



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:28 PM UTC

PDB ID : 5IPM / pdb_00005ipm
Title : SigmaS-transcription initiation complex with 4-nt nascent RNA
Authors : Liu, B.; Zuo, Y.; Steitz, T.A.
Deposited on : 2016-03-09
Resolution : 4.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

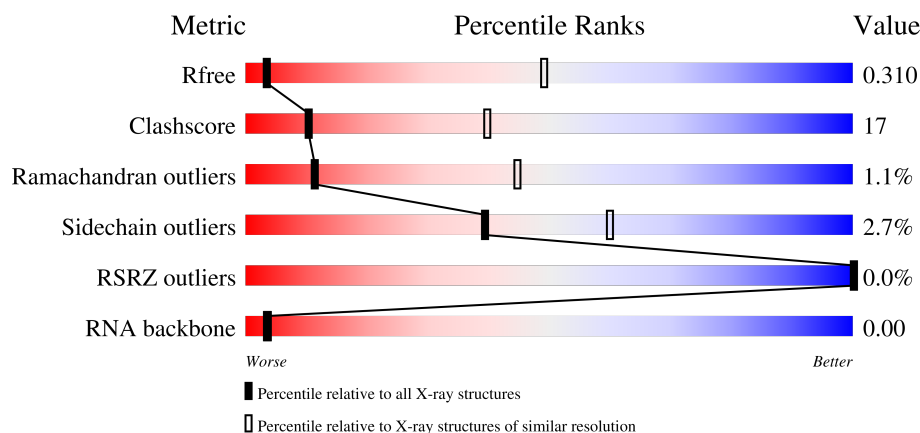
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1004 (4.52-3.88)
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)
RNA backbone	3983	1026 (5.04-3.10)

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	242	
1	B	242	
2	C	1342	
3	D	1407	

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Mol	Chain	Length	Quality of chain
4	E	90	
5	F	336	
6	1	50	
7	2	50	
8	3	4	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	ZN	D	1502	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 29027 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 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1787	1112	317	352	6			
1	B	228	Total	C	N	O	S	0	0	0
			1767	1100	312	349	6			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ALA	-	expression tag	UNP P0A7Z4
A	-5	HIS	-	expression tag	UNP P0A7Z4
A	-4	HIS	-	expression tag	UNP P0A7Z4
A	-3	HIS	-	expression tag	UNP P0A7Z4
A	-2	HIS	-	expression tag	UNP P0A7Z4
A	-1	HIS	-	expression tag	UNP P0A7Z4
A	0	HIS	-	expression tag	UNP P0A7Z4
B	-6	ALA	-	expression tag	UNP P0A7Z4
B	-5	HIS	-	expression tag	UNP P0A7Z4
B	-4	HIS	-	expression tag	UNP P0A7Z4
B	-3	HIS	-	expression tag	UNP P0A7Z4
B	-2	HIS	-	expression tag	UNP P0A7Z4
B	-1	HIS	-	expression tag	UNP P0A7Z4
B	0	HIS	-	expression tag	UNP P0A7Z4

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0	0
			10570	6631	1841	2055	43			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1362	Total	C	N	O	S	0	0	0
			10568	6633	1887	1998	50			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	79	Total	C	N	O	S	0	0	0
			627	382	118	126	1			

- Molecule 5 is a protein called RNA polymerase sigma factor RpoS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	277	Total	C	N	O	S	0	0	0
			2253	1411	415	423	4			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	2	GLY	SER	conflict	UNP P13445
F	33	GLU	GLN	conflict	UNP P13445
F	329	LEU	ARG	conflict	UNP P13445
F	331	HIS	-	expression tag	UNP P13445
F	332	HIS	-	expression tag	UNP P13445
F	333	HIS	-	expression tag	UNP P13445
F	334	HIS	-	expression tag	UNP P13445
F	335	HIS	-	expression tag	UNP P13445
F	336	HIS	-	expression tag	UNP P13445

- Molecule 6 is a DNA chain called synthetic non-template strand DNA (50-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1	33	Total	C	N	O	P	0	0	0
			680	323	124	200	33			

- Molecule 7 is a DNA chain called synthetic template strand DNA (50-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	2	33	Total	C	N	O	P	0	0	0
			675	322	125	196	32			

- Molecule 8 is a RNA chain called nascent RNA 4-mer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	3	4	Total	C	N	O	P	0	0	0
			97	39	17	35	6			

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total	Zn	0	0
			2	2		

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

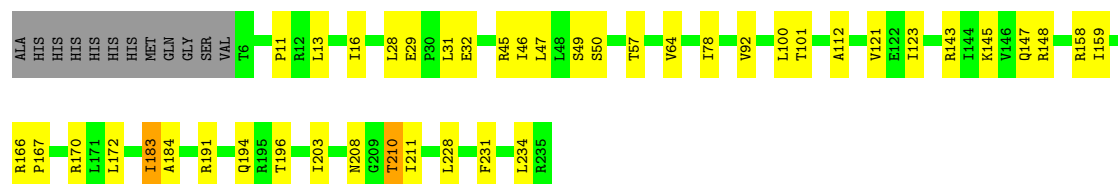
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	1	Total	Mg	0	0
			1	1		

3 Residue-property plots

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

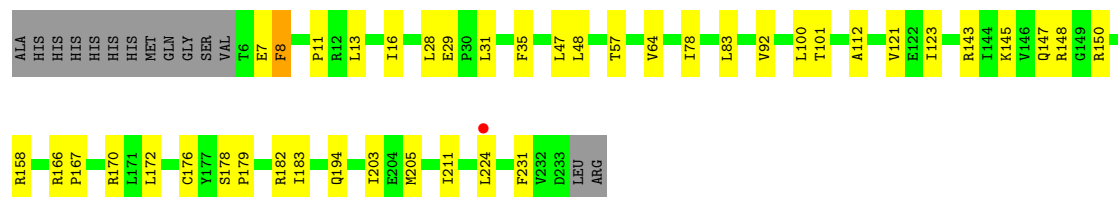
- Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain A: 



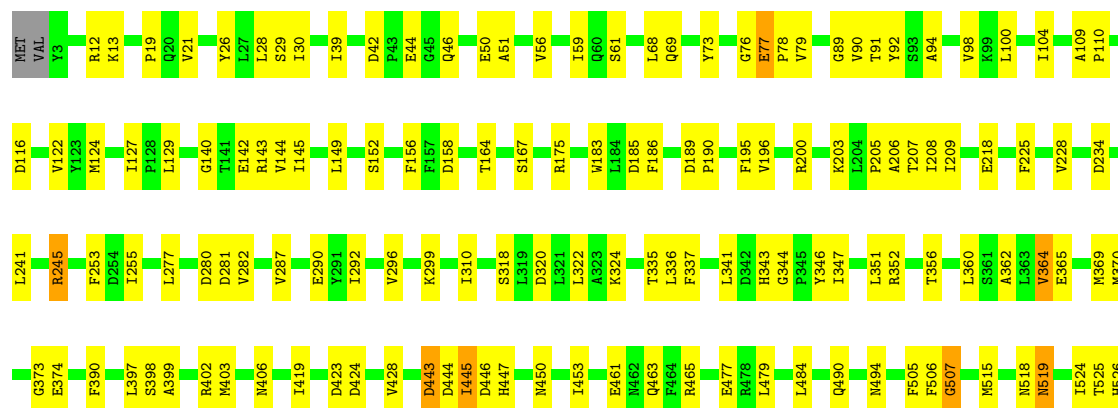
- Molecule 1: DNA-directed RNA polymerase subunit alpha

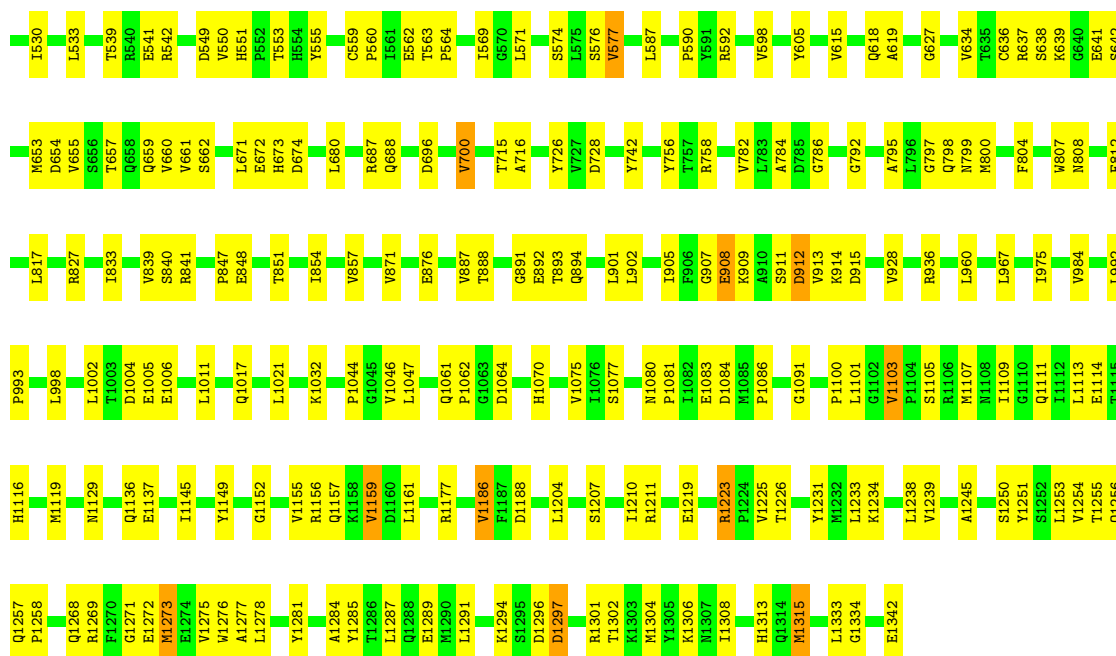
Chain B: 



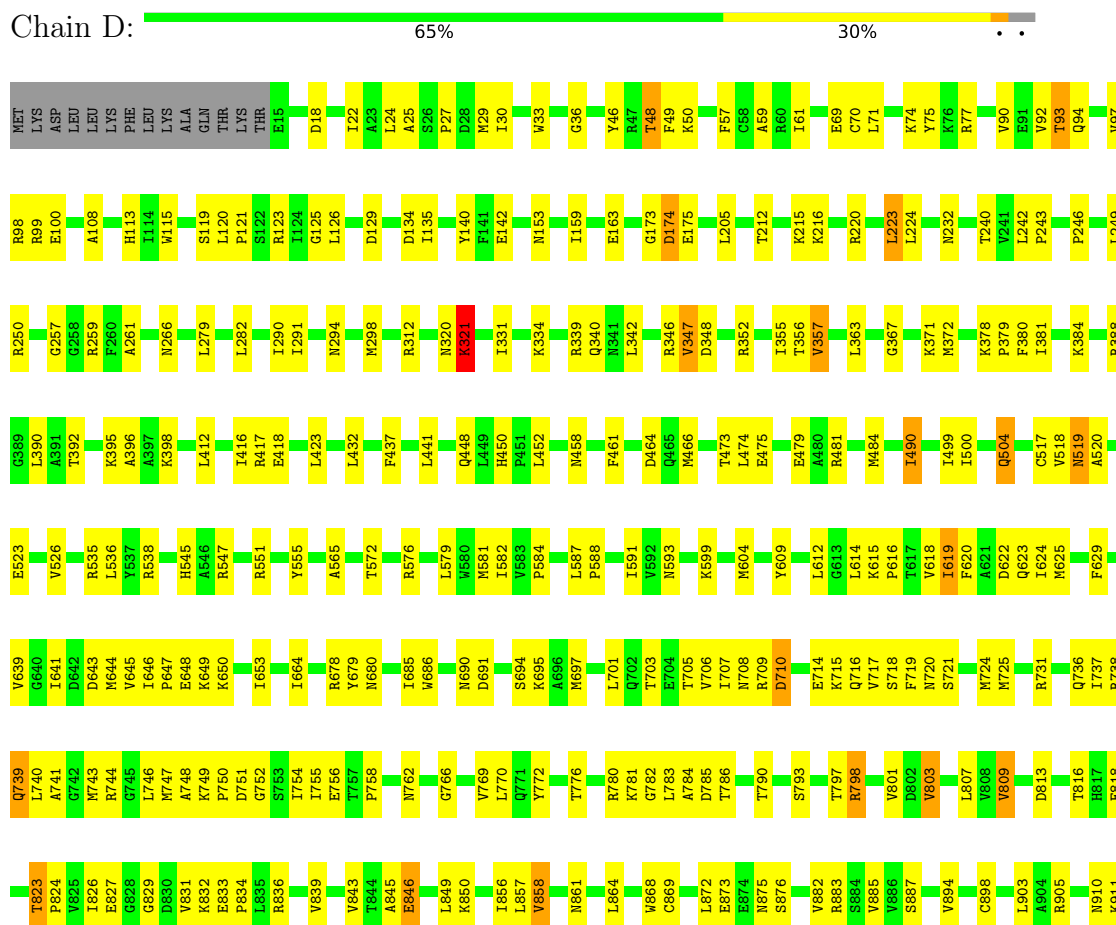
- Molecule 2: DNA-directed RNA polymerase subunit beta

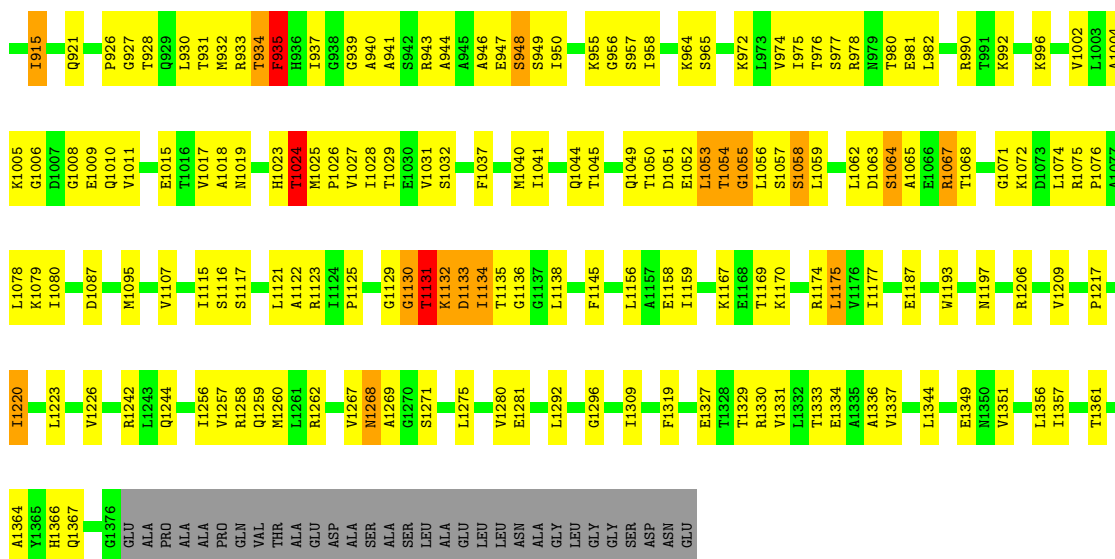
Chain C: 





• Molecule 3: DNA-directed RNA polymerase subunit beta'





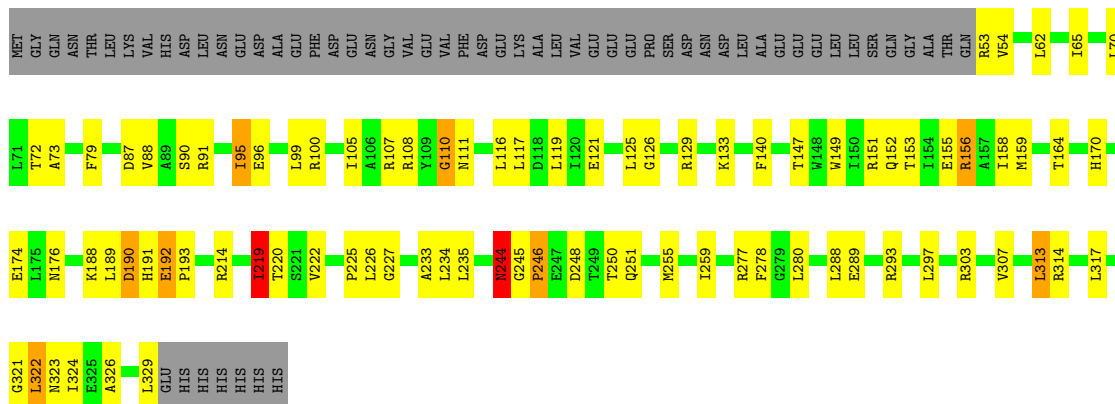
- Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E: 76% 11% 12%



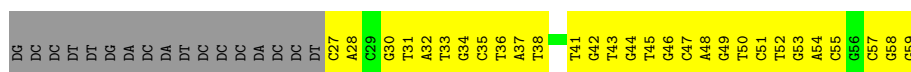
- Molecule 5: RNA polymerase sigma factor RpoS

Chain F: 57% 22% 18%



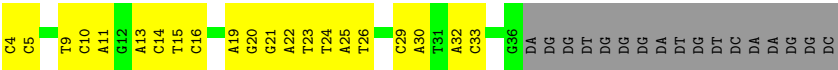
- Molecule 6: synthetic non-template strand DNA (50-MER)

Chain 1: 8% 58% 34%



- Molecule 7: synthetic template strand DNA (50-MER)

Chain 2: 24% 42% 34%



● Molecule 8: nascent RNA 4-mer

Chain 3: 25% 25% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	132.75Å 151.97Å 228.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	126.46 – 4.20 126.46 – 4.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (126.46-4.20) 99.9 (126.46-4.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 4.14Å)	Xtriage
Refinement program	REFMAC 5.8.0123	Depositor
R, R_{free}	0.270 , 0.330 0.258 , 0.310	Depositor DCC
R_{free} test set	1651 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	174.0	Xtriage
Anisotropy	0.560	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 249.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	29027	wwPDB-VP
Average B, all atoms (Å ²)	287.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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: MG, ZN, GTP

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	0.79	0/1809	1.01	1/2450 (0.0%)
1	B	0.75	0/1789	1.00	2/2425 (0.1%)
2	C	0.82	4/10736 (0.0%)	1.03	17/14480 (0.1%)
3	D	0.90	5/10729 (0.0%)	1.13	19/14487 (0.1%)
4	E	0.66	0/629	0.93	1/847 (0.1%)
5	F	0.81	1/2282 (0.0%)	1.09	4/3076 (0.1%)
6	1	0.37	0/762	0.68	0/1175
7	2	0.44	0/757	0.71	0/1167
8	3	0.43	0/72	0.92	0/110
All	All	0.82	10/29565 (0.0%)	1.05	44/40217 (0.1%)

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
5	F	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1131	THR	C-N	39.15	1.88	1.33
3	D	739	GLN	C-N	27.21	1.68	1.33
2	C	444	ASP	CA-C	-10.26	1.40	1.52
2	C	445	ILE	N-CA	-8.88	1.34	1.46
2	C	444	ASP	C-N	-7.30	1.25	1.33
3	D	935	PHE	N-CA	-7.08	1.36	1.45
2	C	152	SER	C-N	5.62	1.41	1.33
5	F	244	ASN	CA-C	5.43	1.59	1.52
3	D	780	ARG	NE-CZ	5.39	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	48	THR	CA-C	-5.21	1.46	1.53

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1131	THR	CA-C-N	-41.10	43.03	121.54
3	D	1131	THR	C-N-CA	-41.10	43.03	121.54
3	D	1131	THR	O-C-N	-24.65	89.81	122.59
3	D	934	THR	N-CA-C	-10.77	101.55	112.97
2	C	444	ASP	CA-C-O	7.69	130.11	121.11
3	D	739	GLN	CA-C-N	-7.45	110.50	120.63
3	D	739	GLN	C-N-CA	-7.45	110.50	120.63
5	F	244	ASN	O-C-N	-7.42	113.84	122.89
3	D	1220	ILE	CB-CA-C	-7.12	102.53	112.14
2	C	1223	ARG	CA-C-N	6.76	126.80	119.90
2	C	1223	ARG	C-N-CA	6.76	126.80	119.90
2	C	245	ARG	N-CA-C	-6.71	104.98	113.43
3	D	915	ILE	CB-CA-C	-6.64	103.35	112.24
2	C	399	ALA	N-CA-C	-6.49	104.29	111.82
3	D	246	PRO	CA-C-N	6.31	125.80	119.24
3	D	246	PRO	C-N-CA	6.31	125.80	119.24
3	D	504	GLN	CB-CA-C	-6.24	108.75	117.23
2	C	255	ILE	CB-CA-C	-6.08	104.66	111.23
1	B	29	GLU	N-CA-C	6.05	113.45	108.07
3	D	357	VAL	CB-CA-C	-5.90	103.14	111.28
5	F	244	ASN	CB-CA-C	5.85	119.65	109.65
3	D	833	GLU	CA-C-N	-5.63	114.15	119.89
3	D	833	GLU	C-N-CA	-5.63	114.15	119.89
1	A	29	GLU	N-CA-C	5.43	113.11	108.22
5	F	95	ILE	CB-CA-C	-5.40	105.06	111.81
2	C	742	TYR	CA-CB-CG	5.36	123.54	113.90
1	B	7	GLU	N-CA-C	-5.31	104.07	110.44
2	C	364	VAL	CB-CA-C	-5.29	105.00	112.14
2	C	444	ASP	CA-C-N	-5.26	111.67	120.30
2	C	444	ASP	C-N-CA	-5.26	111.67	120.30
3	D	934	THR	CA-C-N	-5.26	113.49	122.11
3	D	934	THR	C-N-CA	-5.26	113.49	122.11
2	C	800	MET	N-CA-C	5.25	116.26	108.60
3	D	490	ILE	CB-CA-C	-5.22	105.54	111.55
2	C	827	ARG	N-CA-C	-5.19	106.10	112.90
4	E	6	VAL	N-CA-CB	-5.18	105.44	112.22
3	D	346	ARG	N-CA-C	-5.17	102.83	110.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	577	VAL	N-CA-C	5.11	115.25	110.30
5	F	219	ILE	N-CA-C	5.10	116.58	109.80
2	C	77	GLU	CA-C-N	5.09	125.32	119.83
2	C	77	GLU	C-N-CA	5.09	125.32	119.83
3	D	1226	VAL	N-CA-C	5.07	115.29	110.53
2	C	1315	MET	CA-C-N	-5.04	116.83	123.34
2	C	1315	MET	C-N-CA	-5.04	116.83	123.34

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	244	ASN	Peptide

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	1787	0	1813	35	0
1	B	1767	0	1789	33	0
2	C	10570	0	10579	289	0
3	D	10568	0	10778	562	0
4	E	627	0	634	8	0
5	F	2253	0	2298	94	0
6	1	680	0	373	77	0
7	2	675	0	373	38	0
8	3	97	0	44	7	0
9	D	2	0	0	2	0
10	D	1	0	0	0	0
All	All	29027	0	28681	977	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (977) 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)
3:D:785:ASP:HB3	3:D:935:PHE:CZ	1.23	1.62
3:D:750:PRO:HA	3:D:781:LYS:CD	1.22	1.60
3:D:739:GLN:C	3:D:740:LEU:N	1.68	1.48
3:D:750:PRO:C	3:D:781:LYS:HE3	1.40	1.42
3:D:690:ASN:CG	3:D:738:ARG:HH12	1.21	1.42
3:D:750:PRO:CA	3:D:781:LYS:HD2	1.51	1.38
3:D:1133:ASP:O	3:D:1244:GLN:NE2	1.57	1.36
3:D:750:PRO:C	3:D:781:LYS:CE	1.99	1.34
3:D:785:ASP:CB	3:D:935:PHE:CZ	2.07	1.34
3:D:519:ASN:ND2	3:D:710:ASP:HB2	1.41	1.33
3:D:690:ASN:CG	3:D:738:ARG:NH1	1.84	1.32
3:D:785:ASP:CB	3:D:935:PHE:CE1	2.12	1.31
3:D:785:ASP:HB2	3:D:935:PHE:CE1	1.65	1.31
3:D:749:LYS:O	3:D:781:LYS:NZ	1.64	1.30
3:D:517:CYS:C	3:D:716:GLN:HE22	1.40	1.28
3:D:750:PRO:CA	3:D:781:LYS:CD	2.09	1.27
3:D:690:ASN:OD1	3:D:738:ARG:NH1	1.64	1.22
3:D:690:ASN:ND2	3:D:738:ARG:NH1	1.88	1.22
3:D:519:ASN:HD22	3:D:710:ASP:CB	1.53	1.22
3:D:931:THR:O	3:D:935:PHE:HD2	1.23	1.17
3:D:750:PRO:O	3:D:781:LYS:CE	1.91	1.15
3:D:752:GLY:N	3:D:781:LYS:NZ	1.96	1.14
3:D:680:ASN:OD1	3:D:1023:HIS:CE1	1.99	1.14
3:D:750:PRO:O	3:D:781:LYS:HE3	0.99	1.13
2:C:891:GLY:C	2:C:892:GLU:N	2.08	1.12
3:D:517:CYS:CA	3:D:716:GLN:HE22	1.63	1.12
3:D:518:VAL:HG21	3:D:708:ASN:HD21	1.14	1.11
3:D:750:PRO:HA	3:D:781:LYS:CG	1.81	1.09
3:D:751:ASP:N	3:D:781:LYS:HZ2	1.50	1.09
3:D:708:ASN:HD22	3:D:714:GLU:HG2	1.13	1.08
3:D:320:ASN:OD1	7:2:22:DA:N6	1.85	1.08
5:F:227:GLY:N	7:2:20:DG:O6	1.87	1.07
2:C:911:SER:C	2:C:912:ASP:N	2.12	1.07
3:D:750:PRO:HA	3:D:781:LYS:CE	1.85	1.06
3:D:750:PRO:CA	3:D:781:LYS:CE	2.32	1.06
3:D:518:VAL:N	3:D:716:GLN:HE22	1.53	1.06
3:D:1132:LYS:HG2	3:D:1133:ASP:H	1.18	1.05
3:D:517:CYS:HA	3:D:716:GLN:NE2	1.73	1.03
3:D:826:ILE:HD13	3:D:992:LYS:O	1.57	1.03
3:D:750:PRO:C	3:D:781:LYS:NZ	2.17	1.02
3:D:752:GLY:N	3:D:781:LYS:HZ1	1.49	1.02
3:D:750:PRO:C	3:D:781:LYS:HZ2	1.69	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:518:VAL:N	3:D:716:GLN:NE2	2.07	1.01
3:D:931:THR:O	3:D:935:PHE:CD2	2.13	1.01
3:D:747:MET:HE1	3:D:939:GLY:C	1.85	1.01
3:D:708:ASN:HD22	3:D:714:GLU:CG	1.74	1.00
3:D:701:LEU:CD1	3:D:720:ASN:HD22	1.74	0.99
3:D:708:ASN:ND2	3:D:714:GLU:HG2	1.78	0.99
3:D:965:SER:HB3	3:D:975:ILE:HA	1.44	0.99
3:D:750:PRO:N	3:D:781:LYS:HD2	1.79	0.98
3:D:785:ASP:HB3	3:D:935:PHE:HZ	1.26	0.98
2:C:336:LEU:C	2:C:337:PHE:N	2.22	0.98
3:D:518:VAL:HG21	3:D:708:ASN:ND2	1.79	0.97
2:C:549:ASP:OD2	3:D:750:PRO:HB3	1.64	0.97
2:C:549:ASP:OD2	3:D:750:PRO:CB	2.13	0.96
3:D:957:SER:OG	3:D:1008:GLY:O	1.83	0.94
3:D:517:CYS:C	3:D:716:GLN:NE2	2.24	0.93
3:D:747:MET:HE1	3:D:939:GLY:O	1.69	0.92
3:D:1075:ARG:NH2	3:D:1193:TRP:CZ3	2.36	0.92
3:D:750:PRO:HA	3:D:781:LYS:HD2	0.94	0.92
3:D:1050:THR:HG23	3:D:1056:LEU:O	1.70	0.92
3:D:517:CYS:CA	3:D:716:GLN:NE2	2.31	0.91
3:D:690:ASN:ND2	3:D:738:ARG:CZ	2.34	0.91
3:D:739:GLN:HG3	3:D:744:ARG:HD2	1.51	0.90
3:D:1029:THR:HG22	3:D:1121:LEU:HD11	1.54	0.90
2:C:560:PRO:HB2	3:D:776:THR:HG21	1.52	0.90
3:D:690:ASN:HD21	3:D:738:ARG:NH1	1.63	0.90
3:D:690:ASN:C	3:D:738:ARG:NH2	2.30	0.89
5:F:227:GLY:CA	7:2:20:DG:O6	2.19	0.89
3:D:1005:LYS:HB3	3:D:1009:GLU:OE1	1.73	0.89
6:1:50:DT:H3'	6:1:51:DC:C5'	2.03	0.88
2:C:245:ARG:HD3	2:C:337:PHE:CE1	2.10	0.87
3:D:294:ASN:ND2	5:F:121:GLU:OE2	2.07	0.87
1:A:11:PRO:HG2	1:B:231:PHE:CZ	2.10	0.86
5:F:227:GLY:HA2	7:2:20:DG:O6	1.75	0.86
5:F:192:GLU:HG3	5:F:193:PRO:HD2	1.58	0.86
2:C:967:LEU:HD21	2:C:1021:LEU:HD13	1.56	0.85
3:D:752:GLY:H	3:D:781:LYS:NZ	1.68	0.85
3:D:173:GLY:O	3:D:175:GLU:N	2.10	0.85
3:D:898:CYS:HG	9:D:1502:ZN:ZN	0.86	0.85
3:D:1067:ARG:HD3	3:D:1071:GLY:O	1.75	0.84
3:D:523:GLU:OE1	3:D:710:ASP:OD2	1.95	0.84
3:D:1023:HIS:O	3:D:1024:THR:HB	1.76	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1029:THR:HG23	3:D:1121:LEU:HG	1.59	0.84
3:D:747:MET:CE	3:D:939:GLY:O	2.25	0.84
3:D:1029:THR:CG2	3:D:1121:LEU:HG	2.07	0.84
2:C:200:ARG:HD3	6:1:50:DT:O2	1.78	0.83
5:F:317:LEU:O	5:F:321:GLY:HA3	1.78	0.83
2:C:541:GLU:OE2	6:1:51:DC:N3	2.12	0.82
3:D:1029:THR:HG22	3:D:1121:LEU:CD1	2.09	0.82
2:C:1268:GLN:OE1	3:D:352:ARG:HD2	1.80	0.81
3:D:876:SER:OG	3:D:990:ARG:NH1	2.13	0.81
5:F:107:ARG:NH1	6:1:43:DT:OP1	2.14	0.81
3:D:690:ASN:CG	3:D:738:ARG:CZ	2.52	0.81
6:1:47:DC:C2'	6:1:48:DA:H5'	2.09	0.81
3:D:949:SER:HB2	3:D:1018:ALA:O	1.81	0.81
3:D:1037:PHE:CE2	3:D:1040:MET:HE2	2.16	0.81
2:C:1342:GLU:HG2	3:D:18:ASP:HB2	1.62	0.80
3:D:933:ARG:O	3:D:937:ILE:HG13	1.80	0.80
3:D:1132:LYS:CG	3:D:1133:ASP:H	1.93	0.80
2:C:1284:ALA:HA	3:D:1357:ILE:HD12	1.64	0.80
3:D:933:ARG:C	3:D:935:PHE:H	1.87	0.80
1:A:11:PRO:HG2	1:B:231:PHE:CE2	2.16	0.80
3:D:965:SER:HB2	3:D:974:VAL:O	1.82	0.80
2:C:1287:LEU:CD2	3:D:1357:ILE:HD11	2.12	0.80
3:D:943:ARG:HG2	3:D:944:ALA:H	1.45	0.79
3:D:1132:LYS:HG2	3:D:1133:ASP:N	1.96	0.79
3:D:786:THR:OG1	3:D:935:PHE:HB3	1.82	0.79
3:D:1050:THR:OG1	3:D:1057:SER:HB3	1.82	0.79
3:D:701:LEU:CD1	3:D:720:ASN:ND2	2.46	0.79
2:C:577:VAL:HG23	2:C:661:VAL:O	1.83	0.78
3:D:490:ILE:HD11	3:D:614:LEU:CD1	2.12	0.78
3:D:1344:LEU:HD23	3:D:1349:GLU:HB3	1.64	0.78
3:D:1032:SER:OG	3:D:1117:SER:N	2.16	0.78
3:D:320:ASN:O	3:D:321:LYS:HB3	1.84	0.78
3:D:464:ASP:OD1	8:3:16:G:O2'	2.01	0.78
3:D:739:GLN:CG	3:D:744:ARG:HD2	2.14	0.77
3:D:1133:ASP:O	3:D:1134:ILE:HD13	1.84	0.77
3:D:749:LYS:C	3:D:781:LYS:HD2	2.08	0.77
6:1:45:DT:O3'	6:1:46:DG:O4'	2.03	0.77
3:D:957:SER:HB2	3:D:1010:GLN:HE22	1.48	0.77
1:B:13:LEU:HD21	1:B:16:ILE:HD11	1.66	0.77
3:D:517:CYS:HB2	3:D:719:PHE:HZ	1.50	0.77
2:C:525:THR:HG21	2:C:687:ARG:CD	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1273:MET:HG3	7:2:14:DC:H4'	1.66	0.76
3:D:519:ASN:HD22	3:D:710:ASP:HB2	0.67	0.76
3:D:752:GLY:N	3:D:781:LYS:HZ2	1.82	0.76
1:A:13:LEU:HD21	1:A:16:ILE:HD11	1.67	0.76
3:D:739:GLN:C	3:D:740:LEU:CA	2.57	0.76
3:D:518:VAL:HG23	3:D:716:GLN:HB2	1.66	0.76
2:C:1287:LEU:HD23	3:D:1357:ILE:HD11	1.68	0.76
3:D:1029:THR:CG2	3:D:1121:LEU:CG	2.64	0.76
3:D:749:LYS:O	3:D:781:LYS:CD	2.33	0.76
2:C:46:GLN:HB2	2:C:51:ALA:HA	1.68	0.75
3:D:957:SER:HB2	3:D:1010:GLN:NE2	2.01	0.75
3:D:1133:ASP:O	3:D:1244:GLN:CD	2.30	0.75
3:D:1052:GLU:HG2	3:D:1053:LEU:H	1.50	0.75
2:C:887:VAL:HB	2:C:913:VAL:CG1	2.16	0.75
3:D:1050:THR:HG22	3:D:1051:ASP:N	2.01	0.75
2:C:1287:LEU:HD23	3:D:1357:ILE:CG1	2.17	0.74
3:D:697:MET:SD	3:D:737:ILE:HG22	2.27	0.74
4:E:30:MET:HE1	4:E:37:PRO:HB3	1.68	0.74
3:D:708:ASN:HB2	3:D:714:GLU:C	2.12	0.74
3:D:518:VAL:CG1	3:D:714:GLU:OE1	2.36	0.74
3:D:933:ARG:CD	3:D:937:ILE:HD11	2.18	0.73
6:1:50:DT:H3'	6:1:51:DC:H5''	1.69	0.73
3:D:708:ASN:HB2	3:D:714:GLU:O	1.86	0.73
3:D:785:ASP:HB3	3:D:935:PHE:CE2	2.15	0.73
3:D:749:LYS:O	3:D:781:LYS:CE	2.35	0.73
3:D:1131:THR:N	3:D:1132:LYS:HB2	1.86	0.73
3:D:752:GLY:CA	3:D:781:LYS:HZ1	1.99	0.73
5:F:152:GLN:HG3	6:1:36:DT:O4	1.88	0.73
3:D:708:ASN:ND2	3:D:714:GLU:CG	2.46	0.73
6:1:34:DG:N2	7:2:29:DC:O2	2.18	0.73
3:D:517:CYS:HB2	3:D:719:PHE:CZ	2.24	0.73
3:D:823:THR:HB	3:D:824:PRO:CD	2.19	0.73
3:D:691:ASP:HA	3:D:738:ARG:HH21	1.54	0.73
2:C:549:ASP:OD2	3:D:750:PRO:HB2	1.89	0.72
3:D:943:ARG:HG2	3:D:944:ALA:N	2.04	0.72
6:1:30:DG:N2	7:2:33:DC:O2	2.22	0.72
3:D:517:CYS:HA	3:D:716:GLN:CD	2.14	0.72
3:D:701:LEU:HD12	3:D:720:ASN:HD22	1.55	0.72
2:C:672:GLU:HG3	2:C:673:HIS:CD2	2.25	0.71
3:D:481:ARG:NH1	4:E:3:ARG:O	2.23	0.71
3:D:381:ILE:HD11	3:D:412:LEU:HD13	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:518:VAL:HG11	3:D:714:GLU:OE1	1.91	0.71
3:D:518:VAL:H	3:D:716:GLN:NE2	1.89	0.71
5:F:317:LEU:O	5:F:321:GLY:CA	2.38	0.71
5:F:70:LEU:HD11	6:1:41:DT:C2	2.26	0.71
2:C:205:PRO:O	2:C:208:ILE:HG22	1.91	0.70
3:D:518:VAL:CG2	3:D:716:GLN:HB2	2.21	0.70
3:D:1023:HIS:O	3:D:1024:THR:CB	2.39	0.70
3:D:452:LEU:HB3	3:D:500:ILE:HG23	1.71	0.70
2:C:142:GLU:OE1	2:C:515:MET:HE1	1.91	0.70
3:D:826:ILE:CD1	3:D:992:LYS:O	2.37	0.70
5:F:227:GLY:HA3	7:2:19:DA:C2	2.26	0.70
5:F:176:ASN:OD1	7:2:26:DT:H71	1.92	0.70
2:C:373:GLY:HA3	5:F:54:VAL:HG21	1.74	0.70
2:C:674:ASP:O	3:D:772:TYR:OH	2.03	0.70
3:D:750:PRO:CA	3:D:781:LYS:HE3	2.07	0.69
5:F:317:LEU:O	5:F:321:GLY:N	2.25	0.69
3:D:856:ILE:HG23	3:D:858:VAL:HG23	1.74	0.69
1:A:50:SER:OG	1:B:35:PHE:HZ	1.76	0.69
3:D:739:GLN:HG3	3:D:744:ARG:HA	1.74	0.69
3:D:1067:ARG:NH2	3:D:1076:PRO:HD3	2.08	0.69
2:C:1276:TRP:HH2	3:D:798:ARG:HG2	1.57	0.69
3:D:690:ASN:O	3:D:738:ARG:NH2	2.26	0.69
6:1:47:DC:H2'	6:1:48:DA:H5'	1.74	0.69
2:C:564:PRO:HB3	8:3:14:GTP:O1A	1.92	0.68
3:D:519:ASN:ND2	3:D:710:ASP:CB	2.30	0.68
2:C:245:ARG:CD	2:C:337:PHE:CE1	2.76	0.68
3:D:450:HIS:CE1	3:D:625:MET:HE1	2.28	0.68
3:D:749:LYS:C	3:D:781:LYS:NZ	2.51	0.68
3:D:1029:THR:HG21	3:D:1121:LEU:HD21	1.74	0.68
5:F:147:THR:O	5:F:151:ARG:HG2	1.94	0.68
7:2:15:DT:H5''	7:2:15:DT:H6	1.58	0.68
2:C:1304:MET:HE1	2:C:1315:MET:HA	1.76	0.68
3:D:1037:PHE:CE2	3:D:1040:MET:CE	2.75	0.68
3:D:1050:THR:CG2	3:D:1051:ASP:H	2.06	0.68
2:C:525:THR:HG21	2:C:687:ARG:HD2	1.76	0.67
2:C:1289:GLU:HA	2:C:1315:MET:HE1	1.77	0.67
3:D:708:ASN:HD22	3:D:714:GLU:CB	2.07	0.67
3:D:1050:THR:HG22	3:D:1051:ASP:H	1.58	0.67
3:D:1075:ARG:NH2	3:D:1193:TRP:CE3	2.63	0.67
3:D:396:ALA:HB2	5:F:326:ALA:HB1	1.76	0.67
3:D:1158:GLU:HA	3:D:1223:LEU:HD22	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1006:GLY:N	3:D:1009:GLU:OE1	2.28	0.66
3:D:1134:ILE:CD1	3:D:1244:GLN:HG3	2.25	0.66
1:A:210:THR:HG22	1:A:211:ILE:N	2.09	0.66
1:A:49:SER:HB3	2:C:1083:GLU:OE2	1.95	0.66
2:C:1287:LEU:HD23	3:D:1357:ILE:CD1	2.25	0.66
2:C:156:PHE:CE2	2:C:158:ASP:HB2	2.31	0.66
2:C:1306:LYS:HG2	5:F:250:THR:OG1	1.96	0.66
3:D:898:CYS:SG	9:D:1502:ZN:ZN	1.83	0.66
2:C:453:ILE:HD12	2:C:587:LEU:HD21	1.78	0.65
6:1:32:DA:C2	7:2:32:DA:C2	2.85	0.65
3:D:59:ALA:HB3	3:D:71:LEU:HD11	1.79	0.65
6:1:51:DC:OP1	6:1:51:DC:H2'	1.96	0.65
6:1:44:DG:H4'	6:1:45:DT:OP2	1.95	0.65
3:D:708:ASN:HB3	3:D:714:GLU:HB3	1.78	0.64
3:D:1005:LYS:CB	3:D:1009:GLU:OE1	2.45	0.64
2:C:292:ILE:HD12	2:C:322:LEU:HD22	1.78	0.64
5:F:227:GLY:HA3	7:2:19:DA:H2	1.61	0.64
5:F:100:ARG:HB3	6:1:42:DG:H5''	1.78	0.64
5:F:110:GLY:HA2	5:F:119:LEU:HD11	1.79	0.64
2:C:841:ARG:NH1	3:D:257:GLY:HA2	2.13	0.64
3:D:964:LYS:O	3:D:976:THR:OG1	2.11	0.64
3:D:1044:GLN:O	3:D:1067:ARG:HG2	1.98	0.64
3:D:1050:THR:CG2	3:D:1051:ASP:N	2.60	0.63
7:2:22:DA:H2''	7:2:23:DT:O5'	1.98	0.63
1:B:83:LEU:HD21	3:D:526:VAL:HB	1.80	0.63
3:D:933:ARG:C	3:D:935:PHE:N	2.57	0.63
6:1:45:DT:H2''	6:1:46:DG:N9	2.14	0.63
7:2:16:DC:H6	7:2:16:DC:H5''	1.64	0.63
2:C:490:GLN:HE22	5:F:188:LYS:HE2	1.63	0.63
3:D:955:LYS:HG2	3:D:956:GLY:N	2.13	0.63
2:C:94:ALA:HB2	2:C:129:LEU:HD11	1.80	0.63
3:D:1067:ARG:CD	3:D:1071:GLY:O	2.47	0.63
5:F:190:ASP:C	5:F:190:ASP:OD1	2.42	0.63
2:C:848:GLU:HG2	2:C:888:THR:HG22	1.81	0.62
2:C:206:ALA:O	2:C:209:ILE:HG22	1.99	0.62
3:D:1075:ARG:CZ	3:D:1193:TRP:CE3	2.83	0.62
3:D:645:VAL:HG21	3:D:701:LEU:HB2	1.80	0.62
3:D:981:GLU:OE2	3:D:996:LYS:NZ	2.26	0.62
3:D:1129:GLY:O	3:D:1130:GLY:C	2.43	0.62
3:D:1130:GLY:C	3:D:1132:LYS:HB2	2.23	0.62
2:C:142:GLU:OE1	2:C:515:MET:CE	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:582:ILE:HG23	3:D:623:GLN:HB3	1.80	0.62
3:D:1068:THR:O	3:D:1072:LYS:HG2	2.00	0.62
5:F:72:THR:HG22	5:F:73:ALA:H	1.64	0.62
3:D:205:LEU:HD23	3:D:205:LEU:O	2.00	0.62
2:C:559:CYS:HB2	2:C:662:SER:HB3	1.82	0.62
3:D:714:GLU:HG2	3:D:715:LYS:N	2.15	0.62
3:D:933:ARG:HD2	3:D:937:ILE:HD11	1.80	0.62
3:D:974:VAL:HG11	3:D:1028:ILE:HD13	1.81	0.62
2:C:1107:MET:HE3	3:D:736:GLN:HE21	1.64	0.62
3:D:1267:VAL:O	3:D:1268:ASN:CB	2.48	0.62
5:F:170:HIS:NE2	6:1:32:DA:N7	2.48	0.61
2:C:26:TYR:O	2:C:29:SER:OG	2.16	0.61
2:C:653:MET:HG2	2:C:654:ASP:N	2.13	0.61
2:C:241:LEU:CD2	2:C:277:LEU:HD21	2.31	0.61
2:C:967:LEU:CD2	2:C:1021:LEU:HD13	2.28	0.61
3:D:720:ASN:O	3:D:724:MET:SD	2.58	0.61
3:D:974:VAL:HG11	3:D:1028:ILE:HG21	1.82	0.61
3:D:615:LYS:HB2	3:D:616:PRO:HD3	1.82	0.61
2:C:1302:THR:HG22	5:F:246:PRO:HA	1.80	0.61
3:D:142:GLU:OE2	5:F:53:ARG:NH1	2.32	0.61
5:F:110:GLY:HA2	5:F:119:LEU:CD1	2.31	0.61
2:C:156:PHE:CZ	2:C:445:ILE:HG13	2.36	0.61
3:D:678:ARG:NH1	3:D:756:GLU:OE2	2.33	0.61
3:D:1071:GLY:HA2	3:D:1074:LEU:HD12	1.83	0.61
3:D:331:ILE:HD12	3:D:331:ILE:N	2.16	0.60
3:D:715:LYS:HG2	3:D:716:GLN:N	2.15	0.60
3:D:839:VAL:HG13	3:D:882:VAL:HG11	1.83	0.60
5:F:317:LEU:HD22	5:F:324:ILE:HG21	1.83	0.60
3:D:93:THR:HG22	3:D:94:GLN:H	1.65	0.60
3:D:965:SER:CB	3:D:974:VAL:O	2.48	0.60
3:D:978:ARG:HH12	3:D:1025:MET:CE	2.14	0.60
1:B:47:LEU:HD13	1:B:183:ILE:HD12	1.83	0.60
2:C:494:ASN:ND2	7:2:25:DA:OP1	2.34	0.60
3:D:644:MET:CE	3:D:740:LEU:HD13	2.31	0.60
6:1:44:DG:H3'	6:1:45:DT:H5''	1.84	0.60
3:D:1032:SER:HB3	3:D:1116:SER:HA	1.83	0.60
3:D:1067:ARG:HH22	3:D:1076:PRO:HD3	1.65	0.60
2:C:164:THR:OG1	2:C:167:SER:OG	2.20	0.60
3:D:645:VAL:CG2	3:D:701:LEU:HB2	2.31	0.60
1:A:228:LEU:HD21	1:B:224:LEU:HD23	1.84	0.60
2:C:390:PHE:HA	2:C:419:ILE:HG23	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1101:LEU:HD13	3:D:504:GLN:HG3	1.83	0.60
2:C:1269:ARG:HH22	3:D:340:GLN:HA	1.66	0.60
2:C:69:GLN:O	2:C:100:LEU:HD12	2.02	0.60
3:D:649:LYS:O	3:D:653:ILE:HG13	2.01	0.60
3:D:686:TRP:CG	3:D:758:PRO:HG3	2.36	0.60
2:C:1313:HIS:HB2	3:D:474:LEU:HG	1.84	0.59
3:D:958:ILE:O	3:D:1008:GLY:N	2.33	0.59
6:1:34:DG:C2	7:2:30:DA:C2	2.90	0.59
3:D:782:GLY:O	3:D:935:PHE:CD1	2.56	0.59
6:1:33:DT:H2''	6:1:34:DG:H5'	1.83	0.59
2:C:245:ARG:HD3	2:C:337:PHE:CD1	2.36	0.59
2:C:1251:TYR:OH	3:D:348:ASP:OD2	2.20	0.59
3:D:826:ILE:HG21	3:D:992:LYS:O	2.03	0.59
3:D:690:ASN:C	3:D:738:ARG:HH22	2.07	0.59
3:D:518:VAL:H	3:D:716:GLN:CD	2.11	0.59
1:A:210:THR:O	1:A:211:ILE:C	2.46	0.59
2:C:241:LEU:HD23	2:C:277:LEU:HD21	1.85	0.59
3:D:388:ARG:HB3	3:D:390:LEU:HD13	1.83	0.59
5:F:244:ASN:ND2	5:F:248:ASP:OD2	2.31	0.59
1:A:11:PRO:HG2	1:B:231:PHE:HZ	1.62	0.58
6:1:52:DT:H2''	6:1:53:DG:C8	2.38	0.58
3:D:958:ILE:HG23	3:D:982:LEU:CD1	2.32	0.58
2:C:525:THR:HG21	2:C:687:ARG:HD3	1.85	0.58
1:A:47:LEU:HD13	1:A:183:ILE:HD12	1.85	0.58
2:C:1334:GLY:O	3:D:25:ALA:HB3	2.03	0.58
5:F:277:ARG:HE	5:F:288:LEU:HD21	1.69	0.58
2:C:967:LEU:HD21	2:C:1021:LEU:CD1	2.29	0.58
3:D:24:LEU:HD12	3:D:232:ASN:HB3	1.86	0.58
2:C:356:THR:HG21	2:C:362:ALA:HA	1.85	0.58
2:C:19:PRO:HA	2:C:1156:ARG:HD2	1.86	0.58
2:C:1149:TYR:HB3	2:C:1159:VAL:CG1	2.34	0.58
6:1:46:DG:H2''	6:1:47:DC:O4'	2.03	0.58
2:C:318:SER:OG	2:C:320:ASP:OD1	2.22	0.57
3:D:946:ALA:C	3:D:948:SER:H	2.12	0.57
6:1:45:DT:H2''	6:1:46:DG:C4	2.39	0.57
1:A:50:SER:HG	1:B:35:PHE:HZ	1.52	0.57
1:A:234:LEU:HD23	1:B:13:LEU:HB3	1.86	0.57
7:2:21:DG:H2''	7:2:22:DA:OP2	2.03	0.57
2:C:143:ARG:HH12	2:C:507:GLY:HA2	1.69	0.57
2:C:618:GLN:HE21	3:D:769:VAL:HB	1.70	0.57
3:D:367:GLY:HA3	3:D:448:GLN:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:831:VAL:O	3:D:834:PRO:HD3	2.04	0.57
6:1:31:DT:H2''	6:1:32:DA:OP2	2.05	0.57
2:C:189:ASP:HB2	2:C:190:PRO:HD2	1.85	0.57
2:C:1005:GLU:HG2	2:C:1006:GLU:H	1.69	0.57
3:D:1053:LEU:O	3:D:1054:THR:C	2.47	0.57
2:C:967:LEU:HD21	2:C:1021:LEU:HD22	1.86	0.57
3:D:134:ASP:HB3	3:D:159:ILE:HD11	1.86	0.57
3:D:690:ASN:CG	3:D:738:ARG:NH2	2.62	0.57
3:D:751:ASP:C	3:D:781:LYS:NZ	2.60	0.57
5:F:140:PHE:CG	6:1:37:DA:H2''	2.40	0.57
5:F:317:LEU:CD2	5:F:324:ILE:HD12	2.34	0.57
2:C:1308:ILE:HG23	3:D:380:PHE:CE1	2.38	0.57
3:D:708:ASN:CB	3:D:714:GLU:HB3	2.35	0.57
3:D:572:THR:HG22	3:D:593:ASN:OD1	2.05	0.57
3:D:646:ILE:HG23	3:D:647:PRO:HD2	1.87	0.57
3:D:978:ARG:HH12	3:D:1025:MET:HE2	1.69	0.57
2:C:975:ILE:HD13	2:C:998:LEU:HD21	1.85	0.57
2:C:1313:HIS:HB3	3:D:473:THR:HA	1.87	0.57
3:D:1029:THR:CG2	3:D:1121:LEU:CD1	2.83	0.57
6:1:49:DG:C2'	6:1:50:DT:H5''	2.35	0.57
2:C:1271:GLY:O	2:C:1275:VAL:HG23	2.05	0.56
3:D:591:ILE:HD11	3:D:604:MET:HA	1.87	0.56
3:D:965:SER:CB	3:D:975:ILE:HA	2.29	0.56
3:D:1037:PHE:CZ	3:D:1040:MET:HE1	2.40	0.56
3:D:716:GLN:HG2	3:D:717:VAL:N	2.20	0.56
3:D:716:GLN:OE1	3:D:719:PHE:HE2	1.88	0.56
3:D:972:LYS:HD3	3:D:1002:VAL:HG11	1.87	0.56
1:A:50:SER:OG	1:B:35:PHE:CZ	2.58	0.56
2:C:1255:THR:O	2:C:1256:GLN:HB2	2.05	0.56
3:D:797:THR:O	3:D:801:VAL:HG23	2.05	0.56
2:C:1105:SER:HB2	3:D:731:ARG:HD2	1.87	0.56
3:D:1027:VAL:HG12	3:D:1027:VAL:O	2.04	0.56
3:D:747:MET:SD	3:D:940:ALA:HB2	2.45	0.56
3:D:1024:THR:HG22	3:D:1026:PRO:HD3	1.88	0.56
3:D:1052:GLU:CG	3:D:1053:LEU:H	2.15	0.56
2:C:1129:ASN:OD1	2:C:1177:ARG:NH2	2.37	0.56
3:D:555:TYR:CD1	3:D:565:ALA:HB2	2.41	0.56
7:2:19:DA:H2'	7:2:20:DG:O4'	2.06	0.56
3:D:739:GLN:HG2	3:D:744:ARG:HH11	1.70	0.56
2:C:901:LEU:HD13	5:F:278:PHE:CE2	2.41	0.55
3:D:392:THR:HB	5:F:323:ASN:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1004:ALA:CB	3:D:1017:VAL:HA	2.36	0.55
7:2:10:DC:H2'	7:2:11:DA:C8	2.41	0.55
2:C:907:GLY:O	2:C:909:LYS:N	2.39	0.55
5:F:313:LEU:O	5:F:317:LEU:HG	2.05	0.55
2:C:443:ASP:HB3	2:C:450:ASN:HD21	1.70	0.55
3:D:749:LYS:HB3	3:D:750:PRO:HD2	1.89	0.55
3:D:885:VAL:HG13	3:D:894:VAL:HG11	1.87	0.55
3:D:1064:SER:O	3:D:1072:LYS:NZ	2.39	0.55
3:D:1134:ILE:HD11	3:D:1244:GLN:HG3	1.87	0.55
6:1:47:DC:H2''	6:1:48:DA:H5'	1.84	0.55
2:C:196:VAL:HG23	2:C:206:ALA:HA	1.88	0.55
2:C:390:PHE:HA	2:C:419:ILE:CG2	2.36	0.55
7:2:13:DA:H2''	7:2:14:DC:H5'	1.88	0.55
3:D:242:LEU:HD12	3:D:243:PRO:HD2	1.88	0.55
3:D:1133:ASP:O	3:D:1134:ILE:CD1	2.54	0.55
6:1:32:DA:C2	7:2:32:DA:C4	2.95	0.55
3:D:932:MET:SD	8:3:17:U:H2'	2.47	0.55
2:C:1285:TYR:CD2	3:D:1361:THR:HG21	2.41	0.55
3:D:320:ASN:OD1	7:2:22:DA:C6	2.56	0.55
3:D:1052:GLU:HG2	3:D:1053:LEU:N	2.21	0.55
2:C:782:VAL:HG21	2:C:792:GLY:HA2	1.89	0.55
3:D:432:LEU:HD13	3:D:499:ILE:HG21	1.88	0.55
6:1:48:DA:H8	6:1:48:DA:OP2	1.90	0.55
3:D:1029:THR:CG2	3:D:1121:LEU:HD11	2.31	0.55
2:C:42:ASP:O	2:C:50:GLU:HG2	2.07	0.54
2:C:960:LEU:HD11	2:C:1032:LYS:HG3	1.90	0.54
1:B:47:LEU:HD13	1:B:183:ILE:CD1	2.37	0.54
5:F:151:ARG:HG3	5:F:152:GLN:N	2.23	0.54
2:C:562:GLU:HG2	2:C:574:SER:HB2	1.88	0.54
3:D:1123:ARG:O	3:D:1125:PRO:HD3	2.07	0.54
2:C:183:TRP:CH2	6:1:49:DG:C5	2.95	0.54
3:D:48:THR:O	3:D:50:LYS:N	2.36	0.54
3:D:320:ASN:O	3:D:321:LYS:CB	2.53	0.54
3:D:1049:GLN:O	3:D:1057:SER:HA	2.08	0.54
2:C:660:VAL:HG11	3:D:769:VAL:HG13	1.90	0.54
2:C:797:GLY:HA3	2:C:1233:LEU:HD23	1.89	0.54
3:D:517:CYS:SG	3:D:716:GLN:OE1	2.62	0.54
3:D:694:SER:HB2	3:D:738:ARG:NE	2.22	0.54
1:A:184:ALA:HB2	2:C:1091:GLY:HA3	1.88	0.54
2:C:638:SER:O	2:C:639:LYS:CG	2.55	0.54
3:D:1067:ARG:HH22	3:D:1076:PRO:CD	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:576:SER:OG	2:C:659:GLN:O	2.25	0.54
3:D:1175:LEU:HD12	3:D:1177:ILE:HG12	1.90	0.54
3:D:1280:VAL:HG12	3:D:1281:GLU:N	2.23	0.54
6:1:49:DG:H2''	6:1:50:DT:C4'	2.38	0.54
1:A:159:ILE:HD12	2:C:876:GLU:OE1	2.07	0.53
2:C:1077:SER:HA	3:D:356:THR:OG1	2.08	0.53
3:D:647:PRO:O	3:D:650:LYS:HB2	2.08	0.53
3:D:748:ALA:HB2	3:D:941:ALA:CB	2.38	0.53
3:D:978:ARG:NH1	3:D:1025:MET:CE	2.71	0.53
3:D:1067:ARG:NH1	3:D:1074:LEU:O	2.41	0.53
6:1:53:DG:H1'	6:1:54:DA:H5''	1.91	0.53
7:2:20:DG:H2''	7:2:21:DG:H5'	1.90	0.53
2:C:1044:PRO:HB2	5:F:214:ARG:HG2	1.89	0.53
3:D:644:MET:HE2	3:D:740:LEU:HD13	1.90	0.53
3:D:1159:ILE:HA	3:D:1206:ARG:HG2	1.90	0.53
3:D:1271:SER:OG	3:D:1292:LEU:HD21	2.08	0.53
2:C:902:LEU:HD11	5:F:259:ILE:HD11	1.89	0.53
3:D:518:VAL:HG13	3:D:714:GLU:OE1	2.08	0.53
2:C:808:ASN:HA	3:D:629:PHE:HB3	1.91	0.53
3:D:518:VAL:HG21	3:D:708:ASN:CG	2.32	0.53
3:D:927:GLY:O	3:D:931:THR:OG1	2.21	0.53
3:D:71:LEU:HG	3:D:90:VAL:HG21	1.90	0.53
3:D:123:ARG:HH22	3:D:1334:GLU:HG2	1.73	0.53
2:C:56:VAL:HG12	2:C:59:ILE:HD11	1.90	0.53
3:D:458:ASN:ND2	8:3:17:U:O3'	2.41	0.53
3:D:120:LEU:HA	3:D:121:PRO:C	2.33	0.53
3:D:395:LYS:HG2	5:F:251:GLN:HE22	1.73	0.53
3:D:739:GLN:O	3:D:762:ASN:HB2	2.09	0.53
1:A:158:ARG:NE	1:A:172:LEU:HD11	2.24	0.53
2:C:208:ILE:HD11	2:C:365:GLU:HB2	1.90	0.53
2:C:894:GLN:HA	3:D:77:ARG:HH21	1.73	0.53
3:D:739:GLN:HG2	3:D:744:ARG:NH1	2.24	0.53
3:D:691:ASP:N	3:D:738:ARG:NH2	2.57	0.52
3:D:709:ARG:HG2	3:D:709:ARG:HH11	1.74	0.52
3:D:845:ALA:O	3:D:846:GLU:CB	2.53	0.52
3:D:1006:GLY:H	3:D:1009:GLU:CD	2.17	0.52
2:C:218:GLU:OE2	2:C:299:LYS:HD3	2.09	0.52
2:C:1107:MET:HE3	3:D:736:GLN:HA	1.91	0.52
3:D:755:ILE:HD12	3:D:755:ILE:H	1.75	0.52
2:C:1100:PRO:HB2	3:D:639:VAL:HG23	1.91	0.52
5:F:116:LEU:HA	5:F:119:LEU:HD12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:46:GLN:HB2	2:C:51:ALA:CA	2.39	0.52
2:C:245:ARG:HG2	2:C:337:PHE:CZ	2.44	0.52
3:D:620:PHE:CZ	3:D:624:ILE:HD11	2.44	0.52
3:D:701:LEU:HD11	3:D:720:ASN:HD22	1.67	0.52
3:D:490:ILE:O	3:D:499:ILE:HG22	2.09	0.52
3:D:1134:ILE:O	3:D:1135:THR:C	2.50	0.52
3:D:749:LYS:C	3:D:781:LYS:CD	2.76	0.52
3:D:1045:THR:HG22	3:D:1067:ARG:NE	2.25	0.52
5:F:156:ARG:NH2	6:1:33:DT:H2'	2.24	0.52
5:F:321:GLY:CA	5:F:324:ILE:HG22	2.40	0.52
2:C:200:ARG:CG	2:C:200:ARG:O	2.58	0.52
2:C:1281:TYR:CD2	3:D:484:MET:HE3	2.45	0.52
3:D:418:GLU:CD	4:E:48:VAL:HG21	2.35	0.52
3:D:450:HIS:HE1	3:D:625:MET:HE1	1.69	0.52
3:D:701:LEU:O	3:D:718:SER:CB	2.58	0.52
5:F:317:LEU:HD13	5:F:324:ILE:HD13	1.92	0.52
2:C:397:LEU:O	2:C:398:SER:OG	2.22	0.52
3:D:701:LEU:HD11	3:D:720:ASN:ND2	2.24	0.52
5:F:227:GLY:HA2	7:2:20:DG:C6	2.45	0.51
6:1:32:DA:N3	7:2:32:DA:C2	2.78	0.51
1:A:45:ARG:NH2	2:C:1084:ASP:OD1	2.38	0.51
1:A:92:VAL:O	1:A:148:ARG:NH2	2.43	0.51
1:B:166:ARG:HB3	1:B:167:PRO:HD2	1.93	0.51
2:C:1081:PRO:HB2	2:C:1083:GLU:OE1	2.10	0.51
3:D:1133:ASP:C	3:D:1244:GLN:HE22	2.17	0.51
1:A:47:LEU:HD13	1:A:183:ILE:CD1	2.39	0.51
2:C:696:ASP:O	2:C:795:ALA:HB1	2.10	0.51
2:C:841:ARG:CZ	3:D:257:GLY:HA2	2.39	0.51
3:D:1167:LYS:HB2	3:D:1174:ARG:HD2	1.91	0.51
2:C:1333:LEU:O	3:D:113:HIS:NE2	2.34	0.51
3:D:748:ALA:HB2	3:D:941:ALA:HB2	1.92	0.51
1:B:92:VAL:O	1:B:148:ARG:NH2	2.43	0.51
1:B:158:ARG:NE	1:B:172:LEU:HD11	2.25	0.51
2:C:700:VAL:HG21	2:C:1114:GLU:HG2	1.92	0.51
3:D:705:THR:OG1	3:D:718:SER:HA	2.09	0.51
2:C:200:ARG:O	2:C:200:ARG:HG2	2.10	0.51
2:C:615:VAL:O	2:C:615:VAL:HG13	2.11	0.51
2:C:1103:VAL:HG22	2:C:1111:GLN:NE2	2.26	0.51
2:C:1294:LYS:HD3	3:D:347:VAL:HG13	1.92	0.51
2:C:1334:GLY:O	3:D:25:ALA:CB	2.59	0.51
3:D:108:ALA:HB3	3:D:279:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:620:PHE:CE2	3:D:624:ILE:HD11	2.46	0.51
3:D:70:CYS:SG	3:D:74:LYS:N	2.83	0.51
3:D:334:LYS:HG2	3:D:339:ARG:HD2	1.92	0.51
3:D:751:ASP:N	3:D:781:LYS:NZ	2.35	0.51
3:D:813:ASP:OD1	3:D:883:ARG:NH2	2.39	0.51
3:D:827:GLU:HB3	3:D:832:LYS:HG3	1.91	0.51
3:D:934:THR:HB	3:D:1133:ASP:OD2	2.10	0.51
3:D:943:ARG:CG	3:D:944:ALA:N	2.74	0.51
2:C:461:GLU:OE2	2:C:465:ARG:NH2	2.44	0.51
2:C:590:PRO:HB2	2:C:655:VAL:HG21	1.91	0.51
2:C:892:GLU:OE2	3:D:77:ARG:NH2	2.44	0.51
3:D:1004:ALA:HB3	3:D:1017:VAL:HA	1.93	0.51
3:D:1327:GLU:O	3:D:1331:VAL:HG23	2.11	0.51
2:C:1061:GLN:HB2	2:C:1062:PRO:HD2	1.92	0.51
3:D:1037:PHE:CG	3:D:1040:MET:SD	3.03	0.51
5:F:222:VAL:HG12	5:F:235:LEU:HB2	1.93	0.51
6:1:48:DA:H2'	6:1:49:DG:C1'	2.41	0.51
2:C:374:GLU:OE2	6:1:43:DT:H72	2.10	0.51
3:D:721:SER:O	3:D:725:MET:SD	2.69	0.51
3:D:803:VAL:HG21	3:D:1309:ILE:O	2.11	0.51
3:D:1063:ASP:O	3:D:1065:ALA:N	2.44	0.51
5:F:79:PHE:O	5:F:90:SER:OG	2.24	0.51
3:D:816:THR:HG22	3:D:818:GLU:H	1.76	0.50
3:D:958:ILE:HG23	3:D:982:LEU:HD11	1.93	0.50
3:D:845:ALA:O	3:D:846:GLU:HB3	2.11	0.50
5:F:70:LEU:HD11	6:1:41:DT:N3	2.27	0.50
1:A:166:ARG:HB3	1:A:167:PRO:HD2	1.93	0.50
2:C:127:ILE:HG13	2:C:127:ILE:O	2.11	0.50
2:C:1281:TYR:OH	3:D:432:LEU:HD23	2.12	0.50
3:D:750:PRO:HA	3:D:781:LYS:HG3	1.85	0.50
3:D:1067:ARG:NH2	3:D:1076:PRO:CD	2.74	0.50
1:B:64:VAL:HG13	1:B:78:ILE:HD13	1.93	0.50
3:D:46:TYR:CE2	6:1:31:DT:OP1	2.63	0.50
3:D:716:GLN:HG2	3:D:717:VAL:H	1.77	0.50
2:C:104:ILE:HD12	2:C:116:ASP:HB2	1.93	0.50
3:D:809:VAL:HG22	3:D:915:ILE:HD11	1.93	0.50
3:D:1156:LEU:HD23	3:D:1209:VAL:HA	1.93	0.50
5:F:170:HIS:HE1	6:1:32:DA:H62	1.60	0.50
2:C:1100:PRO:HB2	3:D:639:VAL:CG2	2.41	0.50
3:D:978:ARG:CG	3:D:1197:ASN:HD21	2.25	0.50
1:A:191:ARG:HG3	1:A:196:THR:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:39:ILE:O	2:C:73:TYR:OH	2.30	0.50
2:C:145:ILE:HD11	2:C:506:PHE:CD1	2.47	0.50
2:C:518:ASN:O	2:C:519:ASN:HB2	2.10	0.50
3:D:943:ARG:CG	3:D:944:ALA:H	2.20	0.50
2:C:61:SER:HB3	2:C:479:LEU:HB3	1.94	0.49
2:C:563:THR:OG1	2:C:569:ILE:O	2.24	0.49
2:C:1285:TYR:HD2	3:D:1361:THR:HG21	1.77	0.49
3:D:458:ASN:CG	3:D:458:ASN:O	2.53	0.49
2:C:992:LEU:HB3	2:C:993:PRO:HD2	1.93	0.49
1:A:64:VAL:HG13	1:A:78:ILE:HD13	1.94	0.49
3:D:937:ILE:O	3:D:937:ILE:HG22	2.10	0.49
5:F:321:GLY:HA2	5:F:324:ILE:HG22	1.93	0.49
2:C:894:GLN:NE2	3:D:69:GLU:HG2	2.26	0.49
3:D:475:GLU:OE1	4:E:28:ARG:NH2	2.45	0.49
3:D:518:VAL:O	3:D:520:ALA:N	2.45	0.49
5:F:105:ILE:HD11	5:F:147:THR:HG22	1.94	0.49
3:D:714:GLU:HG2	3:D:715:LYS:H	1.76	0.49
3:D:876:SER:CB	3:D:990:ARG:CZ	2.91	0.49
2:C:533:LEU:HD21	2:C:571:LEU:HD13	1.94	0.49
3:D:1049:GLN:O	3:D:1058:SER:N	2.40	0.49
5:F:100:ARG:CB	6:1:42:DG:H5''	2.42	0.49
6:1:53:DG:H2''	6:1:54:DA:H5'	1.94	0.49
2:C:253:PHE:CZ	2:C:287:VAL:HG12	2.48	0.49
2:C:671:LEU:HD23	2:C:1186:VAL:CG1	2.42	0.49
2:C:847:PRO:HB3	2:C:1047:LEU:HD11	1.95	0.49
2:C:1210:ILE:CG2	2:C:1211:ARG:N	2.75	0.49
3:D:716:GLN:CG	3:D:717:VAL:H	2.26	0.49
3:D:751:ASP:CA	3:D:781:LYS:HZ2	2.22	0.49
3:D:839:VAL:HG12	3:D:864:LEU:HD12	1.94	0.49
3:D:1269:ALA:HB2	3:D:1275:LEU:HD23	1.95	0.49
2:C:673:HIS:CE1	3:D:766:GLY:HA3	2.48	0.49
2:C:839:VAL:O	2:C:839:VAL:HG13	2.12	0.49
3:D:416:ILE:CD1	3:D:441:LEU:HD21	2.42	0.49
3:D:977:SER:OG	3:D:980:THR:OG1	2.16	0.49
3:D:1217:PRO:HA	3:D:1220:ILE:HD12	1.95	0.49
3:D:1259:GLN:OE1	3:D:1262:ARG:NH2	2.46	0.49
6:1:54:DA:N7	6:1:55:DC:N4	2.61	0.49
3:D:868:TRP:O	3:D:872:LEU:HG	2.13	0.49
6:1:49:DG:H2''	6:1:50:DT:OP1	2.12	0.49
2:C:1145:ILE:HG22	2:C:1161:LEU:HD11	1.94	0.48
5:F:129:ARG:HD2	5:F:149:TRP:CZ3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1:32:DA:N1	7:2:32:DA:C6	2.81	0.48
2:C:200:ARG:CD	6:1:50:DT:O2	2.57	0.48
2:C:590:PRO:HG3	2:C:605:TYR:CE1	2.48	0.48
2:C:914:LYS:HG2	2:C:915:ASP:H	1.78	0.48
3:D:555:TYR:HA	3:D:565:ALA:HA	1.96	0.48
3:D:1050:THR:OG1	3:D:1057:SER:CB	2.57	0.48
3:D:1067:ARG:NH1	3:D:1071:GLY:O	2.46	0.48
5:F:317:LEU:HD21	5:F:324:ILE:HD12	1.96	0.48
6:1:53:DG:H1'	6:1:54:DA:C5'	2.43	0.48
6:1:57:DC:H2''	6:1:58:DG:OP2	2.11	0.48
2:C:186:PHE:CE1	2:C:196:VAL:HG22	2.48	0.48
3:D:739:GLN:CA	3:D:740:LEU:N	2.69	0.48
3:D:836:ARG:HB2	3:D:873:GLU:OE2	2.13	0.48
2:C:564:PRO:O	2:C:569:ILE:HA	2.12	0.48
2:C:1287:LEU:O	2:C:1291:LEU:HG	2.13	0.48
2:C:1296:ASP:O	2:C:1297:ASP:C	2.55	0.48
3:D:751:ASP:C	3:D:781:LYS:HZ2	2.20	0.48
3:D:1134:ILE:CG2	3:D:1138:LEU:HG	2.42	0.48
2:C:186:PHE:CD1	2:C:196:VAL:HG22	2.48	0.48
2:C:1287:LEU:HD22	3:D:1357:ILE:HD11	1.94	0.48
3:D:752:GLY:HA2	3:D:781:LYS:HZ1	1.76	0.48
3:D:703:THR:HG23	3:D:703:THR:O	2.14	0.48
6:1:49:DG:H2''	6:1:50:DT:C5'	2.43	0.48
2:C:28:LEU:HD21	2:C:524:ILE:HG13	1.96	0.48
3:D:679:TYR:OH	3:D:754:ILE:O	2.23	0.48
3:D:831:VAL:HB	3:D:834:PRO:HG3	1.94	0.48
3:D:1050:THR:HA	3:D:1057:SER:HA	1.95	0.48
5:F:158:ILE:HG22	5:F:158:ILE:O	2.12	0.48
5:F:65:ILE:HG22	5:F:99:LEU:HD13	1.95	0.48
2:C:90:VAL:HG12	2:C:91:THR:N	2.28	0.48
3:D:739:GLN:HG3	3:D:744:ARG:CD	2.33	0.48
2:C:369:MET:HE3	2:C:370:MET:CG	2.43	0.48
3:D:29:MET:HG3	3:D:33:TRP:CZ2	2.49	0.48
3:D:1134:ILE:HD11	3:D:1244:GLN:CG	2.44	0.48
2:C:673:HIS:CE1	3:D:766:GLY:CA	2.97	0.47
3:D:126:LEU:HD23	3:D:223:LEU:HD11	1.95	0.47
2:C:77:GLU:HB2	2:C:78:PRO:HD2	1.96	0.47
2:C:1273:MET:HE3	7:2:14:DC:O4'	2.14	0.47
3:D:807:LEU:HD11	3:D:894:VAL:HG13	1.95	0.47
3:D:1064:SER:HA	3:D:1067:ARG:HB2	1.95	0.47
3:D:1175:LEU:HD12	3:D:1177:ILE:CG1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1064:ASP:OD1	2:C:1239:VAL:HG12	2.14	0.47
3:D:646:ILE:HG23	3:D:647:PRO:CD	2.43	0.47
3:D:849:LEU:HD23	3:D:857:LEU:HD23	1.96	0.47
2:C:840:SER:O	2:C:840:SER:OG	2.23	0.47
3:D:609:TYR:OH	3:D:905:ARG:O	2.27	0.47
3:D:1364:ALA:O	3:D:1367:GLN:HG2	2.14	0.47
1:A:112:ALA:HB1	1:A:123:ILE:HG21	1.96	0.47
2:C:21:VAL:HG21	2:C:592:ARG:CZ	2.45	0.47
2:C:807:TRP:CZ3	2:C:1086:PRO:HG3	2.50	0.47
2:C:1100:PRO:CB	3:D:639:VAL:HG23	2.44	0.47
2:C:1119:MET:HE2	2:C:1204:LEU:HD22	1.96	0.47
3:D:126:LEU:HG	3:D:223:LEU:CD1	2.44	0.47
3:D:1267:VAL:O	3:D:1268:ASN:HB2	2.13	0.47
2:C:443:ASP:OD1	2:C:443:ASP:N	2.47	0.47
3:D:716:GLN:CG	3:D:717:VAL:N	2.77	0.47
2:C:156:PHE:CZ	2:C:445:ILE:CG1	2.97	0.47
3:D:357:VAL:HG12	3:D:461:PHE:CE2	2.49	0.47
3:D:839:VAL:HG12	3:D:839:VAL:O	2.15	0.47
3:D:933:ARG:HD3	3:D:937:ILE:HD11	1.95	0.47
3:D:958:ILE:HD11	3:D:1011:VAL:HG21	1.96	0.47
3:D:1052:GLU:O	3:D:1053:LEU:C	2.57	0.47
3:D:1132:LYS:O	3:D:1133:ASP:HB3	2.15	0.47
6:1:45:DT:H3'	6:1:45:DT:H6	1.79	0.47
7:2:22:DA:H2''	7:2:23:DT:C5'	2.44	0.47
2:C:905:ILE:CG2	5:F:314:ARG:HD2	2.45	0.47
3:D:490:ILE:HD11	3:D:614:LEU:HD11	1.92	0.47
3:D:876:SER:OG	3:D:990:ARG:CZ	2.63	0.47
3:D:1037:PHE:CZ	3:D:1040:MET:CE	2.97	0.47
3:D:1079:LYS:HE3	3:D:1087:ASP:OD1	2.15	0.47
2:C:13:LYS:NZ	2:C:1149:TYR:O	2.48	0.47
2:C:550:VAL:HG21	3:D:776:THR:HG22	1.96	0.47
2:C:563:THR:H	2:C:680:LEU:HD11	1.80	0.47
2:C:715:THR:HG22	2:C:786:GLY:H	1.80	0.47
2:C:812:PHE:CB	3:D:357:VAL:HG11	2.44	0.47
3:D:46:TYR:OH	6:1:31:DT:OP1	2.33	0.47
3:D:125:GLY:HA2	3:D:135:ILE:HD11	1.97	0.47
3:D:697:MET:SD	3:D:741:ALA:HB3	2.55	0.47
5:F:96:GLU:HA	5:F:99:LEU:HG	1.97	0.47
5:F:323:ASN:OD1	5:F:324:ILE:N	2.48	0.47
2:C:615:VAL:HA	2:C:638:SER:HB3	1.96	0.47
2:C:1044:PRO:HB2	5:F:214:ARG:CG	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:46:TYR:HE2	6:1:31:DT:OP1	1.98	0.47
6:1:48:DA:H2'	6:1:49:DG:O4'	2.15	0.47
3:D:57:PHE:O	3:D:98:ARG:NH2	2.47	0.46
3:D:943:ARG:NH1	3:D:1130:GLY:HA3	2.30	0.46
2:C:1245:ALA:HB2	3:D:372:MET:HG3	1.97	0.46
3:D:363:LEU:HB2	3:D:622:ASP:OD1	2.14	0.46
3:D:392:THR:HG21	5:F:322:LEU:O	2.16	0.46
1:B:112:ALA:HB1	1:B:123:ILE:HG21	1.96	0.46
2:C:799:ASN:HA	2:C:1231:TYR:HA	1.98	0.46
2:C:1119:MET:HG2	2:C:1204:LEU:HD13	1.97	0.46
3:D:706:VAL:O	3:D:714:GLU:O	2.33	0.46
2:C:245:ARG:CG	2:C:337:PHE:CE1	2.99	0.46
2:C:525:THR:CG2	2:C:687:ARG:HD2	2.45	0.46
3:D:690:ASN:CG	3:D:738:ARG:HH22	2.21	0.46
3:D:1029:THR:CG2	3:D:1121:LEU:CD2	2.94	0.46
6:1:31:DT:H2''	6:1:32:DA:H5'	1.96	0.46
2:C:716:ALA:HB3	2:C:784:ALA:HB3	1.98	0.46
3:D:1054:THR:OG1	3:D:1055:GLY:N	2.47	0.46
5:F:100:ARG:HB3	6:1:42:DG:C5'	2.45	0.46
1:A:145:LYS:HD3	1:A:147:GLN:HE21	1.79	0.46
1:B:145:LYS:HD3	1:B:147:GLN:HE21	1.79	0.46
2:C:1070:HIS:NE2	2:C:1114:GLU:OE1	2.46	0.46
2:C:1075:VAL:HG23	3:D:461:PHE:O	2.15	0.46
2:C:1107:MET:HE2	3:D:739:GLN:HB2	1.97	0.46
2:C:1210:ILE:HG22	2:C:1211:ARG:N	2.30	0.46
3:D:423:LEU:HD12	3:D:437:PHE:CD2	2.51	0.46
3:D:691:ASP:CA	3:D:738:ARG:HH21	2.26	0.46
3:D:1045:THR:HG22	3:D:1067:ARG:CZ	2.46	0.46
2:C:914:LYS:HG2	2:C:915:ASP:N	2.31	0.46
2:C:641:GLU:HG2	2:C:642:SER:H	1.81	0.46
2:C:907:GLY:O	2:C:909:LYS:HG3	2.15	0.46
3:D:582:ILE:HG23	3:D:623:GLN:CB	2.45	0.46
3:D:950:ILE:HB	3:D:1018:ALA:HB3	1.98	0.46
5:F:87:ASP:O	5:F:88:VAL:HB	2.16	0.46
3:D:555:TYR:CE1	3:D:565:ALA:HB2	2.50	0.46
3:D:747:MET:HE3	3:D:939:GLY:O	2.13	0.46
2:C:1107:MET:HE3	3:D:736:GLN:NE2	2.30	0.45
3:D:22:ILE:HG22	3:D:1336:ALA:HA	1.98	0.45
3:D:1050:THR:CG2	3:D:1056:LEU:O	2.54	0.45
5:F:289:GLU:O	5:F:293:ARG:HB2	2.15	0.45
3:D:714:GLU:CG	3:D:715:LYS:N	2.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:856:ILE:HG13	3:D:875:ASN:ND2	2.31	0.45
7:2:16:DC:H6	7:2:16:DC:C5'	2.27	0.45
2:C:195:PHE:CG	2:C:203:LYS:HD3	2.51	0.45
2:C:453:ILE:HD12	2:C:587:LEU:CD2	2.45	0.45
3:D:134:ASP:CB	3:D:159:ILE:HD11	2.46	0.45
2:C:98:VAL:HG21	2:C:124:MET:HE3	1.97	0.45
2:C:241:LEU:HD21	2:C:277:LEU:HD21	1.98	0.45
3:D:30:ILE:HG23	3:D:243:PRO:HB3	1.97	0.45
3:D:615:LYS:N	3:D:616:PRO:CD	2.79	0.45
2:C:907:GLY:O	2:C:908:GLU:C	2.59	0.45
2:C:1136:GLN:O	2:C:1137:GLU:HB2	2.16	0.45
3:D:339:ARG:CZ	3:D:798:ARG:HH22	2.29	0.45
3:D:933:ARG:HD2	3:D:937:ILE:CD1	2.45	0.45
3:D:972:LYS:HB3	3:D:1002:VAL:HG13	1.97	0.45
3:D:1005:LYS:HD2	3:D:1011:VAL:HG12	1.97	0.45
5:F:133:LYS:HE3	6:1:35:DC:H5''	1.98	0.45
2:C:726:TYR:CE2	2:C:728:ASP:HB2	2.52	0.45
3:D:646:ILE:CG2	3:D:647:PRO:HD2	2.46	0.45
3:D:1006:GLY:N	3:D:1009:GLU:CD	2.75	0.45
3:D:1031:VAL:HG23	3:D:1080:ILE:HG21	1.98	0.45
3:D:1063:ASP:O	3:D:1064:SER:C	2.60	0.45
2:C:122:VAL:HG22	2:C:490:GLN:HB3	1.98	0.45
2:C:280:ASP:O	2:C:281:ASP:HB3	2.17	0.45
3:D:129:ASP:HB2	3:D:220:ARG:NH1	2.32	0.45
3:D:664:ILE:HD11	3:D:685:ILE:HD11	1.99	0.45
3:D:933:ARG:HG3	3:D:937:ILE:HD12	1.98	0.45
3:D:974:VAL:HG11	3:D:1028:ILE:CD1	2.45	0.45
3:D:1041:ILE:HB	3:D:1044:GLN:HB2	1.97	0.45
5:F:189:LEU:O	5:F:190:ASP:CG	2.59	0.45
2:C:369:MET:HE3	2:C:370:MET:HG3	1.99	0.45
3:D:36:GLY:HA3	3:D:61:ILE:HG23	1.98	0.45
3:D:1037:PHE:CD2	3:D:1040:MET:SD	3.10	0.45
3:D:331:ILE:N	3:D:331:ILE:CD1	2.80	0.45
3:D:720:ASN:O	3:D:724:MET:CG	2.65	0.45
5:F:219:ILE:HG22	5:F:220:THR:N	2.32	0.45
6:1:48:DA:OP2	6:1:48:DA:C8	2.69	0.45
2:C:1234:LYS:HE2	2:C:1238:LEU:HD21	1.98	0.44
3:D:803:VAL:CG2	3:D:1309:ILE:O	2.65	0.44
3:D:843:VAL:HG13	3:D:861:ASN:HA	1.99	0.44
1:B:8:PHE:CD1	1:B:8:PHE:O	2.71	0.44
2:C:89:GLY:HA2	2:C:140:GLY:HA3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:144:VAL:HB	2:C:526:HIS:CE1	2.52	0.44
2:C:403:MET:SD	2:C:403:MET:C	3.00	0.44
2:C:894:GLN:NE2	3:D:69:GLU:CG	2.80	0.44
3:D:1292:LEU:O	3:D:1296:GLY:N	2.51	0.44
6:1:27:DC:H2''	6:1:28:DA:C8	2.52	0.44
6:1:32:DA:C2	7:2:32:DA:C5	3.06	0.44
6:1:45:DT:H2''	6:1:46:DG:C8	2.52	0.44
3:D:1029:THR:CG2	3:D:1121:LEU:HD21	2.44	0.44
2:C:463:GLN:HG3	2:C:505:PHE:HB2	2.00	0.44
3:D:22:ILE:HG13	3:D:1319:PHE:CZ	2.52	0.44
3:D:518:VAL:HG23	3:D:716:GLN:CB	2.42	0.44
3:D:1059:LEU:HB2	3:D:1107:VAL:HB	1.98	0.44
3:D:1131:THR:O	3:D:1133:ASP:N	2.22	0.44
5:F:317:LEU:HD22	5:F:324:ILE:CG2	2.48	0.44
5:F:317:LEU:HD22	5:F:324:ILE:CD1	2.48	0.44
6:1:48:DA:C6	6:1:49:DG:O6	2.70	0.44
1:B:100:LEU:HD11	1:B:121:VAL:HG11	2.00	0.44
1:B:166:ARG:HD2	1:B:170:ARG:HD3	2.00	0.44
2:C:477:GLU:OE1	5:F:108:ARG:HD2	2.18	0.44
3:D:464:ASP:CG	8:3:16:G:O2'	2.60	0.44
3:D:793:SER:OG	3:D:928:THR:HA	2.17	0.44
6:1:34:DG:H2''	6:1:35:DC:C6	2.53	0.44
2:C:911:SER:C	2:C:912:ASP:CA	2.88	0.44
2:C:1276:TRP:CH2	3:D:798:ARG:HG2	2.46	0.44
3:D:831:VAL:CG1	3:D:834:PRO:HG3	2.48	0.44
3:D:836:ARG:HG3	3:D:869:CYS:HB3	1.98	0.44
1:A:32:GLU:CD	1:B:150:ARG:HH22	2.26	0.44
1:B:48:LEU:HD22	3:D:535:ARG:HG3	1.99	0.44
2:C:1287:LEU:HD21	3:D:1351:VAL:HG22	1.99	0.44
3:D:697:MET:CE	3:D:737:ILE:HG22	2.47	0.44
3:D:809:VAL:HB	3:D:911:LYS:HA	1.99	0.44
5:F:126:GLY:HA3	5:F:153:THR:HG21	2.00	0.44
5:F:277:ARG:HE	5:F:288:LEU:CD2	2.30	0.44
2:C:812:PHE:HB2	3:D:357:VAL:HG11	1.99	0.44
3:D:646:ILE:CG2	3:D:647:PRO:CD	2.95	0.44
3:D:933:ARG:CD	3:D:937:ILE:CD1	2.93	0.44
3:D:1169:THR:OG1	3:D:1174:ARG:NH2	2.50	0.44
2:C:68:LEU:HD13	2:C:100:LEU:HD21	2.00	0.44
2:C:758:ARG:HG3	2:C:833:ILE:O	2.18	0.44
3:D:619:ILE:O	3:D:623:GLN:HG2	2.18	0.44
3:D:949:SER:HB3	3:D:1019:ASN:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1040:MET:HE1	3:D:1078:LEU:HD21	2.00	0.44
2:C:871:VAL:HG11	2:C:928:VAL:HG21	2.00	0.43
3:D:115:TRP:O	3:D:119:SER:HB3	2.18	0.43
3:D:785:ASP:HB2	3:D:935:PHE:CD1	2.36	0.43
3:D:1133:ASP:OD1	3:D:1134:ILE:HG12	2.17	0.43
3:D:1333:THR:O	3:D:1337:VAL:HG23	2.18	0.43
2:C:569:ILE:HD13	3:D:784:ALA:HA	1.99	0.43
3:D:115:TRP:CZ2	3:D:1329:THR:HG22	2.53	0.43
5:F:155:GLU:O	5:F:159:MET:HG3	2.18	0.43
3:D:298:MET:SD	5:F:117:LEU:HB3	2.57	0.43
3:D:572:THR:CG2	3:D:593:ASN:OD1	2.66	0.43
3:D:612:LEU:HB3	3:D:616:PRO:HG2	2.00	0.43
3:D:823:THR:HB	3:D:824:PRO:HD2	1.97	0.43
5:F:152:GLN:HE21	6:1:35:DC:H41	1.67	0.43
1:A:11:PRO:HG2	1:B:231:PHE:HE2	1.74	0.43
1:A:46:ILE:HG12	1:B:35:PHE:CE1	2.53	0.43
2:C:804:PHE:O	2:C:1225:VAL:HG13	2.18	0.43
3:D:518:VAL:HG23	3:D:716:GLN:CD	2.44	0.43
3:D:1040:MET:SD	3:D:1078:LEU:HD23	2.58	0.43
3:D:1080:ILE:HD12	3:D:1115:ILE:HD11	2.00	0.43
4:E:29:GLN:HB3	4:E:35:LYS:HG3	2.00	0.43
2:C:1017:GLN:O	2:C:1021:LEU:HG	2.19	0.43
3:D:334:LYS:HA	3:D:339:ARG:HD2	2.01	0.43
5:F:164:THR:HB	5:F:219:ILE:HD11	2.00	0.43
2:C:344:GLY:HA3	2:C:346:TYR:CZ	2.54	0.43
2:C:696:ASP:HB3	2:C:798:GLN:HG2	2.00	0.43
2:C:1004:ASP:N	2:C:1004:ASP:OD1	2.52	0.43
2:C:1313:HIS:CD2	4:E:31:GLN:NE2	2.87	0.43
3:D:99:ARG:HG3	3:D:100:GLU:HG3	2.00	0.43
3:D:981:GLU:HG2	3:D:996:LYS:HD3	2.00	0.43
3:D:1063:ASP:OD1	3:D:1065:ALA:HB3	2.18	0.43
1:B:182:ARG:HD2	3:D:581:MET:HE1	2.00	0.43
2:C:76:GLY:O	2:C:94:ALA:HB1	2.19	0.43
2:C:638:SER:O	2:C:639:LYS:HG2	2.18	0.43
2:C:936:ARG:HD2	2:C:1046:VAL:O	2.19	0.43
2:C:1157:GLN:O	2:C:1157:GLN:HG3	2.17	0.43
2:C:1301:ARG:CD	5:F:246:PRO:HG3	2.49	0.43
3:D:823:THR:HB	3:D:824:PRO:HD3	1.98	0.43
5:F:225:PRO:HA	5:F:233:ALA:HA	2.00	0.43
5:F:227:GLY:CA	7:2:19:DA:C2	2.99	0.43
5:F:321:GLY:O	5:F:324:ILE:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:LEU:HA	1:A:231:PHE:CD2	2.54	0.43
1:B:11:PRO:HB3	1:B:31:LEU:HD23	2.01	0.43
2:C:1234:LYS:CE	2:C:1238:LEU:HD21	2.49	0.43
3:D:30:ILE:HD13	3:D:243:PRO:HD3	2.00	0.43
1:A:100:LEU:HD11	1:A:121:VAL:HG11	2.01	0.43
2:C:183:TRP:CZ2	6:1:49:DG:C5	3.07	0.43
2:C:296:VAL:HG13	2:C:352:ARG:HH22	1.84	0.43
2:C:541:GLU:OE2	6:1:51:DC:C4	2.70	0.43
3:D:250:ARG:HD2	3:D:266:ASN:OD1	2.19	0.43
3:D:746:LEU:N	3:D:746:LEU:HD12	2.34	0.43
3:D:1027:VAL:N	3:D:1122:ALA:O	2.47	0.43
6:1:54:DA:C8	6:1:55:DC:C5	3.07	0.43
2:C:207:THR:HG21	2:C:351:LEU:HG	2.00	0.42
2:C:817:LEU:HD11	2:C:1080:ASN:HB2	2.00	0.42
3:D:714:GLU:CG	3:D:715:LYS:H	2.31	0.42
3:D:1175:LEU:O	3:D:1187:GLU:HA	2.19	0.42
6:1:49:DG:H2''	6:1:50:DT:H5''	2.01	0.42
2:C:104:ILE:HD13	2:C:484:LEU:HB3	2.00	0.42
2:C:653:MET:HE2	2:C:653:MET:HB3	1.86	0.42
2:C:673:HIS:CD2	2:C:1113:LEU:HD13	2.55	0.42
2:C:680:LEU:HD23	3:D:783:LEU:HD21	2.01	0.42
3:D:809:VAL:HG22	3:D:915:ILE:CD1	2.49	0.42
3:D:903:LEU:H	3:D:903:LEU:HD12	1.83	0.42
5:F:91:ARG:O	5:F:95:ILE:HG13	2.18	0.42
6:1:48:DA:H2'	6:1:49:DG:N9	2.34	0.42
2:C:539:THR:HB	2:C:542:ARG:HG3	2.01	0.42
3:D:173:GLY:O	3:D:174:ASP:C	2.62	0.42
3:D:282:LEU:CD2	5:F:125:LEU:HD21	2.49	0.42
3:D:1005:LYS:HE3	3:D:1015:GLU:OE1	2.19	0.42
3:D:1032:SER:CB	3:D:1116:SER:HA	2.49	0.42
5:F:317:LEU:HD22	5:F:324:ILE:HD12	2.00	0.42
6:1:51:DC:H2''	6:1:52:DT:O5'	2.18	0.42
7:2:4:DC:H2''	7:2:5:DC:H5'	2.02	0.42
2:C:109:ALA:HB1	2:C:110:PRO:HD2	2.02	0.42
3:D:1050:THR:HA	3:D:1056:LEU:O	2.19	0.42
2:C:90:VAL:CG1	2:C:91:THR:N	2.82	0.42
2:C:402:ARG:HD2	2:C:406:ASN:HD21	1.84	0.42
3:D:720:ASN:O	3:D:724:MET:HG3	2.19	0.42
3:D:949:SER:HB3	3:D:1019:ASN:HD22	1.85	0.42
6:1:33:DT:C2'	6:1:34:DG:H5'	2.49	0.42
2:C:228:VAL:HB	2:C:335:THR:OG1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1330:ARG:NH2	7:2:9:DT:O3'	2.53	0.42
6:1:32:DA:C2	7:2:32:DA:C6	3.07	0.42
1:A:11:PRO:HB3	1:A:31:LEU:HD23	2.02	0.42
2:C:550:VAL:HG21	3:D:776:THR:CG2	2.50	0.42
2:C:1002:LEU:CD1	2:C:1011:LEU:HD11	2.50	0.42
3:D:363:LEU:HD23	3:D:618:VAL:HG13	2.00	0.42
3:D:584:PRO:HD3	3:D:620:PHE:CD1	2.55	0.42
3:D:818:GLU:HB3	3:D:887:SER:HB2	2.01	0.42
5:F:176:ASN:OD1	7:2:26:DT:C7	2.65	0.42
5:F:227:GLY:CA	7:2:19:DA:H2	2.30	0.42
6:1:37:DA:H4'	6:1:38:DT:OP1	2.19	0.42
3:D:708:ASN:HD22	3:D:715:LYS:N	2.18	0.42
3:D:1063:ASP:C	3:D:1065:ALA:N	2.77	0.42
1:B:83:LEU:HD11	3:D:526:VAL:O	2.20	0.42
3:D:220:ARG:O	3:D:224:LEU:HG	2.20	0.42
3:D:885:VAL:HG12	3:D:1258:ARG:HD2	2.01	0.42
3:D:1005:LYS:CA	3:D:1009:GLU:OE1	2.68	0.42
1:A:166:ARG:HD2	1:A:170:ARG:HD3	2.01	0.42
1:B:178:SER:HA	1:B:179:PRO:HD2	1.91	0.42
2:C:149:LEU:HB2	2:C:530:ILE:CG2	2.49	0.42
3:D:75:TYR:HB2	3:D:92:VAL:HG21	2.01	0.42
3:D:750:PRO:CA	3:D:781:LYS:CG	2.74	0.42
2:C:641:GLU:HG2	2:C:642:SER:N	2.34	0.41
2:C:892:GLU:HG2	2:C:893:THR:N	2.35	0.41
2:C:1277:ALA:HA	3:D:921:GLN:HE22	1.85	0.41
5:F:62:LEU:O	5:F:65:ILE:HG12	2.19	0.41
1:B:101:THR:HG22	1:B:143:ARG:HG2	2.02	0.41
2:C:1109:ILE:HD12	3:D:644:MET:HE1	2.02	0.41
2:C:424:ASP:O	2:C:428:VAL:HG23	2.20	0.41
2:C:447:HIS:HA	2:C:551:HIS:CE1	2.55	0.41
2:C:1116:HIS:CE1	2:C:1226:THR:HG23	2.55	0.41
2:C:1278:LEU:HD23	3:D:484:MET:HE1	2.02	0.41
5:F:321:GLY:O	5:F:324:ILE:HG22	2.20	0.41
2:C:183:TRP:CZ2	6:1:49:DG:C6	3.08	0.41
2:C:619:ALA:HB2	2:C:654:ASP:HB2	2.03	0.41
6:1:51:DC:P	6:1:51:DC:H6	2.43	0.41
2:C:310:ILE:HG23	2:C:324:LYS:HE2	2.02	0.41
2:C:905:ILE:HG23	5:F:314:ARG:HD2	2.02	0.41
2:C:1284:ALA:N	3:D:479:GLU:OE1	2.53	0.41
3:D:94:GLN:O	3:D:97:VAL:HG22	2.20	0.41
3:D:738:ARG:O	3:D:743:MET:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:65:ASP:HB3	4:E:69:ARG:HH21	1.85	0.41
6:1:58:DG:H2"	6:1:59:DG:C8	2.55	0.41
2:C:634:VAL:HG12	2:C:636:CYS:SG	2.60	0.41
2:C:1005:GLU:HG2	2:C:1006:GLU:N	2.34	0.41
2:C:1257:GLN:HB2	2:C:1258:PRO:HD2	2.03	0.41
3:D:140:TYR:OH	3:D:312:ARG:NH1	2.53	0.41
3:D:212:THR:HA	3:D:215:LYS:HE3	2.02	0.41
3:D:587:LEU:HB3	3:D:588:PRO:HD2	2.02	0.41
3:D:588:PRO:O	3:D:591:ILE:HG22	2.21	0.41
3:D:849:LEU:HD23	3:D:857:LEU:CD2	2.51	0.41
3:D:958:ILE:O	3:D:1008:GLY:CA	2.68	0.41
4:E:6:VAL:HG12	4:E:6:VAL:O	2.21	0.41
5:F:329:LEU:HD23	5:F:329:LEU:HA	1.90	0.41
7:2:24:DT:H2"	7:2:25:DA:OP2	2.20	0.41
2:C:92:TYR:CE2	2:C:129:LEU:HB2	2.56	0.41
2:C:277:LEU:CD1	2:C:282:VAL:HG21	2.51	0.41
2:C:657:THR:HG21	2:C:1188:ASP:HB2	2.03	0.41
2:C:688:GLN:NE2	8:3:14:GTP:O3'	2.53	0.41
2:C:967:LEU:HD21	2:C:1021:LEU:CD2	2.50	0.41
2:C:1149:TYR:CG	2:C:1159:VAL:HG11	2.56	0.41
3:D:643:ASP:O	3:D:645:VAL:N	2.49	0.41
3:D:754:ILE:N	3:D:754:ILE:HD12	2.35	0.41
3:D:926:PRO:O	3:D:930:LEU:HG	2.21	0.41
5:F:303:ARG:O	5:F:307:VAL:HG23	2.20	0.41
1:A:57:THR:O	1:A:172:LEU:HD12	2.21	0.41
2:C:360:LEU:O	2:C:364:VAL:HG23	2.21	0.41
3:D:694:SER:CB	3:D:738:ARG:HE	2.34	0.41
3:D:1025:MET:O	3:D:1026:PRO:C	2.62	0.41
1:B:57:THR:O	1:B:172:LEU:HD12	2.21	0.41
2:C:337:PHE:HE2	2:C:343:HIS:CD2	2.38	0.41
2:C:848:GLU:CG	2:C:888:THR:HG22	2.49	0.41
3:D:290:ILE:HG23	3:D:291:ILE:HG13	2.02	0.41
3:D:355:ILE:HG21	3:D:466:MET:SD	2.61	0.41
3:D:832:LYS:HB3	3:D:1242:ARG:HD3	2.03	0.41
3:D:856:ILE:HG13	3:D:875:ASN:HD21	1.86	0.41
3:D:975:ILE:HD13	3:D:980:THR:HG21	2.02	0.41
3:D:1145:PHE:CD1	3:D:1256:ILE:HG21	2.56	0.41
3:D:1280:VAL:CG1	3:D:1281:GLU:N	2.82	0.41
5:F:65:ILE:HG22	5:F:99:LEU:CD1	2.51	0.41
1:A:101:THR:HG22	1:A:143:ARG:HG2	2.02	0.41
2:C:79:VAL:HG21	5:F:191:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:555:TYR:CD2	2:C:637:ARG:NH2	2.89	0.41
2:C:700:VAL:HG21	2:C:1114:GLU:CG	2.50	0.41
2:C:1289:GLU:HG2	2:C:1294:LYS:HE3	2.03	0.41
3:D:518:VAL:CG1	3:D:714:GLU:CD	2.93	0.41
3:D:576:ARG:HD3	3:D:593:ASN:HA	2.03	0.41
3:D:905:ARG:NH1	3:D:910:ASN:OD1	2.54	0.41
3:D:1134:ILE:C	3:D:1136:GLY:N	2.78	0.40
5:F:189:LEU:C	5:F:191:HIS:H	2.29	0.40
6:1:58:DG:C6	6:1:59:DG:C6	3.09	0.40
7:2:13:DA:C2'	7:2:14:DC:H5'	2.52	0.40
1:A:158:ARG:HB3	1:A:172:LEU:HD21	2.03	0.40
1:B:176:CYS:HB3	3:D:535:ARG:NH2	2.37	0.40
2:C:225:PHE:CE2	2:C:347:ILE:HB	2.56	0.40
2:C:564:PRO:CB	8:3:14:GTP:O1A	2.65	0.40
2:C:854:ILE:HB	2:C:857:VAL:HG21	2.03	0.40
2:C:887:VAL:HB	2:C:913:VAL:HG11	1.99	0.40
2:C:1254:VAL:HG13	3:D:249:LEU:HD23	2.01	0.40
3:D:1357:ILE:H	3:D:1357:ILE:HG13	1.65	0.40
2:C:911:SER:CA	2:C:912:ASP:N	2.83	0.40
2:C:1152:GLY:CA	2:C:1155:VAL:HG23	2.51	0.40
3:D:261:ALA:HA	5:F:220:THR:O	2.20	0.40
3:D:694:SER:HB2	3:D:738:ARG:HE	1.86	0.40
5:F:226:LEU:HD11	5:F:234:LEU:HD23	2.04	0.40
1:A:210:THR:HG22	1:A:211:ILE:CA	2.50	0.40
2:C:175:ARG:HD3	6:1:50:DT:H73	2.04	0.40
2:C:598:VAL:HA	2:C:627:GLY:O	2.21	0.40
3:D:416:ILE:HD13	3:D:441:LEU:HD21	2.02	0.40
3:D:1257:VAL:HA	3:D:1260:MET:HE2	2.03	0.40
1:B:205:MET:HE3	1:B:205:MET:HB2	2.00	0.40
2:C:228:VAL:HG23	2:C:337:PHE:HA	2.03	0.40
2:C:984:VAL:O	2:C:984:VAL:HG13	2.21	0.40
3:D:378:LYS:N	3:D:379:PRO:HD2	2.36	0.40
3:D:604:MET:HE2	3:D:604:MET:HB3	2.01	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	228/242 (94%)	216 (95%)	10 (4%)	2 (1%)	14	49
1	B	226/242 (93%)	214 (95%)	11 (5%)	1 (0%)	30	66
2	C	1332/1342 (99%)	1242 (93%)	82 (6%)	8 (1%)	21	58
3	D	1360/1407 (97%)	1258 (92%)	81 (6%)	21 (2%)	8	38
4	E	77/90 (86%)	74 (96%)	3 (4%)	0	100	100
5	F	275/336 (82%)	258 (94%)	12 (4%)	5 (2%)	6	33
All	All	3498/3659 (96%)	3262 (93%)	199 (6%)	37 (1%)	11	45

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	908	GLU
3	D	174	ASP
3	D	519	ASN
3	D	1024	THR
3	D	1053	LEU
3	D	1132	LYS
3	D	1268	ASN
5	F	322	LEU
2	C	756	TYR
3	D	710	ASP
3	D	829	GLY
3	D	948	SER
3	D	1054	THR
3	D	1064	SER
3	D	1130	GLY
5	F	297	LEU
1	A	208	ASN
2	C	1297	ASP
3	D	321	LYS
3	D	947	GLU

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Mol	Chain	Res	Type
3	D	1133	ASP
5	F	110	GLY
1	A	210	THR
1	B	8	PHE
2	C	234	ASP
2	C	1103	VAL
2	C	519	ASN
3	D	846	GLU
3	D	858	VAL
5	F	111	ASN
2	C	507	GLY
3	D	49	PHE
3	D	1134	ILE
5	F	245	GLY
3	D	1055	GLY
2	C	1186	VAL
3	D	823	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	198/208 (95%)	194 (98%)	4 (2%)	48	65
1	B	196/208 (94%)	192 (98%)	4 (2%)	48	65
2	C	1155/1157 (100%)	1134 (98%)	21 (2%)	51	66
3	D	1135/1168 (97%)	1091 (96%)	44 (4%)	28	50
4	E	67/74 (90%)	67 (100%)	0	100	100
5	F	240/292 (82%)	231 (96%)	9 (4%)	29	51
All	All	2991/3107 (96%)	2909 (97%)	82 (3%)	39	60

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU

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Mol	Chain	Res	Type
1	A	183	ILE
1	A	194	GLN
1	A	203	ILE
1	B	28	LEU
1	B	194	GLN
1	B	203	ILE
1	B	211	ILE
2	C	12	ARG
2	C	30	ILE
2	C	44	GLU
2	C	185	ASP
2	C	290	GLU
2	C	341	LEU
2	C	423	ASP
2	C	443	ASP
2	C	446	ASP
2	C	553	THR
2	C	700	VAL
2	C	851	THR
2	C	912	ASP
2	C	1159	VAL
2	C	1207	SER
2	C	1219	GLU
2	C	1223	ARG
2	C	1250	SER
2	C	1253	LEU
2	C	1272	GLU
2	C	1273	MET
3	D	27	PRO
3	D	93	THR
3	D	153	ASN
3	D	163	GLU
3	D	216	LYS
3	D	223	LEU
3	D	240	THR
3	D	259	ARG
3	D	321	LYS
3	D	342	LEU
3	D	347	VAL
3	D	371	LYS
3	D	384	LYS
3	D	398	LYS

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Mol	Chain	Res	Type
3	D	417	ARG
3	D	536	LEU
3	D	538	ARG
3	D	545	HIS
3	D	547	ARG
3	D	551	ARG
3	D	579	LEU
3	D	599	LYS
3	D	619	ILE
3	D	641	ILE
3	D	648	GLU
3	D	695	LYS
3	D	707	ILE
3	D	770	LEU
3	D	790	THR
3	D	798	ARG
3	D	803	VAL
3	D	809	VAL
3	D	850	LYS
3	D	935	PHE
3	D	1024	THR
3	D	1058	SER
3	D	1062	LEU
3	D	1067	ARG
3	D	1095	MET
3	D	1131	THR
3	D	1170	LYS
3	D	1175	LEU
3	D	1356	LEU
3	D	1366	HIS
5	F	156	ARG
5	F	174	GLU
5	F	190	ASP
5	F	192	GLU
5	F	219	ILE
5	F	246	PRO
5	F	255	MET
5	F	280	LEU
5	F	313	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	66	HIS
1	A	132	HIS
1	A	147	GLN
1	A	186	ASN
1	B	66	HIS
1	B	132	HIS
1	B	147	GLN
2	C	46	GLN
2	C	165	HIS
2	C	238	GLN
2	C	273	HIS
2	C	450	ASN
2	C	462	ASN
2	C	490	GLN
2	C	526	HIS
2	C	618	GLN
2	C	688	GLN
2	C	767	GLN
2	C	894	GLN
2	C	1220	GLN
2	C	1237	HIS
2	C	1257	GLN
2	C	1312	ASN
2	C	1313	HIS
3	D	104	HIS
3	D	153	ASN
3	D	196	GLN
3	D	340	GLN
3	D	341	ASN
3	D	364	HIS
3	D	424	ASN
3	D	450	HIS
3	D	458	ASN
3	D	504	GLN
3	D	545	HIS
3	D	623	GLN
3	D	690	ASN
3	D	702	GLN
3	D	708	ASN
3	D	716	GLN
3	D	720	ASN
3	D	736	GLN

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Mol	Chain	Res	Type
3	D	865	HIS
3	D	921	GLN
3	D	929	GLN
3	D	954	ASN
3	D	1010	GLN
3	D	1019	ASN
3	D	1098	GLN
3	D	1114	GLN
3	D	1197	ASN
3	D	1218	HIS
3	D	1227	HIS
3	D	1244	GLN
4	E	31	GLN
4	E	43	ASN
5	F	152	GLN
5	F	187	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	3	2/4 (50%)	2 (100%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	3	16	G
8	3	17	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	3
3	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	336:LEU	C	337:PHE	N	2.22
1	C	911:SER	C	912:ASP	N	2.12
1	C	891:GLY	C	892:GLU	N	2.08
1	D	1131:THR	C	1132:LYS	N	1.88
1	D	739:GLN	C	740:LEU	N	1.68

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	230/242 (95%)	-0.86	0 100 100	183, 279, 356, 428	0
1	B	228/242 (94%)	-0.85	1 (0%) 88 77	193, 298, 382, 466	0
2	C	1340/1342 (99%)	-0.91	0 100 100	140, 249, 396, 562	0
3	D	1362/1407 (96%)	-0.91	0 100 100	138, 279, 418, 529	0
4	E	79/90 (87%)	-0.96	0 100 100	245, 321, 482, 519	0
5	F	277/336 (82%)	-0.87	0 100 100	227, 330, 432, 542	0
6	1	33/50 (66%)	-0.58	0 100 100	272, 339, 468, 483	0
7	2	33/50 (66%)	-0.59	0 100 100	232, 318, 425, 477	0
8	3	3/4 (75%)	-0.97	0 100 100	298, 298, 327, 338	0
All	All	3585/3763 (95%)	-0.90	1 (0%) 100 100	138, 277, 415, 562	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	224	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	MG	D	1503	1/1	0.96	0.07	343,343,343,343	0
9	ZN	D	1502	1/1	1.00	0.03	298,298,298,298	0
9	ZN	D	1501	1/1	1.00	0.01	316,316,316,316	0

6.5 Other polymers [i](#)

There are no such residues in this entry.