE:C	7:E:30:ILE:HD12	2.42	0.45
4:A:1148:ILE:HD11	4:A:1198:ASP:HA	1.99	0.45
5:B:549:THR:HB	5:B:628:THR:HB	1.99	0.45
6:C:265:MET:HE1	12:K:21:ILE:HD12	1.99	0.45
11:J:21:TYR:CZ	11:J:25:LEU:HD11	2.52	0.45
4:A:81:PHE:CD2	4:A:240:PRO:HB2	2.52	0.45
5:B:216:GLU:HB3	5:B:500:THR:HG23	1.99	0.45
6:C:142:VAL:HG11	11:J:5:VAL:HG13	1.99	0.45
6:C:255:VAL:CG1	12:K:91:CYS:HB3	2.47	0.45
6:C:259:LEU:O	6:C:263:THR:HG23	2.17	0.45
8:F:111:LEU:HD12	8:F:114:GLU:O	2.17	0.45
4:A:483:ASP:OD1	4:A:483:ASP:N	2.49	0.44
5:B:1002:THR:HG23	5:B:1004:GLU:H	1.82	0.44
8:F:74:ILE:H	8:F:74:ILE:HD12	1.82	0.44
4:A:662:PHE:HB3	5:B:829:CYS:SG	2.57	0.44
4:A:898:ARG:HB2	4:A:933:TYR:CE1	2.51	0.44
5:B:901:PRO:HA	5:B:949:VAL:HB	1.98	0.44
6:C:123:ASN:OD1	6:C:125:MET:HG3	2.17	0.44
9:H:11:GLN:OE1	9:H:12:VAL:N	2.50	0.44
10:I:69:PRO:HB2	10:I:85:PHE:CE2	2.52	0.44
5:B:48:LEU:HD23	5:B:173:MET:SD	2.57	0.44
5:B:193:LYS:HB3	5:B:787:VAL:HG11	1.98	0.44
8:F:128:LYS:HE3	8:F:128:LYS:HB3	1.79	0.44
11:J:4:PRO:O	11:J:14:VAL:HG23	2.17	0.44
4:A:457:ALA:O	4:A:507:VAL:HG23	2.17	0.44
4:A:806:ARG:HH11	5:B:729:ILE:HD11	1.82	0.44
4:A:899:VAL:HG11	4:A:908:LEU:HD12	1.98	0.44
5:B:1106:ARG:CZ	5:B:1118:PRO:HB3	2.46	0.44
5:B:1163:CYS:O	5:B:1167:GLY:N	2.48	0.44
7:E:46:TYR:CD1	7:E:58:MET:HE3	2.52	0.44
12:K:81:TYR:CE2	12:K:86:ALA:HB2	2.52	0.44
4:A:57:ARG:C	4:A:68:GLN:HB3	2.41	0.44
4:A:71:GLN:O	4:A:71:GLN:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:298:PHE:O	4:A:302:THR:HG22	2.17	0.44
4:A:738:LYS:HB2	4:A:740:LEU:HG	1.99	0.44
5:B:437:GLU:CD	5:B:437:GLU:H	2.25	0.44
5:B:763:GLN:HG2	5:B:766:ARG:HG2	2.00	0.44
7:E:6:GLU:HA	7:E:9:ILE:HD13	1.99	0.44
8:F:111:LEU:HD23	8:F:111:LEU:H	1.82	0.44
4:A:368:LYS:HE2	4:A:368:LYS:HB2	1.77	0.44
4:A:461:LYS:HD2	4:A:461:LYS:HA	1.67	0.44
5:B:313:MET:O	5:B:316:PRO:HD2	2.17	0.44
5:B:619:ILE:HD12	10:I:65:ASP:HB2	1.98	0.44
5:B:638:PHE:O	5:B:740:HIS:HB3	2.18	0.44
9:H:6:PHE:HD1	9:H:129:TYR:HE2	1.65	0.44
11:J:58:GLU:O	11:J:62:ARG:HG2	2.17	0.44
4:A:305:ASP:CG	4:A:326:ARG:HH11	2.25	0.44
4:A:1351:GLU:O	4:A:1355:VAL:HG23	2.17	0.44
5:B:21:GLU:O	5:B:654:ARG:HB3	2.17	0.44
5:B:117:ALA:HA	5:B:122:LEU:HB2	2.00	0.44
5:B:798:TYR:CD2	11:J:4:PRO:HG3	2.52	0.44
6:C:162:GLY:HA3	6:C:170:TRP:CD2	2.53	0.44
9:H:8:ASP:OD1	9:H:9:ILE:N	2.47	0.44
4:A:89:PRO:HD2	4:A:205:GLU:HG2	2.00	0.44
4:A:497:THR:HG23	5:B:1146:PHE:HB2	1.98	0.44
4:A:1336:MET:HG3	4:A:1341:ILE:HD12	1.99	0.44
5:B:760:ASP:OD1	5:B:760:ASP:N	2.50	0.44
9:H:104:PHE:HE2	9:H:134:ASN:O	2.01	0.44
4:A:279:LEU:HD13	4:A:289:ILE:HG22	2.00	0.44
4:A:344:ARG:O	5:B:1155:SER:HB2	2.18	0.44
4:A:22:PHE:CD2	4:A:27:VAL:HG23	2.53	0.43
4:A:82:GLY:O	4:A:240:PRO:HA	2.18	0.43
4:A:407:ARG:HD2	4:A:413:ILE:HD11	1.99	0.43
4:A:529:CYS:O	4:A:533:LYS:HG3	2.17	0.43
5:B:845:SER:HB3	11:J:8:PHE:HB3	1.99	0.43
10:I:69:PRO:HB2	10:I:85:PHE:CZ	2.53	0.43
13:L:51:CYS:SG	13:L:52:GLY:N	2.90	0.43
4:A:662:PHE:CE2	4:A:746:MET:HE2	2.54	0.43
4:A:1021:LEU:O	4:A:1024:SER:OG	2.30	0.43
7:E:65:THR:O	7:E:69:ILE:HG23	2.18	0.43
9:H:38:LEU:HD13	9:H:125:LEU:HD13	2.00	0.43
11:J:45:CYS:O	11:J:48:ARG:HG2	2.18	0.43
2:T:3:DT:H6	2:T:3:DT:H2'	1.66	0.43
4:A:54:ASN:C	4:A:56:PRO:HD3	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:270:LEU:HD23	4:A:274:ILE:HD13	2.00	0.43
4:A:508:PRO:HA	4:A:511:ILE:HG13	1.99	0.43
4:A:885:THR:HG23	4:A:1024:SER:HB3	2.00	0.43
4:A:901:LEU:HD13	4:A:919:ILE:HG12	2.01	0.43
5:B:1006:ILE:HD13	11:J:44:TYR:CZ	2.54	0.43
6:C:35:ARG:NH1	12:K:41:THR:OG1	2.40	0.43
7:E:26:ARG:O	7:E:75:MET:HE1	2.18	0.43
11:J:49:MET:HE3	11:J:49:MET:HB3	1.92	0.43
12:K:18:LYS:HG3	12:K:19:LEU:CD1	2.48	0.43
2:T:10:DT:H1'	2:T:11:DC:H5'	2.01	0.43
4:A:34:LYS:HE2	4:A:83:HIS:NE2	2.33	0.43
4:A:490:HIS:HB3	5:B:1150:ARG:HH21	1.83	0.43
4:A:1436:ILE:HD13	5:B:1139:ILE:HG23	2.00	0.43
4:A:215:SER:O	4:A:218:ASP:HB2	2.17	0.43
4:A:298:PHE:CE2	4:A:312:PRO:HB2	2.52	0.43
4:A:990:VAL:O	4:A:994:GLN:HG3	2.17	0.43
4:A:1155:ASP:HB2	4:A:1162:VAL:HG22	2.00	0.43
5:B:219:ALA:O	5:B:241:ARG:NH1	2.52	0.43
5:B:308:TRP:HA	5:B:311:LEU:HD12	2.01	0.43
6:C:77:ILE:HD12	6:C:77:ILE:HA	1.93	0.43
8:F:82:THR:O	8:F:136:ARG:NH2	2.52	0.43
12:K:12:LEU:HD12	12:K:12:LEU:H	1.84	0.43
12:K:60:ALA:O	12:K:73:LEU:HA	2.17	0.43
3:N:7:DA:OP1	4:A:101:LYS:NZ	2.46	0.43
4:A:174:ILE:HD11	4:A:181:LEU:HB3	2.01	0.43
4:A:356:ASP:OD2	12:K:65:HIS:NE2	2.51	0.43
4:A:746:MET:HB3	4:A:752:LYS:O	2.18	0.43
4:A:830:LYS:HA	4:A:830:LYS:HD3	1.82	0.43
4:A:1427:ASN:O	4:A:1431:GLY:N	2.52	0.43
5:B:483:LEU:HD23	5:B:484:ASN:N	2.33	0.43
7:E:170:LEU:HD13	7:E:175:LEU:HD22	2.01	0.43
4:A:661:GLY:HA3	5:B:1081:LEU:HD22	2.01	0.43
5:B:1188:LYS:H	5:B:1188:LYS:HD2	1.83	0.43
4:A:90:VAL:HG13	4:A:297:GLN:HG3	2.01	0.43
4:A:274:ILE:O	4:A:278:THR:HG23	2.19	0.43
4:A:326:ARG:HG3	4:A:1406:VAL:HG11	2.01	0.43
4:A:353:ILE:HG21	4:A:487:MET:HG3	2.01	0.43
4:A:1076:ALA:HA	4:A:1079:MET:HG3	2.01	0.43
5:B:544:CYS:HB2	5:B:634:TYR:CZ	2.54	0.43
5:B:788:ARG:NH1	5:B:790:ASP:OD1	2.52	0.43
5:B:815:ARG:O	11:J:54:VAL:HG21	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:1106:ARG:NH1	5:B:1118:PRO:HB3	2.34	0.43
9:H:133:ASN:OD1	9:H:133:ASN:N	2.52	0.43
4:A:464:PRO:HB2	12:K:4:PRO:HD3	2.00	0.43
4:A:688:LYS:HE2	4:A:688:LYS:HB2	1.71	0.43
4:A:898:ARG:O	4:A:1029:ARG:NH1	2.52	0.43
5:B:173:MET:HB2	5:B:203:PHE:CE1	2.45	0.43
6:C:44:LEU:HB2	6:C:77:ILE:HD13	2.00	0.43
6:C:204:SER:O	6:C:207:CYS:HB2	2.19	0.43
7:E:56:LYS:HB2	7:E:57:MET:HE2	2.00	0.43
8:F:109:VAL:HG12	8:F:124:GLU:HG3	2.01	0.43
4:A:490:HIS:HB3	5:B:1150:ARG:HE	1.84	0.43
4:A:987:VAL:O	4:A:991:LYS:HG3	2.19	0.43
5:B:34:ILE:HD13	5:B:747:MET:HE3	2.00	0.43
5:B:984:HIS:NE2	5:B:1028:GLU:OE2	2.40	0.43
6:C:66:ARG:O	6:C:70:ILE:HG12	2.19	0.43
7:E:96:PHE:CA	7:E:99:HIS:CD2	2.91	0.43
4:A:51:GLY:C	4:A:56:PRO:HB3	2.43	0.42
4:A:884:ASP:HB3	4:A:896:ARG:HH22	1.83	0.42
4:A:1329:THR:HG22	4:A:1331:SER:H	1.83	0.42
5:B:466:TRP:CE3	5:B:466:TRP:HA	2.54	0.42
5:B:975:GLN:O	5:B:990:ILE:HD12	2.18	0.42
4:A:533:LYS:HB3	4:A:533:LYS:HE2	1.83	0.42
4:A:902:LEU:HD11	4:A:926:GLN:HG2	2.01	0.42
4:A:1220:PHE:HE1	4:A:1224:LEU:HD22	1.83	0.42
5:B:251:ILE:H	5:B:251:ILE:HD12	1.83	0.42
5:B:500:THR:OG1	5:B:537:LYS:NZ	2.51	0.42
7:E:90:VAL:CG2	7:E:119:SER:HB2	2.49	0.42
9:H:6:PHE:CE2	9:H:125:LEU:HD21	2.54	0.42
3:N:7:DA:H2"	3:N:8:DG:C8	2.54	0.42
4:A:662:PHE:O	5:B:828:ALA:HA	2.19	0.42
4:A:915:SER:O	4:A:919:ILE:HB	2.18	0.42
4:A:1209:MET:HE2	4:A:1236:LEU:HD22	2.01	0.42
5:B:175:ARG:HG3	5:B:200:GLY:HA3	2.02	0.42
5:B:857:ARG:HH11	5:B:945:GLU:CD	2.27	0.42
5:B:886:LYS:HG2	5:B:936:ASP:OD2	2.20	0.42
10:I:68:LEU:HA	10:I:69:PRO:HD3	1.88	0.42
4:A:289:ILE:HG13	4:A:290:GLU:N	2.35	0.42
4:A:630:ILE:HG23	4:A:642:CYS:SG	2.59	0.42
5:B:33:VAL:HG12	5:B:681:TRP:HZ3	1.83	0.42
5:B:616:ILE:HG12	5:B:697:GLU:HA	2.00	0.42
6:C:24:ASN:O	6:C:24:ASN:ND2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:89:PRO:HG3	4:A:237:THR:HG22	2.01	0.42
4:A:1325:THR:HA	7:E:147:HIS:HA	2.00	0.42
4:A:1345:ARG:NH1	4:A:1373:ASP:OD1	2.53	0.42
7:E:112:TYR:CD1	7:E:116:ILE:HD11	2.54	0.42
10:I:108:HIS:CE1	10:I:110:PHE:HB3	2.55	0.42
13:L:55:ILE:HD12	13:L:55:ILE:O	2.20	0.42
4:A:492:PRO:HB3	4:A:497:THR:HG22	2.02	0.42
4:A:1441:PHE:CZ	8:F:89:GLU:HA	2.55	0.42
5:B:67:SER:HB2	5:B:92:PHE:CD1	2.54	0.42
4:A:777:PHE:HB3	4:A:782:ARG:H	1.83	0.42
4:A:1371:LEU:O	4:A:1375:MET:HG3	2.20	0.42
5:B:112:LEU:HD13	5:B:122:LEU:HD12	2.01	0.42
6:C:76:ASP:C	6:C:129:ILE:HD11	2.44	0.42
8:F:131:PRO:O	8:F:132:LEU:HG	2.20	0.42
10:I:86:PHE:CE2	10:I:89:GLN:HG2	2.53	0.42
4:A:70:CYS:SG	4:A:80:HIS:CE1	3.12	0.42
4:A:770:VAL:HA	4:A:822:GLU:OE2	2.20	0.42
4:A:999:VAL:HG23	4:A:1053:PHE:HZ	1.85	0.42
5:B:69:LEU:HD13	5:B:69:LEU:HA	1.92	0.42
5:B:370:PHE:O	5:B:374:LYS:HG3	2.20	0.42
5:B:518:HIS:HB3	5:B:522:VAL:CG2	2.49	0.42
6:C:44:LEU:HB2	6:C:77:ILE:CD1	2.50	0.42
7:E:7:ARG:HG3	7:E:8:ASN:N	2.34	0.42
11:J:44:TYR:HA	11:J:47:ARG:HB2	2.01	0.42
2:T:20:DC:OP2	4:A:332:LYS:NZ	2.47	0.42
4:A:472:LEU:HD11	5:B:835:GLN:HE22	1.85	0.42
5:B:839:MET:HE3	5:B:988:GLY:HA3	2.00	0.42
6:C:255:VAL:O	6:C:259:LEU:HD12	2.19	0.42
4:A:51:GLY:HA2	4:A:56:PRO:HB3	2.02	0.42
4:A:513:SER:OG	4:A:518:LYS:O	2.38	0.42
4:A:820:GLY:O	4:A:824:LEU:HG	2.19	0.42
5:B:429:PHE:O	5:B:433:GLN:HG3	2.20	0.42
5:B:466:TRP:NE1	5:B:479:VAL:HG11	2.35	0.42
6:C:98:VAL:H	6:C:122:SER:CB	2.32	0.42
6:C:260:LEU:O	6:C:264:GLN:HG3	2.20	0.42
7:E:17:ARG:HA	7:E:20:LYS:HE2	2.02	0.42
10:I:55:THR:HG22	10:I:55:THR:O	2.19	0.42
4:A:780:VAL:HG12	4:A:789:LYS:HE3	2.01	0.41
4:A:814:PHE:CE1	5:B:514:LEU:HD21	2.55	0.41
4:A:973:ILE:HG21	4:A:1036:ARG:O	2.20	0.41
5:B:782:LEU:HB3	5:B:784:ASN:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:999:MET:CE	5:B:1008:PRO:HG2	2.50	0.41
6:C:254:LYS:HB3	6:C:254:LYS:HE3	1.87	0.41
4:A:67:CYS:O	4:A:68:GLN:HG3	2.20	0.41
4:A:1376:THR:HG22	7:E:212:ARG:HH12	1.84	0.41
5:B:118:ARG:HA	5:B:207:GLY:HA2	2.02	0.41
5:B:322:PHE:CE2	10:I:30:ARG:HB2	2.55	0.41
5:B:446:LEU:HB3	5:B:447:ALA:H	1.66	0.41
5:B:451:LYS:O	5:B:455:SER:HB3	2.21	0.41
6:C:186:LEU:HB3	6:C:188:HIS:CD2	2.56	0.41
9:H:101:ALA:HB2	9:H:116:TYR:CD1	2.55	0.41
4:A:597:LEU:HD23	4:A:597:LEU:HA	1.93	0.41
4:A:873:MET:SD	4:A:957:PRO:HG3	2.61	0.41
4:A:896:ARG:HB3	4:A:897:TYR:CD1	2.55	0.41
4:A:1276:VAL:HB	4:A:1279:ILE:HD13	2.01	0.41
5:B:193:LYS:NZ	11:J:65:PRO:HG2	2.35	0.41
5:B:424:LEU:HD12	5:B:424:LEU:HA	1.80	0.41
5:B:579:ARG:HB3	5:B:586:TRP:NE1	2.35	0.41
5:B:797:TYR:HB3	5:B:798:TYR:CD1	2.56	0.41
5:B:992:ILE:HG13	12:K:67:PHE:HE1	1.85	0.41
4:A:199:LEU:HD12	4:A:199:LEU:HA	1.91	0.41
4:A:674:PRO:O	4:A:677:ARG:HG2	2.21	0.41
4:A:874:ASP:O	4:A:878:ILE:HG13	2.19	0.41
5:B:230:ALA:O	5:B:261:ARG:NH2	2.53	0.41
5:B:286:PHE:CE1	5:B:375:ALA:HB1	2.55	0.41
5:B:599:THR:O	5:B:603:LEU:HG	2.20	0.41
10:I:17:ARG:NH1	10:I:18:GLU:O	2.53	0.41
13:L:40:LEU:HD23	13:L:40:LEU:H	1.85	0.41
4:A:482:PHE:HB2	5:B:836:GLU:O	2.20	0.41
4:A:881:GLN:OE1	4:A:961:ARG:NH1	2.53	0.41
5:B:112:LEU:HD21	5:B:117:ALA:HB2	2.02	0.41
5:B:211:VAL:HG21	5:B:483:LEU:HG	2.03	0.41
5:B:839:MET:HE2	5:B:839:MET:HB3	1.93	0.41
6:C:6:PRO:O	12:K:104:ASN:ND2	2.54	0.41
6:C:164:ALA:HA	6:C:167:HIS:O	2.20	0.41
10:I:59:VAL:HG12	10:I:60:GLN:N	2.36	0.41
4:A:259:GLU:HB3	4:A:264:PHE:CZ	2.55	0.41
4:A:666:ILE:O	4:A:670:ILE:HG13	2.21	0.41
4:A:910:PRO:HA	4:A:916:GLY:HA3	2.03	0.41
4:A:1370:LEU:O	4:A:1374:VAL:HG23	2.20	0.41
5:B:241:ARG:HG2	5:B:253:THR:HG22	2.03	0.41
5:B:856:PHE:HB3	5:B:967:ARG:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:999:MET:HE3	5:B:999:MET:HB3	1.78	0.41
7:E:170:LEU:HD23	7:E:170:LEU:HA	1.95	0.41
9:H:12:VAL:HG12	9:H:53:ASP:O	2.21	0.41
3:N:9:DA:H2"	3:N:10:DG:C5	2.55	0.41
4:A:451:HIS:HB3	4:A:453:MET:H	1.86	0.41
4:A:1236:LEU:HD23	4:A:1236:LEU:HA	1.89	0.41
4:A:1433:MET:HE1	8:F:92:ARG:HH21	1.84	0.41
5:B:71:LEU:O	5:B:87:LYS:HA	2.20	0.41
5:B:361:LEU:HD12	5:B:361:LEU:HA	1.95	0.41
5:B:487:THR:HG22	5:B:488:TYR:N	2.36	0.41
6:C:107:SER:OG	6:C:111:THR:OG1	2.38	0.41
7:E:29:PHE:HB2	7:E:65:THR:HG22	2.02	0.41
11:J:48:ARG:O	11:J:52:THR:OG1	2.21	0.41
3:N:11:DA:H2'	3:N:12:DG:C8	2.56	0.41
4:A:519:PRO:O	4:A:624:SER:HB2	2.21	0.41
5:B:288:ALA:HB1	5:B:331:LEU:HD23	2.03	0.41
5:B:486:TYR:CE2	5:B:778:MET:HG2	2.56	0.41
5:B:800:GLN:HB3	11:J:52:THR:HB	2.02	0.41
10:I:56:ALA:O	10:I:89:GLN:HG3	2.21	0.41
2:T:14:DG:C2	2:T:15:DC:C2	3.09	0.41
4:A:15:LYS:HG2	5:B:1218:THR:O	2.21	0.41
4:A:399:HIS:CD2	4:A:400:PRO:HA	2.56	0.41
4:A:525:GLN:NE2	5:B:836:GLU:OE2	2.54	0.41
4:A:761:MET:HE1	5:B:1018:PRO:HA	2.02	0.41
5:B:189:LEU:HD22	5:B:194:GLU:HB2	2.02	0.41
5:B:228:LYS:HD2	5:B:228:LYS:HA	1.87	0.41
5:B:229:ALA:O	5:B:261:ARG:NH2	2.53	0.41
5:B:309:GLN:HE22	10:I:50:THR:CG2	2.31	0.41
5:B:789:MET:HE3	5:B:965:LYS:HB3	2.03	0.41
7:E:67:GLU:H	7:E:67:GLU:CD	2.23	0.41
8:F:136:ARG:HD2	8:F:146:TRP:CD1	2.56	0.41
12:K:21:ILE:HG23	12:K:31:VAL:HG21	2.03	0.41
4:A:305:ASP:OD1	4:A:326:ARG:NH1	2.54	0.41
4:A:326:ARG:CD	4:A:1406:VAL:HG11	2.52	0.41
4:A:347:PHE:HA	5:B:1107:ALA:HA	2.02	0.41
4:A:455:MET:HE1	5:B:1130:PHE:CE1	2.56	0.41
4:A:586:ILE:HD13	4:A:586:ILE:HA	1.89	0.41
4:A:843:LYS:HD2	4:A:843:LYS:HA	1.65	0.41
5:B:736:THR:HG23	5:B:737:THR:HG23	2.02	0.41
6:C:137:LYS:H	6:C:137:LYS:HG2	1.57	0.41
8:F:133:VAL:HG21	8:F:145:ASP:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:19:ASP:HB3	10:I:24:ARG:HG3	2.03	0.41
12:K:108:GLU:O	12:K:112:GLN:HG2	2.21	0.41
4:A:11:LEU:HA	5:B:1193:GLN:O	2.20	0.40
4:A:601:LYS:HB2	4:A:603:ASN:CG	2.47	0.40
4:A:618:GLU:OE2	4:A:620:LYS:HB2	2.21	0.40
4:A:1341:ILE:HG13	4:A:1376:THR:HG23	2.03	0.40
5:B:261:ARG:HA	5:B:261:ARG:HD3	1.76	0.40
5:B:542:MET:SD	5:B:747:MET:HG3	2.61	0.40
5:B:563:MET:SD	5:B:588:GLY:HA3	2.61	0.40
6:C:91:HIS:HB2	6:C:96:SER:OG	2.21	0.40
6:C:194:GLU:H	6:C:200:GLU:CD	2.30	0.40
10:I:8:ARG:HG3	10:I:9:ASP:N	2.36	0.40
10:I:78:CYS:SG	10:I:79:HIS:N	2.94	0.40
4:A:919:ILE:HG13	4:A:925:LEU:HD12	2.03	0.40
4:A:923:LEU:O	4:A:927:VAL:HG13	2.21	0.40
4:A:1428:VAL:HG13	5:B:1151:LEU:HD23	2.02	0.40
6:C:39:ALA:HB1	6:C:165:LYS:HG3	2.03	0.40
6:C:148:ARG:HD3	11:J:61:LEU:O	2.21	0.40
7:E:13:TRP:HB2	7:E:42:PHE:CE2	2.55	0.40
7:E:77:SER:HG	7:E:106:GLN:H	1.69	0.40
7:E:151:PRO:HD2	7:E:153:HIS:HE1	1.86	0.40
10:I:91:ARG:HH11	10:I:95:THR:HG21	1.82	0.40
4:A:102:VAL:HG13	4:A:211:PHE:CZ	2.56	0.40
4:A:115:LEU:HB2	4:A:122:MET:HE3	2.02	0.40
4:A:182:VAL:HG12	4:A:201:VAL:HG13	2.02	0.40
4:A:549:MET:HE1	4:A:656:TRP:HD1	1.86	0.40
4:A:960:ILE:CB	4:A:1025:ARG:HD3	2.51	0.40
5:B:301:ILE:HG21	5:B:314:LEU:HD21	2.03	0.40
5:B:492:LEU:O	5:B:496:ARG:HG3	2.21	0.40
6:C:60:ASP:HB2	13:L:67:PHE:CZ	2.57	0.40
7:E:166:LYS:HA	7:E:166:LYS:HD2	1.93	0.40
9:H:130:ARG:HD3	9:H:134:ASN:ND2	2.36	0.40
11:J:48:ARG:HG2	11:J:48:ARG:HH11	1.86	0.40
2:T:24:DT:OP1	5:B:1122:ARG:NH1	2.54	0.40
4:A:883:LEU:O	4:A:886:ILE:HG22	2.21	0.40
4:A:1151:GLU:HB3	4:A:1153:TYR:CE1	2.55	0.40
4:A:1157:ASP:HB3	4:A:1160:SER:O	2.21	0.40
5:B:276:ILE:HG22	5:B:278:GLN:O	2.21	0.40
6:C:97:VAL:HG21	6:C:129:ILE:HG22	2.04	0.40
7:E:61:GLN:HG2	7:E:79:TRP:HE3	1.85	0.40
9:H:38:LEU:HD11	9:H:123:MET:HE2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:16:GLU:CD	4:A:1418:LEU:HD21	2.46	0.40
4:A:956:LEU:HD23	4:A:956:LEU:HA	1.78	0.40
4:A:1051:ALA:O	4:A:1055:ARG:HG3	2.21	0.40
4:A:1208:THR:O	4:A:1212:VAL:HG23	2.22	0.40
6:C:61:GLU:H	6:C:61:GLU:HG2	1.64	0.40
9:H:37:LYS:NZ	9:H:126:GLU:OE2	2.55	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)
4:A:917:SER:OG	10:I:21:GLU:OE1[4_546]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	1371/1733 (79%)	1334 (97%)	36 (3%)	1 (0%)	48	76
5	B	1101/1224 (90%)	1078 (98%)	23 (2%)	0	100	100
6	C	265/318 (83%)	260 (98%)	5 (2%)	0	100	100
7	E	211/215 (98%)	205 (97%)	6 (3%)	0	100	100
8	F	84/155 (54%)	82 (98%)	2 (2%)	0	100	100
9	H	129/146 (88%)	124 (96%)	5 (4%)	0	100	100
10	I	116/122 (95%)	112 (97%)	4 (3%)	0	100	100
11	J	63/70 (90%)	62 (98%)	1 (2%)	0	100	100
12	K	112/120 (93%)	111 (99%)	1 (1%)	0	100	100
13	L	41/70 (59%)	39 (95%)	2 (5%)	0	100	100
All	All	3493/4173 (84%)	3407 (98%)	85 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	958	VAL

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	
4	A	1194/1520 (79%)	1194 (100%)	0	100	100
5	B	955/1061 (90%)	955 (100%)	0	100	100
6	C	235/274 (86%)	235 (100%)	0	100	100
7	E	192/197 (98%)	192 (100%)	0	100	100
8	F	73/137 (53%)	73 (100%)	0	100	100
9	H	116/128 (91%)	116 (100%)	0	100	100
10	I	109/116 (94%)	109 (100%)	0	100	100
11	J	60/65 (92%)	60 (100%)	0	100	100
12	K	99/102 (97%)	99 (100%)	0	100	100
13	L	37/57 (65%)	37 (100%)	0	100	100
All	All	3070/3657 (84%)	3070 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	297	GLN
4	A	394	ASN
4	A	399	HIS
4	A	427	GLN
4	A	479	ASN
4	A	493	GLN
4	A	517	ASN
4	A	548	ASN

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Mol	Chain	Res	Type
4	A	589	GLN
4	A	626	ASN
4	A	838	GLN
4	A	877	HIS
4	A	881	GLN
4	A	953	ASN
4	A	1106	ASN
4	A	1128	GLN
4	A	1187	GLN
4	A	1218	GLN
4	A	1265	ASN
4	A	1367	HIS
5	B	47	GLN
5	B	110	HIS
5	B	433	GLN
5	B	465	ASN
5	B	573	GLN
5	B	667	GLN
5	B	958	GLN
5	B	1040	ASN
5	B	1093	GLN
5	B	1141	HIS
5	B	1187	ASN
6	C	131	HIS
7	E	153	HIS
8	F	104	ASN
9	H	35	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	9/10 (90%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	9	G

There are no RNA pucker outliers to report.

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

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
2	8OG	T	19	1,2	22,25,26	4.09	18 (81%)	26,37,40	1.68	7 (26%)

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
2	8OG	T	19	1,2	-	3/7/21/22	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	19	8OG	C8-N7	7.45	1.52	1.38
2	T	19	8OG	C8-N9	6.09	1.51	1.40
2	T	19	8OG	C2-N3	6.01	1.47	1.33
2	T	19	8OG	C4-N3	5.81	1.47	1.34
2	T	19	8OG	C2-N2	4.96	1.45	1.34
2	T	19	8OG	O4'-C1'	-4.86	1.31	1.42
2	T	19	8OG	C5-C4	4.72	1.43	1.37
2	T	19	8OG	O3'-C3'	4.28	1.52	1.43
2	T	19	8OG	C5-N7	4.28	1.44	1.37
2	T	19	8OG	C2-N1	4.24	1.47	1.37
2	T	19	8OG	C2'-C1'	3.72	1.62	1.52
2	T	19	8OG	C6-N1	3.62	1.45	1.38
2	T	19	8OG	C5-C6	3.43	1.52	1.41
2	T	19	8OG	C5'-C4'	-3.05	1.42	1.51
2	T	19	8OG	C4-N9	2.88	1.44	1.39
2	T	19	8OG	O6-C6	-2.41	1.19	1.23
2	T	19	8OG	C3'-C4'	2.41	1.59	1.53
2	T	19	8OG	O8-C8	-2.34	1.18	1.23

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	19	8OG	C2-N3-C4	4.50	120.05	112.30
2	T	19	8OG	O6-C6-C5	-3.11	119.77	127.26
2	T	19	8OG	C2-N1-C6	-2.71	120.19	125.11
2	T	19	8OG	C5-C6-N1	2.68	119.49	112.13
2	T	19	8OG	C5-N7-C8	-2.50	106.02	109.47
2	T	19	8OG	N9-C4-N3	2.47	129.22	126.13
2	T	19	8OG	C4-C5-N7	2.40	110.46	106.06

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	T	19	8OG	O4'-C4'-C5'-O5'
2	T	19	8OG	C3'-C4'-C5'-O5'
2	T	19	8OG	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	PPV	A	1804	-	6,8,8	0.79	0	12,13,13	0.80	0

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	PPV	A	1804	-	-	1/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

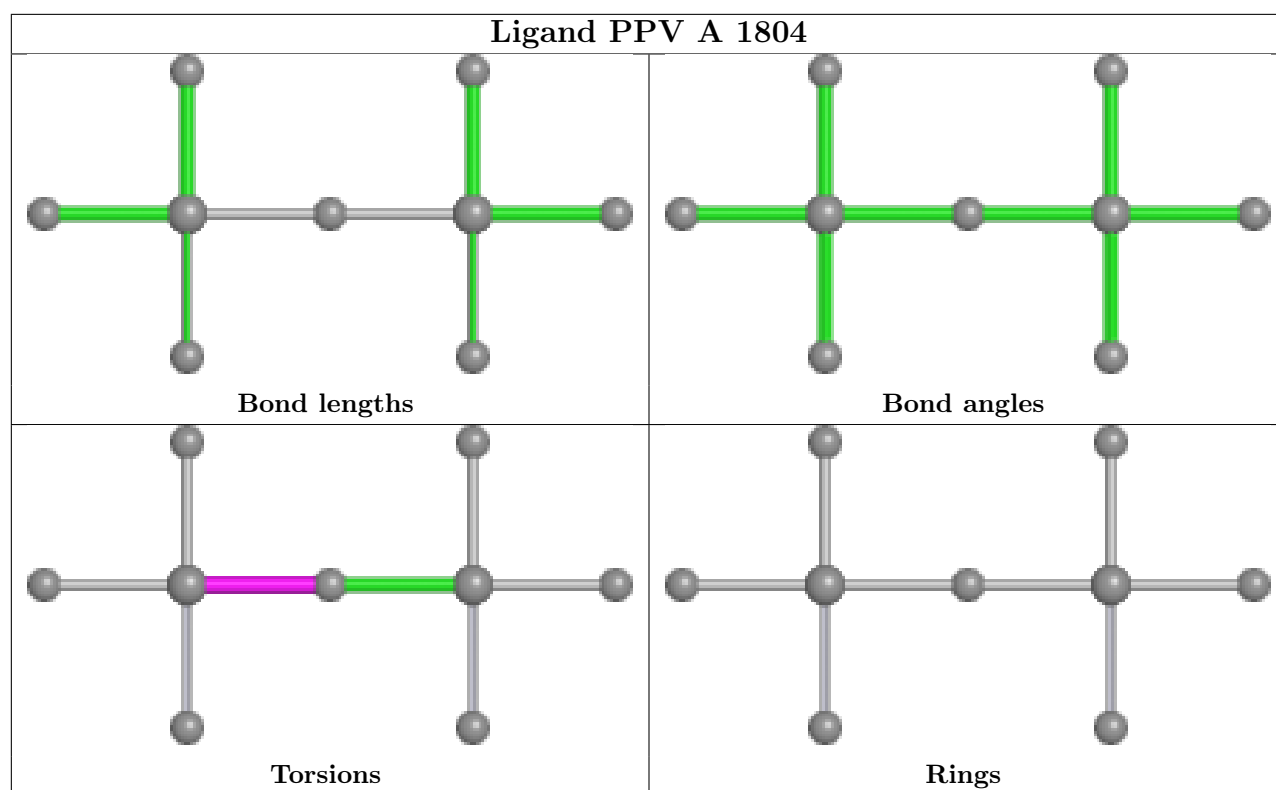
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	A	1804	PPV	P1-OPP-P2-O32

There are no ring outliers.

No monomer is involved in short contacts.

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

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	R	10/10 (100%)	0.18	1 (10%) 12 12	81, 94, 140, 153	0
2	T	25/29 (86%)	0.37	0 100 100	76, 155, 214, 221	0
3	N	15/18 (83%)	0.15	0 100 100	150, 173, 221, 227	0
4	A	1385/1733 (79%)	0.56	72 (5%) 33 23	45, 87, 157, 209	0
5	B	1121/1224 (91%)	0.45	33 (2%) 53 39	48, 84, 142, 186	0
6	C	267/318 (83%)	0.31	6 (2%) 62 46	53, 86, 119, 147	0
7	E	213/215 (99%)	0.76	22 (10%) 12 11	61, 119, 178, 195	0
8	F	86/155 (55%)	0.27	2 (2%) 61 45	68, 93, 127, 156	0
9	H	133/146 (91%)	0.56	8 (6%) 27 20	83, 107, 147, 177	0
10	I	118/122 (96%)	0.42	2 (1%) 69 53	68, 100, 123, 135	0
11	J	65/70 (92%)	0.33	2 (3%) 51 38	59, 81, 108, 128	0
12	K	114/120 (95%)	0.32	0 100 100	52, 85, 111, 130	0
13	L	43/70 (61%)	0.81	4 (9%) 14 13	68, 120, 165, 186	0
All	All	3595/4230 (84%)	0.50	152 (4%) 40 28	45, 89, 156, 227	0

All (152) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	E	83	CYS	4.8
7	E	121	MET	4.7
4	A	1332	PHE	4.7
7	E	110	PHE	4.4
7	E	93	MET	4.4
4	A	1108	ALA	4.4
5	B	819	ALA	4.1
5	B	1214	PRO	4.0
7	E	82	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
7	E	46	TYR	3.8
4	A	141	LEU	3.7
4	A	103	CYS	3.7
5	B	386	LEU	3.5
9	H	63	LEU	3.4
13	L	32	ALA	3.4
7	E	100	ILE	3.4
6	C	178	PHE	3.3
4	A	1257	ASP	3.3
4	A	464	PRO	3.3
4	A	1220	PHE	3.3
7	E	12	LEU	3.2
4	A	289	ILE	3.2
4	A	1271	ILE	3.2
4	A	776	ALA	3.2
4	A	646	PHE	3.1
5	B	751	VAL	3.1
5	B	733	HIS	3.1
4	A	162	VAL	3.1
4	A	1061	GLY	3.1
7	E	92	THR	3.0
4	A	355	GLY	3.0
9	H	86	ASP	3.0
4	A	234	MET	3.0
4	A	21	LEU	2.9
5	B	162	SER	2.9
5	B	260	GLY	2.9
4	A	873	MET	2.9
4	A	1192	LEU	2.9
5	B	525	ALA	2.9
7	E	188	LEU	2.9
4	A	3	GLY	2.8
9	H	90	ALA	2.8
5	B	1016	ALA	2.8
4	A	276	LEU	2.8
4	A	867	ILE	2.8
13	L	66	GLN	2.8
5	B	714	GLU	2.8
7	E	144	ILE	2.8
4	A	1328	TYR	2.8
5	B	212	LEU	2.8
9	H	88	SER	2.8

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Mol	Chain	Res	Type	RSRZ
4	A	1344	GLY	2.7
5	B	409	ALA	2.7
10	I	82	GLU	2.7
4	A	769	SER	2.7
13	L	28	LYS	2.7
4	A	323	LYS	2.7
4	A	1329	THR	2.7
4	A	844	ALA	2.7
4	A	339	ASN	2.7
9	H	134	ASN	2.7
4	A	815	PHE	2.6
7	E	9	ILE	2.6
4	A	448	PRO	2.6
4	A	885	THR	2.6
4	A	1156	PRO	2.6
7	E	16	PHE	2.6
5	B	466	TRP	2.5
5	B	509	ALA	2.5
4	A	308	ILE	2.5
4	A	850	VAL	2.5
4	A	279	LEU	2.5
7	E	124	VAL	2.5
5	B	1212	ILE	2.5
5	B	300	HIS	2.5
5	B	799	PRO	2.5
1	R	10	C	2.4
4	A	242	PRO	2.4
4	A	588	LEU	2.4
9	H	23	VAL	2.4
4	A	1209	MET	2.4
4	A	1193	LEU	2.4
11	J	65	PRO	2.4
5	B	830	TYR	2.4
5	B	524	PRO	2.4
5	B	779	GLY	2.3
6	C	171	GLY	2.3
4	A	577	ILE	2.3
8	F	93	ILE	2.3
5	B	314	LEU	2.3
6	C	251	LEU	2.3
4	A	682	THR	2.3
4	A	1141	THR	2.3

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Mol	Chain	Res	Type	RSRZ
5	B	1077	THR	2.3
4	A	235	ILE	2.3
4	A	1219	THR	2.3
4	A	503	GLN	2.3
4	A	1002	GLY	2.3
11	J	16	ASP	2.3
4	A	696	GLU	2.2
4	A	574	GLY	2.2
8	F	85	MET	2.2
4	A	318	SER	2.2
4	A	316	GLN	2.2
6	C	26	ASP	2.2
7	E	109	ILE	2.2
5	B	721	LEU	2.2
4	A	829	VAL	2.2
4	A	138	ILE	2.2
4	A	1315	GLU	2.2
4	A	1081	LEU	2.2
4	A	1313	LEU	2.2
4	A	91	PHE	2.2
4	A	1225	PHE	2.2
4	A	106	VAL	2.2
9	H	139	ASN	2.2
4	A	952	ALA	2.2
4	A	105	CYS	2.2
7	E	184	VAL	2.1
4	A	53	LEU	2.1
5	B	521	LEU	2.1
7	E	123	LEU	2.1
4	A	1112	LYS	2.1
5	B	735	ALA	2.1
5	B	753	ALA	2.1
5	B	764	SER	2.1
5	B	919	SER	2.1
6	C	141	GLY	2.1
4	A	854	ASN	2.1
4	A	335	ARG	2.1
7	E	90	VAL	2.1
4	A	257	ARG	2.1
7	E	108	GLY	2.1
10	I	23	ASN	2.1
5	B	334	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
5	B	336	ARG	2.1
5	B	1165	ILE	2.1
7	E	132	ILE	2.1
4	A	44	THR	2.1
4	A	849	MET	2.1
4	A	1267	MET	2.1
4	A	1073	GLY	2.1
9	H	104	PHE	2.0
7	E	178	ILE	2.0
4	A	437	MET	2.0
7	E	44	ALA	2.0
5	B	832	GLY	2.0
5	B	1087	PHE	2.0
4	A	56	PRO	2.0
6	C	51	VAL	2.0
4	A	722	LEU	2.0
13	L	55	ILE	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($\text{\AA}^2$)	Q<0.9
2	8OG	T	19	23/24	0.71	0.12	86,107,128,146	0

6.3 Carbohydrates [i](#)

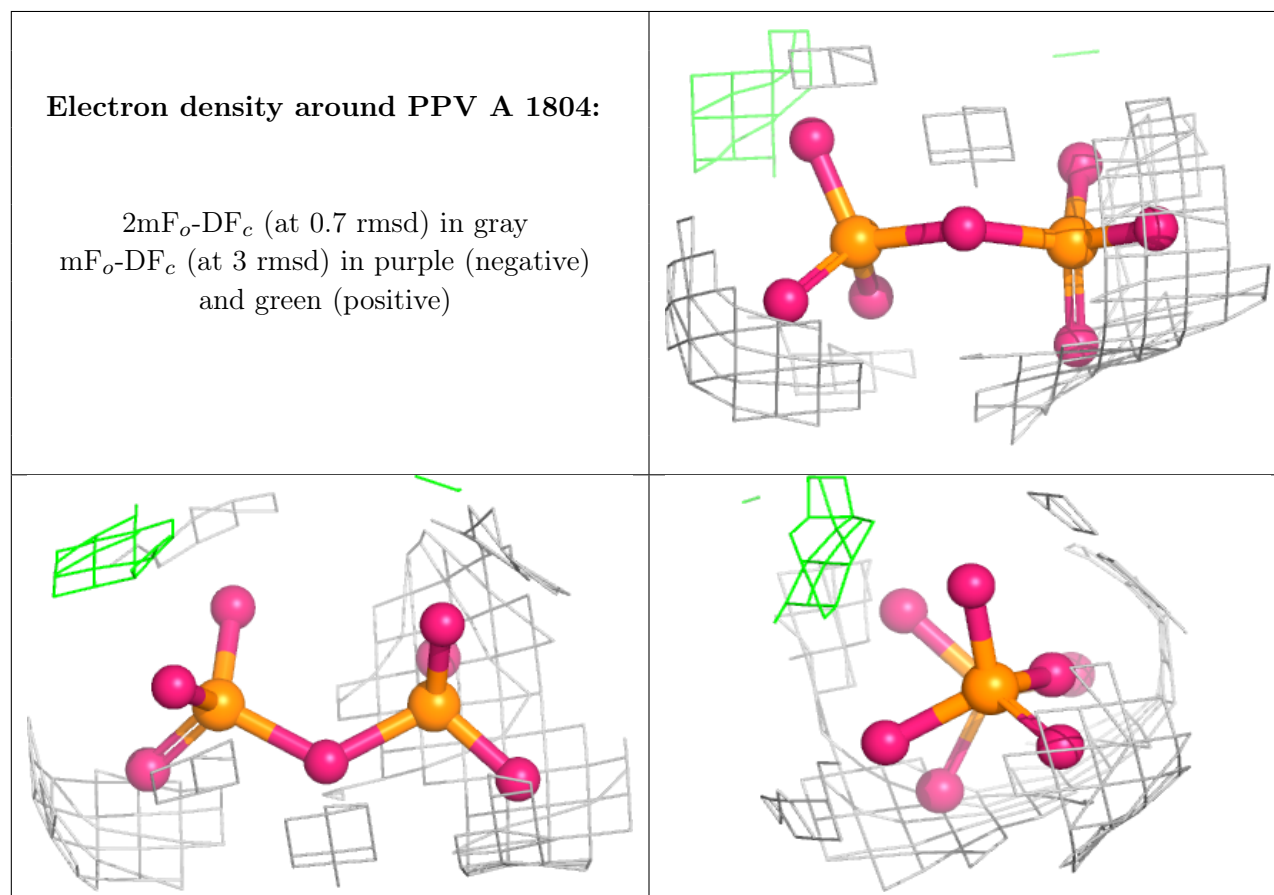
There are no oligosaccharides in this entry.

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
16	PPV	A	1804	9/9	0.42	0.12	134,142,165,171	0
14	ZN	L	101	1/1	0.75	0.14	174,174,174,174	0
15	MG	A	1803	1/1	0.83	0.08	88,88,88,88	0
14	ZN	I	202	1/1	0.86	0.10	157,157,157,157	0
14	ZN	B	1301	1/1	0.95	0.06	163,163,163,163	0
14	ZN	J	101	1/1	0.96	0.11	88,88,88,88	0
14	ZN	A	1801	1/1	0.96	0.05	233,233,233,233	0
14	ZN	I	201	1/1	0.97	0.04	89,89,89,89	0
14	ZN	A	1802	1/1	0.97	0.04	161,161,161,161	0
14	ZN	C	401	1/1	1.00	0.09	100,100,100,100	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 ⓘ

There are no such residues in this entry.