



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2016 – 12:39 PM EDT

PDB ID : 5IPM
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027790

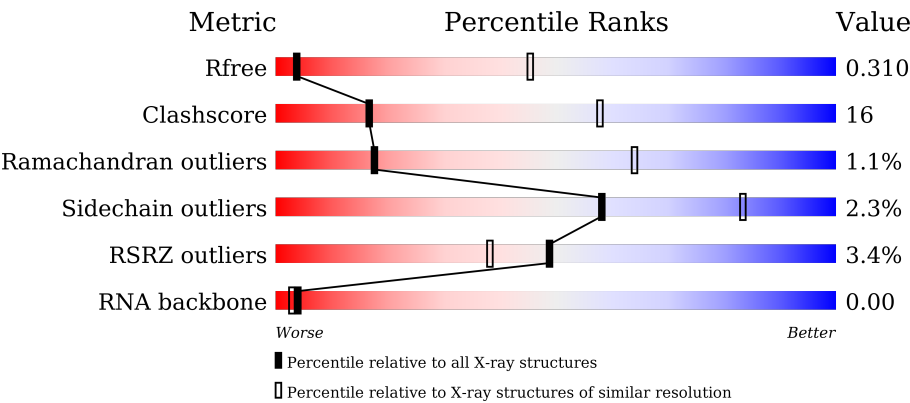
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	1039 (4.80-3.60)
Clashscore	102246	1140 (4.80-3.60)
Ramachandran outliers	100387	1083 (4.80-3.60)
Sidechain outliers	100360	1067 (4.80-3.60)
RSRZ outliers	91569	1042 (4.80-3.60)
RNA backbone	2183	1087 (5.60-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 (three-letter code: ZN) (formula: Zn).

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

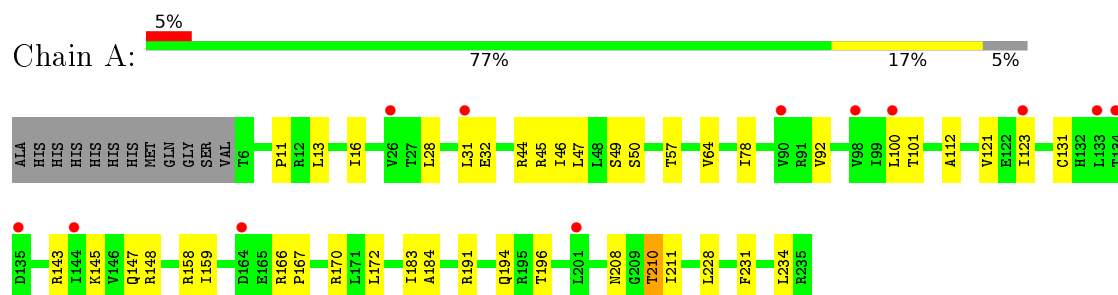
- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

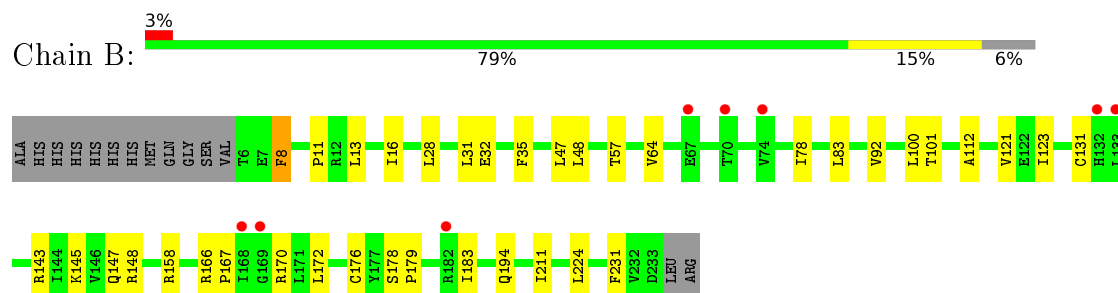
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

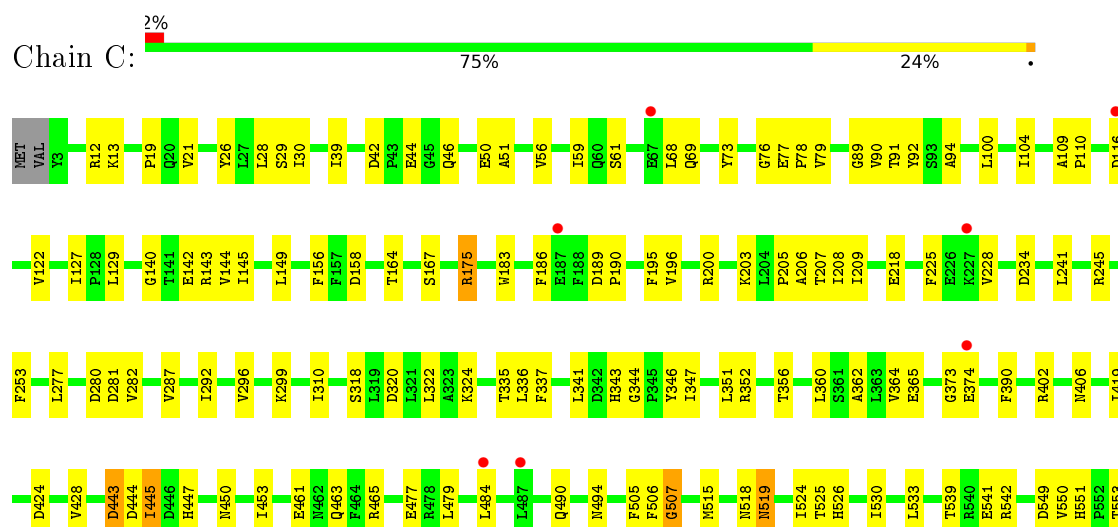
- Molecule 1: DNA-directed RNA polymerase subunit alpha



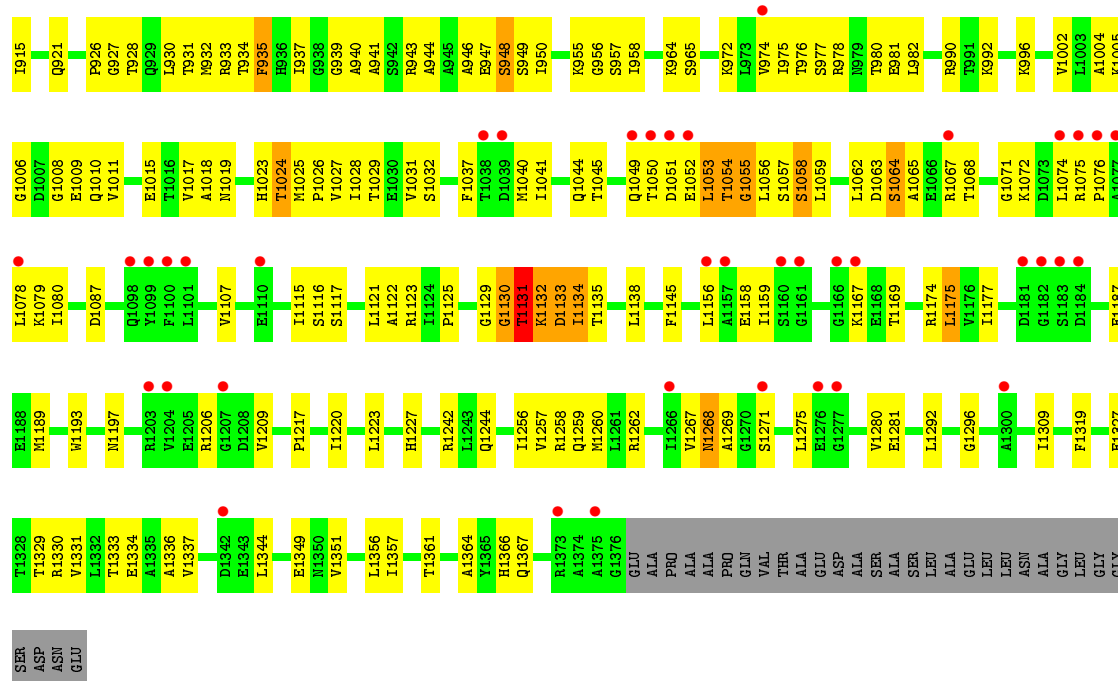
- Molecule 1: DNA-directed RNA polymerase subunit alpha



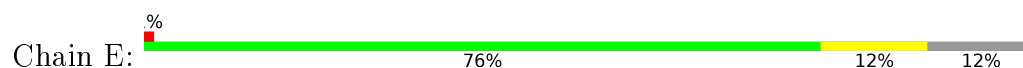
- Molecule 2: DNA-directed RNA polymerase subunit beta



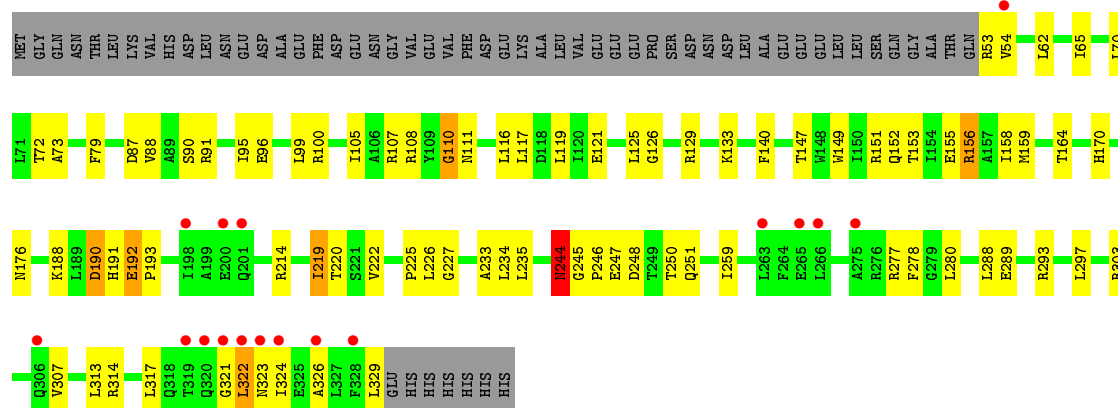




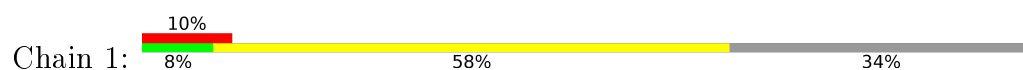
- Molecule 4: DNA-directed RNA polymerase subunit omega

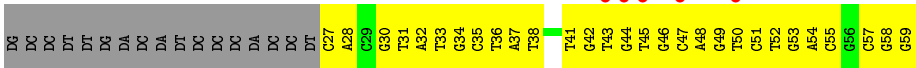


- Molecule 5: RNA polymerase sigma factor RpoS

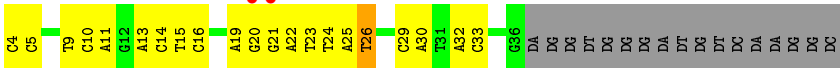
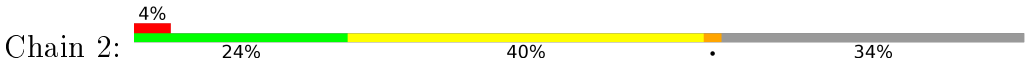


- Molecule 6: synthetic non-template strand DNA (50-MER)





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



● Molecule 8: nascent RNA 4-mer



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 49.99 – 4.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (126.46-4.20) 100.0 (49.99-4.20)	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 (5.05%)	DCC
Wilson B-factor (Å ²)	174.0	Xtriage
Anisotropy	0.560	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 225.4	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	0.94	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 [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.55	0/1809	0.73	1/2450 (0.0%)
1	B	0.53	0/1789	0.71	0/2425
2	C	0.61	1/10736 (0.0%)	0.79	8/14480 (0.1%)
3	D	0.62	2/10729 (0.0%)	0.86	8/14487 (0.1%)
4	E	0.53	0/629	0.73	0/847
5	F	0.64	2/2282 (0.1%)	0.87	1/3076 (0.0%)
6	1	0.39	0/762	0.66	0/1175
7	2	0.52	1/757 (0.1%)	0.68	0/1167
8	3	0.34	0/72	0.62	0/110
All	All	0.60	6/29565 (0.0%)	0.80	18/40217 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	F	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1131	THR	C-N	23.67	1.88	1.34
3	D	739	GLN	C-N	14.94	1.68	1.34
5	F	247	GLU	CD-OE1	8.12	1.34	1.25
5	F	247	GLU	CG-CD	7.43	1.63	1.51
2	C	445	ILE	N-CA	-5.76	1.34	1.46
7	2	26	DT	O3'-P	-5.14	1.54	1.61

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1131	THR	C-N-CA	-31.47	43.03	121.70
3	D	1131	THR	CA-C-N	-24.32	63.71	117.20
3	D	1131	THR	O-C-N	-20.56	89.81	122.70
3	D	780	ARG	NE-CZ-NH1	7.07	123.83	120.30
2	C	742	TYR	CB-CG-CD1	-6.56	117.06	121.00
2	C	175	ARG	NE-CZ-NH2	-6.54	117.03	120.30
2	C	1273	MET	CG-SD-CE	6.16	110.05	100.20
2	C	444	ASP	CA-C-N	-5.85	104.33	117.20
3	D	311	ARG	NE-CZ-NH2	-5.76	117.42	120.30
2	C	1106	ARG	NE-CZ-NH2	-5.60	117.50	120.30
5	F	244	ASN	O-C-N	-5.50	113.84	123.20
3	D	311	ARG	NE-CZ-NH1	5.37	122.98	120.30
2	C	742	TYR	CA-CB-CG	5.34	123.54	113.40
1	A	44	ARG	NE-CZ-NH2	-5.29	117.65	120.30
3	D	731	ARG	NE-CZ-NH2	-5.21	117.69	120.30
2	C	175	ARG	NE-CZ-NH1	5.19	122.90	120.30
3	D	783	LEU	CB-CG-CD2	-5.13	102.28	111.00
2	C	742	TYR	CB-CG-CD2	5.11	124.07	121.00

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

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	34	0
1	B	1767	0	1789	30	0
2	C	10570	0	10579	275	0
3	D	10568	0	10778	547	0
4	E	627	0	634	7	0
5	F	2253	0	2298	92	0
6	1	680	0	373	77	0
7	2	675	0	373	37	0
8	3	97	0	44	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	D	2	0	0	2	0
10	D	1	0	0	0	0
All	All	29027	0	28681	949	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 16.

All (949) 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	1.43
3:D:750:PRO:CA	3:D:781:LYS:HD2	1.51	1.38
3:D:750:PRO:C	3:D:781:LYS:HE3	1.40	1.38
3:D:690:ASN:CG	3:D:738:ARG:HH12	1.21	1.37
3:D:1133:ASP:O	3:D:1244:GLN:NE2	1.57	1.36
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: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:690:ASN:OD1	3:D:738:ARG:NH1	1.64	1.30
3:D:749:LYS:O	3:D:781:LYS:NZ	1.64	1.30
3:D:750:PRO:C	3:D:781:LYS:CE	1.99	1.29
3:D:690:ASN:CG	3:D:738:ARG:NH1	1.84	1.28
3:D:750:PRO:CA	3:D:781:LYS:CD	2.09	1.27
3:D:517:CYS:C	3:D:716:GLN:HE22	1.40	1.24
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
3:D:517:CYS:CA	3:D:716:GLN:HE22	1.63	1.12
3:D:752:GLY:N	3:D:781:LYS:HZ1	1.48	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	1.08
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:227:GLY:N	7:2:20:DG:O6	1.87	1.07
2:C:891:GLY:C	2:C:892:GLU:N	2.08	1.07
3:D:750:PRO:CA	3:D:781:LYS:CE	2.32	1.06
3:D:750:PRO:HA	3:D:781:LYS:CE	1.85	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
2:C:911:SER:C	2:C:912:ASP:N	2.12	1.02
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: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
3:D:750:PRO:C	3:D:781:LYS:NZ	2.17	0.98
3:D:518:VAL:HG21	3:D:708:ASN:ND2	1.79	0.97
3:D:750:PRO:C	3:D:781:LYS:HZ2	1.68	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
2:C:336:LEU:C	2:C:337:PHE:N	2.22	0.93
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
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
3:D:517:CYS:C	3:D:716:GLN:NE2	2.24	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:690:ASN:C	3:D:738:ARG:NH2	2.30	0.85
3:D:1067:ARG:HD3	3:D:1071:GLY:O	1.75	0.84
3:D:1023:HIS:O	3:D:1024:THR:HB	1.76	0.84
3:D:1029:THR:HG23	3:D:1121:LEU:HG	1.59	0.84
3:D:523:GLU:OE1	3:D:710:ASP:OD2	1.95	0.84
3:D:1029:THR:CG2	3:D:1121:LEU:HG	2.07	0.84
3:D:747:MET:CE	3:D:939:GLY:O	2.25	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
5:F:107:ARG:NH1	6:1:43:DT:OP1	2.14	0.81
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
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
2:C:1342:GLU:HG2	3:D:18:ASP:HB2	1.62	0.80
3:D:1132:LYS:CG	3:D:1133:ASP:H	1.93	0.80
3:D:933:ARG:O	3:D:937:ILE:HG13	1.80	0.80
2:C:1284:ALA:HA	3:D:1357:ILE:HD12	1.64	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:747:MET:HE3	3:D:939:GLY:O	1.80	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
1:A:50:SER:HG	1:B:35:PHE:HZ	1.30	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:1344:LEU:HD23	3:D:1349:GLU:HB3	1.64	0.78
3:D:490:ILE:HD11	3:D:614:LEU:CD1	2.12	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:1133:ASP:O	3:D:1134:ILE:HD13	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:739:GLN:CG	3:D:744:ARG:HD2	2.14	0.77
3:D:933:ARG:C	3:D:935:PHE:H	1.87	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
3:D:690:ASN:CG	3:D:738:ARG:CZ	2.52	0.77
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
1:A:13:LEU:HD21	1:A:16:ILE:HD11	1.67	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:898:CYS:HG	9:D:1502:ZN:ZN	0.99	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
2:C:674:ASP:O	3:D:772:TYR:OH	2.03	0.74
3:D:697:MET:SD	3:D:737:ILE:HG22	2.27	0.74
3:D:752:GLY:N	3:D:781:LYS:HZ2	1.84	0.74
3:D:518:VAL:CG1	3:D:714:GLU:OE1	2.36	0.74
6:1:50:DT:H3'	6:1:51:DC:H5''	1.69	0.73
3:D:933:ARG:CD	3:D:937:ILE:HD11	2.18	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:1131:THR:N	3:D:1132:LYS:HB2	1.86	0.73
3:D:749:LYS:O	3:D:781:LYS:CE	2.35	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:752:GLY:CA	3:D:781:LYS:HZ1	2.00	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
3:D:749:LYS:C	3:D:781:LYS:HD2	2.08	0.73
2:C:549:ASP:OD2	3:D:750:PRO:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:701:LEU:HD12	3:D:720:ASN:HD22	1.55	0.72
3:D:1037:PHE:CZ	3:D:1040:MET:HE1	2.25	0.72
3:D:739:GLN:C	3:D:740:LEU:CA	2.57	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
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:1023:HIS:O	3:D:1024:THR:CB	2.39	0.70
3:D:1133:ASP:O	3:D:1244:GLN:CD	2.30	0.70
3:D:518:VAL:CG2	3:D:716:GLN:HB2	2.21	0.70
3:D:452:LEU:HB3	3:D:500:ILE:HG23	1.71	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
3:D:644:MET:HE2	3:D:740:LEU:HD13	1.73	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
3:D:708:ASN:HB2	3:D:714:GLU:C	2.12	0.69
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:1067:ARG:NH2	3:D:1076:PRO:HD3	2.08	0.69
3:D:739:GLN:HG3	3:D:744:ARG:HA	1.74	0.69
6:1:47:DC:H2'	6:1:48:DA:H5'	1.74	0.69
2:C:1276:TRP:HH2	3:D:798:ARG:HG2	1.57	0.69
3:D:1037:PHE:CE2	3:D:1040:MET:CE	2.75	0.69
3:D:690:ASN:O	3:D:738:ARG:NH2	2.26	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:1029:THR:HG21	3:D:1121:LEU:HD21	1.74	0.68
7:2:15:DT:H5''	7:2:15:DT:H6	1.58	0.68
5:F:147:THR:O	5:F:151:ARG:HG2	1.94	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:708:ASN:HD22	3:D:714:GLU:CB	2.07	0.67
3:D:517:CYS:HA	3:D:716:GLN:CD	2.14	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
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:1306:LYS:HG2	5:F:250:THR:OG1	1.96	0.66
2:C:156:PHE:CE2	2:C:158:ASP:HB2	2.31	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:747:MET:HE1	3:D:939:GLY:C	2.16	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
3:D:1037:PHE:CE2	3:D:1040:MET:HE2	2.32	0.64
2:C:292:ILE:HD12	2:C:322:LEU:HD22	1.78	0.64
3:D:981:GLU:OE2	3:D:996:LYS:NZ	2.26	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:749:LYS:C	3:D:781:LYS:NZ	2.51	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
7:2:22:DA:H2''	7:2:23:DT:O5'	1.98	0.63
3:D:1050:THR:CG2	3:D:1051:ASP:N	2.60	0.63
1:B:83:LEU:HD21	3:D:526:VAL:HB	1.80	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:C:142:GLU:OE1	2:C:515:MET:CE	2.47	0.62
3:D:1068:THR:O	3:D:1072:LYS:HG2	2.00	0.62
3:D:582:ILE:HG23	3:D:623:GLN:HB3	1.80	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:974:VAL:HG11	3:D:1028:ILE:HD13	1.81	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: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
5:F:110:GLY:HA2	5:F:119:LEU:CD1	2.31	0.61
3:D:142:GLU:OE2	5:F:53:ARG:NH1	2.32	0.61
2:C:156:PHE:CZ	2:C:445:ILE:HG13	2.36	0.61
3:D:1071:GLY:HA2	3:D:1074:LEU:HD12	1.83	0.61
3:D:678:ARG:NH1	3:D:756:GLU:OE2	2.33	0.61
3:D:747:MET:HE1	3:D:939:GLY:O	1.99	0.61
3:D:331:ILE:N	3:D:331:ILE:HD12	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:978:ARG:HH12	3:D:1025:MET:CE	2.14	0.60
3:D:93:THR:HG22	3:D:94:GLN:H	1.65	0.60
3:D:747:MET:HE3	3:D:940:ALA:HA	1.82	0.60
3:D:965:SER:CB	3:D:974:VAL:O	2.48	0.60
6:1:44:DG:H3'	6:1:45:DT:H5''	1.84	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1067:ARG:HH22	3:D:1076:PRO:HD3	1.65	0.60
3:D:1032:SER:HB3	3:D:1116:SER:HA	1.83	0.60
2:C:164:THR:OG1	2:C:167:SER:OG	2.20	0.60
2:C:142:GLU:OE1	2:C:515:MET:HE2	2.02	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
2:C:1269:ARG:HH22	3:D:340:GLN:HA	1.66	0.60
2:C:1101:LEU:HD13	3:D:504:GLN:HG3	1.83	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
3:D:958:ILE:O	3:D:1008:GLY:N	2.33	0.59
2:C:1313:HIS:HB2	3:D:474:LEU:HG	1.84	0.59
6:1:34:DG:C2	7:2:30:DA:C2	2.90	0.59
6:1:33:DT:H2''	6:1:34:DG:H5'	1.83	0.59
3:D:782:GLY:O	3:D:935:PHE:CD1	2.56	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
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
5:F:190:ASP:OD1	5:F:190:ASP:C	2.42	0.58
2:C:356:THR:HG21	2:C:362:ALA:HA	1.85	0.58
6:1:46:DG:H2''	6:1:47:DC:O4'	2.03	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
6:1:45:DT:H2''	6:1:46:DG:C4	2.39	0.57
3:D:1129:GLY:O	3:D:1130:GLY:C	2.43	0.57
3:D:1130:GLY:C	3:D:1132:LYS:HB2	2.23	0.57
7:2:21:DG:H2''	7:2:22:DA:OP2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:LEU:HD23	1:B:13:LEU:HB3	1.86	0.57
6:1:31:DT:H2"	6:1:32:DA:OP2	2.05	0.57
2:C:143:ARG:HH12	2:C:507:GLY:HA2	1.69	0.57
3:D:367:GLY:HA3	3:D:448:GLN:HB2	1.87	0.57
2:C:618:GLN:HE21	3:D:769:VAL:HB	1.70	0.57
3:D:831:VAL:O	3:D:834:PRO:HD3	2.04	0.57
2:C:1005:GLU:HG2	2:C:1006:GLU:H	1.69	0.57
2:C:189:ASP:HB2	2:C:190:PRO:HD2	1.85	0.57
5:F:140:PHE:CG	6:1:37:DA:H2"	2.40	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
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
2:C:975:ILE:HD13	2:C:998:LEU:HD21	1.85	0.57
6:1:49:DG:C2'	6:1:50:DT:H5"	2.35	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
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: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
3:D:747:MET:CE	3:D:939:GLY:C	2.74	0.56
2:C:1105:SER:HB2	3:D:731:ARG:HD2	1.87	0.56
3:D:1027:VAL:O	3:D:1027:VAL:HG12	2.04	0.56
3:D:1024:THR:HG22	3:D:1026:PRO:HD3	1.88	0.56
3:D:747:MET:SD	3:D:940:ALA:HB2	2.45	0.56
3:D:1052:GLU:CG	3:D:1053:LEU:H	2.15	0.56
7:2:19:DA:H2'	7:2:20:DG:O4'	2.06	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
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
7:2:10:DC:H2'	7:2:11:DA:C8	2.41	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
3:D:392:THR:HB	5:F:323:ASN:HA	1.87	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
6:1:47:DC:H2''	6:1:48:DA:H5'	1.84	0.55
2:C:443:ASP:HB3	2:C:450:ASN:HD21	1.70	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
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
7:2:13:DA:H2''	7:2:14:DC:H5'	1.88	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
6:1:32:DA:C2	7:2:32:DA:C4	2.95	0.55
3:D:1133:ASP:O	3:D:1134:ILE:CD1	2.54	0.55
3:D:242:LEU:HD12	3:D:243:PRO:HD2	1.88	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:1052:GLU:HG2	3:D:1053:LEU:N	2.21	0.55
3:D:320:ASN:OD1	7:2:22:DA:C6	2.56	0.55
3:D:690:ASN:C	3:D:738:ARG:HH22	2.07	0.55
6:1:48:DA:H8	6:1:48:DA:OP2	1.90	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
3:D:1029:THR:CG2	3:D:1121:LEU:HD11	2.31	0.55
2:C:960:LEU:HD11	2:C:1032:LYS:HG3	1.90	0.54
2:C:42:ASP:O	2:C:50:GLU:HG2	2.07	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
3:D:1131:THR:O	3:D:1133:ASP:N	2.22	0.54
2:C:183:TRP:CH2	6:1:49:DG:C5	2.95	0.54
3:D:1049:GLN:O	3:D:1057:SER:HA	2.08	0.54
3:D:320:ASN:O	3:D:321:LYS:CB	2.53	0.54
3:D:48:THR:O	3:D:50:LYS:N	2.36	0.54
3:D:518:VAL:H	3:D:716:GLN:CD	2.11	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
2:C:660:VAL:HG11	3:D:769:VAL:HG13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:THR:O	1:A:211:ILE:C	2.46	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
3:D:1132:LYS:CG	3:D:1133:ASP:N	2.63	0.54
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
6:1:49:DG:H2"	6:1:50:DT:C4'	2.38	0.54
3:D:1280:VAL:HG12	3:D:1281:GLU:N	2.23	0.54
1:A:159:ILE:HD12	2:C:876:GLU:OE1	2.07	0.53
3:D:1067:ARG:NH1	3:D:1074:LEU:O	2.41	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
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
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:1044:PRO:HB2	5:F:214:ARG:HG2	1.89	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:927:GLY:O	3:D:931:THR:OG1	2.21	0.53
3:D:123:ARG:HH22	3:D:1334:GLU:HG2	1.73	0.53
3:D:71:LEU:HG	3:D:90:VAL:HG21	1.90	0.53
3:D:458:ASN:ND2	8:3:17:U:O3'	2.41	0.53
2:C:56:VAL:HG12	2:C:59:ILE:HD11	1.90	0.53
3:D:946:ALA:C	3:D:948:SER:H	2.12	0.53
3:D:739:GLN:O	3:D:762:ASN:HB2	2.09	0.53
3:D:395:LYS:HG2	5:F:251:GLN:HE22	1.73	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:1053:LEU:O	3:D:1054:THR:C	2.47	0.53
3:D:690:ASN:CG	3:D:738:ARG:NH2	2.62	0.53
3:D:739:GLN:HG2	3:D:744:ARG:NH1	2.24	0.53
3:D:709:ARG:HG2	3:D:709:ARG:HH11	1.74	0.52
3:D:691:ASP:N	3:D:738:ARG:NH2	2.57	0.52
3:D:751:ASP:C	3:D:781:LYS:NZ	2.60	0.52
3:D:845:ALA:O	3:D:846:GLU:CB	2.53	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:218:GLU:OE2	2:C:299:LYS:HD3	2.09	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
2:C:245:ARG:HG2	2:C:337:PHE:CZ	2.44	0.52
2:C:46:GLN:HB2	2:C:51:ALA:CA	2.39	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:933:ARG:C	3:D:935:PHE:N	2.57	0.52
3:D:490:ILE:O	3:D:499:ILE:HG22	2.09	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:318:SER:OG	2:C:320:ASP:OD1	2.22	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
3:D:701:LEU:HD11	3:D:720:ASN:ND2	2.24	0.52
6:1:32:DA:N3	7:2:32:DA:C2	2.78	0.51
5:F:227:GLY:HA2	7:2:20:DG:C6	2.45	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
1:A:45:ARG:NH2	2:C:1084:ASP:OD1	2.38	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
3:D:1167:LYS:HB2	3:D:1174:ARG:HD2	1.91	0.51
2:C:841:ARG:CZ	3:D:257:GLY:HA2	2.39	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
3:D:937:ILE:HG22	3:D:937:ILE:O	2.10	0.51
1:B:158:ARG:NE	1:B:172:LEU:HD11	2.25	0.51
1:B:92:VAL:O	1:B:148:ARG:NH2	2.43	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:1103:VAL:HG22	2:C:1111:GLN:NE2	2.26	0.51
2:C:200:ARG:HG2	2:C:200:ARG:O	2.10	0.51
2:C:615:VAL:HG13	2:C:615:VAL:O	2.11	0.51
3:D:108:ALA:HB3	3:D:279:LEU:HD23	1.92	0.51
2:C:1334:GLY:O	3:D:25:ALA:CB	2.59	0.51
2:C:1294:LYS:HD3	3:D:347:VAL:HG13	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:334:LYS:HG2	3:D:339:ARG:HD2	1.92	0.51
3:D:70:CYS:SG	3:D:74:LYS:N	2.83	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:1107:MET:HE2	3:D:739:GLN:HB2	1.92	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
6:1:48:DA:H2'	6:1:49:DG:C1'	2.41	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
2:C:374:GLU:OE2	6:1:43:DT:H72	2.10	0.51
3:D:1063:ASP:O	3:D:1065:ALA:N	2.44	0.51
3:D:803:VAL:HG21	3:D:1309:ILE:O	2.11	0.51
3:D:721:SER:O	3:D:725:MET:SD	2.69	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:O	2:C:127:ILE:HG13	2.11	0.50
2:C:1281:TYR:OH	3:D:432:LEU:HD23	2.12	0.50
3:D:1067:ARG:NH2	3:D:1076:PRO:CD	2.74	0.50
3:D:750:PRO:HA	3:D:781:LYS:HG3	1.85	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
5:F:170:HIS:HE1	6:1:32:DA:H62	1.60	0.50
2:C:104:ILE:HD12	2:C:116:ASP:HB2	1.93	0.50
3:D:1156:LEU:HD23	3:D:1209:VAL:HA	1.93	0.50
3:D:809:VAL:HG22	3:D:915:ILE:HD11	1.93	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:1285:TYR:HD2	3:D:1361:THR:HG21	1.77	0.49
2:C:563:THR:OG1	2:C:569:ILE:O	2.24	0.49
2:C:61:SER:HB3	2:C:479:LEU:HB3	1.94	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
2:C:839:VAL:HG13	2:C:839:VAL:O	2.12	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:518:VAL:O	3:D:520:ALA:N	2.45	0.49
3:D:475:GLU:OE1	4:E:28:ARG:NH2	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
6:1:53:DG:H2''	6:1:54:DA:H5'	1.94	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
2:C:1210:ILE:CG2	2:C:1211:ARG:N	2.75	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
3:D:1269:ALA:HB2	3:D:1275:LEU:HD23	1.95	0.49
3:D:716:GLN:CG	3:D:717:VAL:H	2.26	0.49
3:D:839:VAL:HG12	3:D:864:LEU:HD12	1.94	0.49
6:1:54:DA:N7	6:1:55:DC:N4	2.61	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
3:D:416:ILE:CD1	3:D:441:LEU:HD21	2.42	0.49
2:C:673:HIS:CE1	3:D:766:GLY:HA3	2.48	0.49
6:1:49:DG:H2''	6:1:50:DT:OP1	2.12	0.49
3:D:868:TRP:O	3:D:872:LEU:HG	2.13	0.49
5:F:158:ILE:O	5:F:158:ILE:HG22	2.12	0.49
6:1:32:DA:N1	7:2:32:DA:C6	2.81	0.48
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
2:C:200:ARG:CD	6:1:50:DT:O2	2.57	0.48
6:1:53:DG:H1'	6:1:54:DA:C5'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1:57:DC:H2"	6:1:58:DG:OP2	2.11	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: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
3:D:555:TYR:HA	3:D:565:ALA:HA	1.96	0.48
5:F:317:LEU:HD21	5:F:324:ILE:HD12	1.96	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:1287:LEU:O	2:C:1291:LEU:HG	2.13	0.48
2:C:564:PRO:O	2:C:569:ILE:HA	2.12	0.48
3:D:1134:ILE:CG2	3:D:1138:LEU:HG	2.42	0.48
3:D:518:VAL:HG21	3:D:708:ASN:CG	2.32	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
6:1:49:DG:H2"	6:1:50:DT:C5'	2.43	0.48
3:D:120:LEU:HA	3:D:121:PRO:C	2.33	0.48
3:D:703:THR:HG23	3:D:703:THR:O	2.14	0.48
2:C:28:LEU:HD21	2:C:524:ILE:HG13	1.96	0.48
3:D:1050:THR:HA	3:D:1057:SER:HA	1.95	0.48
3:D:831:VAL:HB	3:D:834:PRO:HG3	1.94	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
3:D:1134:ILE:HD11	3:D:1244:GLN:CG	2.44	0.48
3:D:29:MET:HG3	3:D:33:TRP:CZ2	2.49	0.48
3:D:751:ASP:CA	3:D:781:LYS:HZ2	2.24	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
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
3:D:807:LEU:HD11	3:D:894:VAL:HG13	1.95	0.47
2:C:1064:ASP:OD1	2:C:1239:VAL:HG12	2.14	0.47
3:D:1037:PHE:CE2	3:D:1040:MET:HE1	2.48	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:OG	2:C:840:SER:O	2.23	0.47
3:D:1134:ILE:O	3:D:1135:THR:C	2.50	0.47
3:D:1364:ALA:O	3:D:1367:GLN:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:752:GLY:HA2	3:D:781:LYS:HZ1	1.77	0.47
3:D:609:TYR:OH	3:D:905:ARG:O	2.27	0.47
1:A:112:ALA:HB1	1:A:123:ILE:HG21	1.96	0.47
2:C:1100:PRO:CB	3:D:639:VAL:HG23	2.44	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
3:D:1267:VAL:O	3:D:1268:ASN:HB2	2.13	0.47
3:D:126:LEU:HG	3:D:223:LEU:CD1	2.44	0.47
2:C:443:ASP:N	2:C:443:ASP:OD1	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:1132:LYS:O	3:D:1133:ASP:HB3	2.15	0.47
3:D:357:VAL:HG12	3:D:461:PHE:CE2	2.49	0.47
3:D:418:GLU:CD	4:E:48:VAL:HG21	2.35	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
3:D:958:ILE:HD11	3:D:1011:VAL:HG21	1.96	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
5:F:79:PHE:O	5:F:90:SER:OG	2.24	0.47
2:C:905:ILE:CG2	5:F:314:ARG:HD2	2.45	0.47
3:D:1079:LYS:HE3	3:D:1087:ASP:OD1	2.15	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
2:C:13:LYS:NZ	2:C:1149:TYR:O	2.48	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:125:GLY:HA2	3:D:135:ILE:HD11	1.97	0.47
3:D:46:TYR:OH	6:1:31:DT:OP1	2.33	0.47
3:D:697:MET:SD	3:D:741:ALA:HB3	2.55	0.47
2:C:550:VAL:HG21	3:D:776:THR:HG22	1.96	0.47
5:F:323:ASN:OD1	5:F:324:ILE:N	2.48	0.47
5:F:96:GLU:HA	5:F:99:LEU:HG	1.97	0.47
6:1:48:DA:H2'	6:1:49:DG:O4'	2.15	0.47
2:C:615:VAL:HA	2:C:638:SER:HB3	1.96	0.47
3:D:46:TYR:HE2	6:1:31:DT:OP1	1.98	0.47
2:C:1044:PRO:HB2	5:F:214:ARG:CG	2.45	0.47
3:D:943:ARG:NH1	3:D:1130:GLY:HA3	2.30	0.46
3:D:57:PHE:O	3:D:98:ARG:NH2	2.47	0.46
2:C:1245:ALA:HB2	3:D:372:MET:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:1119:MET:HG2	2:C:1204:LEU:HD13	1.97	0.46
2:C:799:ASN:HA	2:C:1231:TYR:HA	1.98	0.46
3:D:706:VAL:O	3:D:714:GLU:O	2.33	0.46
6:1:31:DT:H2''	6:1:32:DA:H5'	1.96	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:1029:THR:CG2	3:D:1121:LEU:CD2	2.94	0.46
3:D:977:SER:OG	3:D:980:THR:OG1	2.16	0.46
2:C:142:GLU:OE1	2:C:515:MET:HE1	2.14	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:1136:GLN:O	2:C:1137:GLU:HB2	2.16	0.46
2:C:1210:ILE:HG22	2:C:1211:ARG:N	2.30	0.46
3:D:1006:GLY:H	3:D:1009:GLU:CD	2.17	0.46
3:D:1045:THR:HG22	3:D:1067:ARG:CZ	2.46	0.46
3:D:423:LEU:HD12	3:D:437:PHE:CD2	2.51	0.46
2:C:1075:VAL:HG23	3:D:461:PHE:O	2.15	0.46
3:D:691:ASP:CA	3:D:738:ARG:HH21	2.26	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:1050:THR:CG2	3:D:1056:LEU:O	2.54	0.45
3:D:22:ILE:HG22	3:D:1336:ALA:HA	1.98	0.45
5:F:289:GLU:O	5:F:293:ARG:HB2	2.15	0.45
7:2:16:DC:H6	7:2:16:DC:C5'	2.27	0.45
3:D:714:GLU:CG	3:D:715:LYS:N	2.78	0.45
3:D:856:ILE:HG13	3:D:875:ASN:ND2	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
3:D:458:ASN:O	3:D:458:ASN:CG	2.53	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
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:1031:VAL:HG23	3:D:1080:ILE:HG21	1.98	0.45
3:D:646:ILE:CG2	3:D:647:PRO:HD2	2.46	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:1041:ILE:HB	3:D:1044:GLN:HB2	1.97	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:1037:PHE:CD2	3:D:1040:MET:SD	3.10	0.45
3:D:36:GLY:HA3	3:D:61:ILE:HG23	1.98	0.45
6:1:48:DA:OP2	6:1:48:DA:C8	2.69	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
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
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
1:B:8:PHE:CD1	1:B:8:PHE:O	2.71	0.44
2:C:144:VAL:HB	2:C:526:HIS:CE1	2.52	0.44
2:C:894:GLN:NE2	3:D:69:GLU:CG	2.80	0.44
2:C:89:GLY:HA2	2:C:140:GLY:HA3	1.99	0.44
3:D:1292:LEU:O	3:D:1296:GLY:N	2.51	0.44
3:D:1029:THR:CG2	3:D:1121:LEU:HD21	2.44	0.44
6:1:48:DA:C6	6:1:49:DG:O6	2.70	0.44
2:C:463:GLN:HG3	2:C:505:PHE:HB2	2.00	0.44
3:D:1059:LEU:HB2	3:D:1107:VAL:HB	1.98	0.44
3:D:22:ILE:HG13	3:D:1319:PHE:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:518:VAL:HG23	3:D:716:GLN:CB	2.42	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
6:1:34:DG:H2"	6:1:35:DC:C6	2.53	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
3:D:793:SER:OG	3:D:928:THR:HA	2.17	0.44
2:C:477:GLU:OE1	5:F:108:ARG:HD2	2.18	0.44
2:C:788:SER:OG	2:C:795:ALA:O	2.24	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
2:C:1287:LEU:HD21	3:D:1351:VAL:HG22	1.99	0.44
1:B:48:LEU:HD22	3:D:535:ARG:HG3	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
3:D:1169:THR:OG1	3:D:1174:ARG:NH2	2.50	0.44
3:D:1257:VAL:HA	3:D:1260:MET:HE2	1.99	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
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
2:C:1296:ASP:O	2:C:1297:ASP:C	2.55	0.43
2:C:871:VAL:HG11	2:C:928:VAL:HG21	2.00	0.43
3:D:1133:ASP:OD1	3:D:1134:ILE:HG12	2.17	0.43
3:D:115:TRP:O	3:D:119:SER:HB3	2.18	0.43
3:D:1333:THR:O	3:D:1337:VAL:HG23	2.18	0.43
3:D:785:ASP:HB2	3:D:935:PHE:CD1	2.36	0.43
3:D:115:TRP:CZ2	3:D:1329:THR:HG22	2.53	0.43
3:D:1133:ASP:C	3:D:1244:GLN:HE22	2.17	0.43
2:C:569:ILE:HD13	3:D:784:ALA:HA	1.99	0.43
5:F:155:GLU:O	5:F:159:MET:HG3	2.18	0.43
5:F:152:GLN:HE21	6:1:35:DC:H41	1.67	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:823:THR:HB	3:D:824:PRO:HD2	1.97	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: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:1004:ASP:OD1	2:C:1004:ASP:N	2.52	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
3:D:99:ARG:HG3	3:D:100:GLU:HG3	2.00	0.43
3:D:1063:ASP:OD1	3:D:1065:ALA:HB3	2.18	0.43
3:D:981:GLU:HG2	3:D:996:LYS:HD3	2.00	0.43
2:C:1313:HIS:CD2	4:E:31:GLN:NE2	2.87	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:638:SER:O	2:C:639:LYS:HG2	2.18	0.43
2:C:76:GLY:O	2:C:94:ALA:HB1	2.19	0.43
2:C:1301:ARG:CD	5:F:246:PRO:HG3	2.49	0.43
5:F:227:GLY:CA	7:2:19:DA:C2	2.99	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:321:GLY:O	5:F:324:ILE:N	2.52	0.43
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
2:C:183:TRP:CZ2	6:1:49:DG:C5	3.07	0.43
6:1:54:DA:C8	6:1:55:DC:C5	3.07	0.43
1:A:100:LEU:HD11	1:A:121:VAL:HG11	2.01	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:1027:VAL:N	3:D:1122:ALA:O	2.47	0.43
3:D:250:ARG:HD2	3:D:266:ASN:OD1	2.19	0.43
3:D:746:LEU:HD12	3:D:746:LEU:N	2.34	0.43
6:1:49:DG:H2"	6:1:50:DT:H5"	2.01	0.42
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1175:LEU:O	3:D:1187:GLU:HA	2.19	0.42
3:D:714:GLU:CG	3:D:715:LYS:H	2.31	0.42
6:1:48:DA:H2'	6:1:49:DG:N9	2.34	0.42
2:C:673:HIS:CD2	2:C:1113:LEU:HD13	2.55	0.42
2:C:104:ILE:HD13	2:C:484:LEU:HB3	2.00	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
6:1:51: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:539:THR:HB	2:C:542:ARG:HG3	2.01	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
3:D:282:LEU:CD2	5:F:125:LEU:HD21	2.49	0.42
5:F:317:LEU:HD22	5:F:324:ILE:HD12	2.00	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
3:D:1052:GLU:O	3:D:1053:LEU:C	2.57	0.42
6:1:33:DT:C2'	6:1:34:DG:H5'	2.49	0.42
2:C:402:ARG:HD2	2:C:406:ASN:HD21	1.84	0.42
2:C:800:MET:HE2	2:C:800:MET:HB3	1.97	0.42
2:C:90:VAL:CG1	2:C:91:THR:N	2.82	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
6:1:32:DA:C2	7:2:32:DA:C6	3.07	0.42
2:C:228:VAL:HB	2:C:335:THR:OG1	2.20	0.42
3:D:1330:ARG:NH2	7:2:9:DT:O3'	2.53	0.42
3:D:750:PRO:CA	3:D:781:LYS:NZ	2.76	0.42
6:1:37:DA:H4'	6:1:38:DT:OP1	2.19	0.42
5:F:227:GLY:CA	7:2:19:DA:H2	2.30	0.42
1:A:11:PRO:HB3	1:A:31:LEU:HD23	2.02	0.42
2:C:1002:LEU:CD1	2:C:1011:LEU:HD11	2.50	0.42
2:C:550:VAL:HG21	3:D:776:THR:CG2	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
3:D:708:ASN:HD22	3:D:715:LYS:N	2.18	0.42
3:D:1005:LYS:CA	3:D:1009:GLU:OE1	2.68	0.42
3:D:885:VAL:HG12	3:D:1258:ARG:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:220:ARG:O	3:D:224:LEU:HG	2.20	0.42
1:B:83:LEU:HD11	3:D:526:VAL:O	2.20	0.42
3:D:978:ARG:HH12	3:D:1025:MET:HE3	1.85	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
3:D:690:ASN:CG	3:D:738:ARG:HH22	2.21	0.41
2:C:1116:HIS:CE1	2:C:1226:THR:HG23	2.55	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
5:F:321:GLY:O	5:F:324:ILE:HG22	2.20	0.41
6:1:51:DC:P	6:1:51:DC:H6	2.43	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
6:1:58:DG:H2'	6:1:59:DG:C8	2.55	0.41
2:C:310:ILE:HG23	2:C:324:LYS:HE2	2.02	0.41
2:C:1284:ALA:N	3:D:479:GLU:OE1	2.53	0.41
3:D:738:ARG:O	3:D:743:MET:N	2.54	0.41
3:D:94:GLN:O	3:D:97:VAL:HG22	2.20	0.41
4:E:65:ASP:HB3	4:E:69:ARG:HH21	1.85	0.41
2:C:905:ILE:HG23	5:F:314:ARG:HD2	2.02	0.41
7:2:24:DT:H2'	7:2:25:DA:OP2	2.20	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
2:C:634:VAL:HG12	2:C:636:CYS:SG	2.60	0.41
3:D:958:ILE:O	3:D:1008:GLY:CA	2.68	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
4:E:6:VAL:O	4:E:6:VAL:HG12	2.21	0.41
5:F:329:LEU:HD23	5:F:329:LEU:HA	1.90	0.41
2:C:688:GLN:NE2	8:3:14:GTP:O3'	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1149:TYR:CG	2:C:1159:VAL:HG11	2.56	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:967:LEU:HD21	2:C:1021:LEU:CD2	2.50	0.41
3:D:643:ASP:O	3:D:645:VAL:N	2.49	0.41
3:D:754:ILE:HD12	3:D:754:ILE:N	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:751:ASP:C	3:D:781:LYS:HZ2	2.22	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:1145:PHE:CD1	3:D:1256:ILE:HG21	2.56	0.41
3:D:355:ILE:HG21	3:D:466:MET:SD	2.61	0.41
3:D:752:GLY:H	3:D:781:LYS:HZ2	1.48	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:1280:VAL:CG1	3:D:1281:GLU:N	2.82	0.41
3:D:290:ILE:HG23	3:D:291:ILE:HG13	2.02	0.41
3:D:975:ILE:HD13	3:D:980:THR:HG21	2.02	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:1289:GLU:HG2	2:C:1294:LYS:HE3	2.03	0.41
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:79:VAL:HG21	5:F:191:HIS:CE1	2.56	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
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
2:C:564:PRO:CB	8:3:14:GTP:O1A	2.65	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: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:907:GLY:O	2:C:908:GLU:C	2.59	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1357:ILE:H	3:D:1357:ILE:HG13	1.65	0.40
2:C:1254:VAL:HG13	3:D:249:LEU:HD23	2.01	0.40
2:C:1152:GLY:CA	2:C:1155:VAL:HG23	2.51	0.40
2:C:911:SER:CA	2:C:912:ASP:N	2.83	0.40
3:D:1006:GLY:N	3:D:1009:GLU:CD	2.75	0.40
3:D:1063:ASP:O	3:D:1064:SER:C	2.60	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
2:C:228:VAL:HG23	2:C:337:PHE:HA	2.03	0.40
2:C:984:VAL:HG13	2:C:984:VAL:O	2.21	0.40
3:D:378:LYS:N	3:D:379:PRO:HD2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	228/242 (94%)	216 (95%)	10 (4%)	2 (1%)	21	67
1	B	226/242 (93%)	214 (95%)	11 (5%)	1 (0%)	39	80
2	C	1332/1342 (99%)	1242 (93%)	82 (6%)	8 (1%)	30	74
3	D	1360/1407 (97%)	1258 (92%)	81 (6%)	21 (2%)	13	58
4	E	77/90 (86%)	74 (96%)	3 (4%)	0	100	100
5	F	275/336 (82%)	258 (94%)	12 (4%)	5 (2%)	11	55
All	All	3498/3659 (96%)	3262 (93%)	199 (6%)	37 (1%)	17	64

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
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%)	63	86
1	B	196/208 (94%)	191 (97%)	5 (3%)	54	81
2	C	1155/1157 (100%)	1139 (99%)	16 (1%)	74	89
3	D	1135/1168 (97%)	1099 (97%)	36 (3%)	46	78
4	E	67/74 (90%)	65 (97%)	2 (3%)	48	79
5	F	240/292 (82%)	235 (98%)	5 (2%)	61	85
All	All	2991/3107 (96%)	2923 (98%)	68 (2%)	58	83

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	32	GLU
1	A	131	CYS
1	A	194	GLN
1	B	28	LEU
1	B	32	GLU
1	B	131	CYS
1	B	194	GLN
1	B	211	ILE
2	C	12	ARG
2	C	30	ILE
2	C	44	GLU
2	C	341	LEU
2	C	443	ASP
2	C	553	THR
2	C	554	HIS
2	C	700	VAL
2	C	851	THR
2	C	1207	SER
2	C	1223	ARG
2	C	1240	ASP
2	C	1250	SER

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Mol	Chain	Res	Type
2	C	1253	LEU
2	C	1272	GLU
2	C	1273	MET
3	D	27	PRO
3	D	93	THR
3	D	99	ARG
3	D	153	ASN
3	D	163	GLU
3	D	216	LYS
3	D	223	LEU
3	D	227	PHE
3	D	240	THR
3	D	259	ARG
3	D	321	LYS
3	D	347	VAL
3	D	384	LYS
3	D	398	LYS
3	D	399	LYS
3	D	417	ARG
3	D	505	ASP
3	D	538	ARG
3	D	551	ARG
3	D	579	LEU
3	D	599	LYS
3	D	641	ILE
3	D	648	GLU
3	D	695	LYS
3	D	707	ILE
3	D	798	ARG
3	D	850	LYS
3	D	935	PHE
3	D	1058	SER
3	D	1062	LEU
3	D	1131	THR
3	D	1175	LEU
3	D	1189	MET
3	D	1227	HIS
3	D	1356	LEU
3	D	1366	HIS
4	E	43	ASN
4	E	45	LYS
5	F	156	ARG

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Mol	Chain	Res	Type
5	F	190	ASP
5	F	192	GLU
5	F	219	ILE
5	F	280	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	GLN
1	B	147	GLN
2	C	343	HIS
2	C	450	ASN
2	C	490	GLN
2	C	526	HIS
2	C	618	GLN
2	C	894	GLN
2	C	1116	HIS
2	C	1220	GLN
2	C	1257	GLN
2	C	1313	HIS
3	D	153	ASN
3	D	196	GLN
3	D	341	ASN
3	D	450	HIS
3	D	458	ASN
3	D	545	HIS
3	D	623	GLN
3	D	690	ASN
3	D	708	ASN
3	D	716	GLN
3	D	720	ASN
3	D	736	GLN
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	1244	GLN

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Mol	Chain	Res	Type
3	D	1279	GLN
4	E	31	GLN
4	E	43	ASN
5	F	152	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	230/242 (95%)	0.13	12 (5%) 31 24	183, 279, 356, 428	0
1	B	228/242 (94%)	-0.02	8 (3%) 48 37	193, 298, 382, 466	0
2	C	1340/1342 (99%)	-0.16	25 (1%) 70 60	140, 249, 396, 562	0
3	D	1362/1407 (96%)	0.04	52 (3%) 44 34	138, 279, 418, 529	0
4	E	79/90 (87%)	-0.03	1 (1%) 79 71	245, 321, 482, 519	0
5	F	277/336 (82%)	0.25	17 (6%) 25 17	227, 330, 432, 542	0
6	1	33/50 (66%)	0.21	5 (15%) 3 4	272, 339, 468, 483	0
7	2	33/50 (66%)	0.16	2 (6%) 25 17	232, 318, 425, 477	0
8	3	3/4 (75%)	0.40	0 100 100	298, 298, 327, 338	0
All	All	3585/3763 (95%)	-0.02	122 (3%) 49 38	138, 277, 415, 562	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	F	323	ASN	11.1
3	D	1076	PRO	9.0
2	C	1004	ASP	7.0
3	D	1075	ARG	6.3
2	C	982	GLY	6.0
5	F	324	ILE	5.6
3	D	1050	THR	5.0
2	C	990	ASP	4.9
3	D	854	ALA	4.9
3	D	1161	GLY	4.9
3	D	1166	GLY	4.9
3	D	1183	SER	4.6
3	D	1203	ARG	4.6
3	D	1052	GLU	4.5
3	D	1051	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
5	F	322	LEU	4.1
3	D	855	ASP	4.1
3	D	878	ASP	4.0
5	F	320	GLN	3.9
5	F	198	ILE	3.9
2	C	1003	THR	3.8
2	C	777	VAL	3.7
1	B	70	THR	3.6
3	D	1373	ARG	3.5
5	F	326	ALA	3.5
1	A	133	LEU	3.4
1	B	169	GLY	3.4
3	D	853	THR	3.3
2	C	740	GLU	3.3
5	F	321	GLY	3.2
2	C	911	SER	3.2
3	D	1100	PHE	3.2
2	C	116	ASP	3.1
3	D	1101	LEU	3.1
6	1	44	DG	3.1
1	A	134	THR	3.1
5	F	263	LEU	3.1
2	C	487	LEU	3.1
3	D	879	ALA	3.1
5	F	328	PHE	3.0
6	1	50	DT	3.0
3	D	1078	LEU	3.0
1	B	168	ILE	3.0
5	F	265	GLU	3.0
3	D	1077	ALA	3.0
3	D	1156	LEU	2.9
3	D	214	ARG	2.9
4	E	2	ALA	2.9
2	C	912	ASP	2.9
1	A	144	ILE	2.9
3	D	1110	GLU	2.9
3	D	1342	ASP	2.9
6	1	47	DC	2.9
1	B	133	LEU	2.8
1	A	123	ILE	2.8
2	C	1180	MET	2.8
3	D	1204	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
2	C	913	VAL	2.7
3	D	877	VAL	2.7
3	D	1074	LEU	2.7
1	A	135	ASP	2.7
3	D	1271	SER	2.7
3	D	1167	LYS	2.7
3	D	1067	ARG	2.7
2	C	227	LYS	2.6
3	D	852	GLY	2.6
5	F	275	ALA	2.6
2	C	987	GLU	2.6
3	D	1099	TYR	2.5
1	B	74	VAL	2.5
2	C	374	GLU	2.5
3	D	880	VAL	2.5
3	D	1098	GLN	2.5
1	A	164	ASP	2.5
3	D	1277	GLY	2.5
3	D	1181	ASP	2.5
5	F	201	GLN	2.4
5	F	266	LEU	2.4
5	F	54	VAL	2.4
1	A	100	LEU	2.4
3	D	1184	ASP	2.4
3	D	1160	SER	2.4
2	C	721	GLY	2.4
2	C	906	PHE	2.4
3	D	686	TRP	2.4
1	A	98	VAL	2.3
2	C	991	LYS	2.3
3	D	974	VAL	2.3
7	2	21	DG	2.3
3	D	1207	GLY	2.3
3	D	1049	GLN	2.3
2	C	484	LEU	2.3
6	1	45	DT	2.3
3	D	1039	ASP	2.3
1	B	67	GLU	2.3
1	A	31	LEU	2.3
2	C	187	GLU	2.3
3	D	314	ARG	2.3
2	C	937	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
5	F	306	GLN	2.2
3	D	1266	ILE	2.2
5	F	319	THR	2.2
3	D	20	ILE	2.2
3	D	1182	GLY	2.2
2	C	1005	GLU	2.2
1	A	26	VAL	2.2
1	A	90	VAL	2.2
2	C	905	ILE	2.2
3	D	149	GLY	2.2
1	B	132	HIS	2.1
3	D	1038	THR	2.1
2	C	67	GLU	2.1
3	D	1276	GLU	2.1
2	C	722	GLY	2.1
3	D	1300	ALA	2.1
1	A	201	LEU	2.0
1	B	182	ARG	2.0
6	1	43	DT	2.0
7	2	20	DG	2.0
3	D	1157	ALA	2.0
3	D	1375	ALA	2.0
5	F	200	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
9	ZN	D	1502	1/1	0.93	0.13	0.12	298,298,298,298	0
9	ZN	D	1501	1/1	0.99	0.08	-1.30	316,316,316,316	0
10	MG	D	1503	1/1	0.92	0.07	-1.89	343,343,343,343	0

6.5 Other polymers [i](#)

There are no such residues in this entry.