



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 18, 2017 – 08:22 AM EDT

PDB ID : 5VI5
Title : Structure of Mycobacterium smegmatis transcription initiation complex with a full transcription bubble
Authors : Darst, S.A.; Campbell, E.A.; Lilic, M.
Deposited on : unknown
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029824

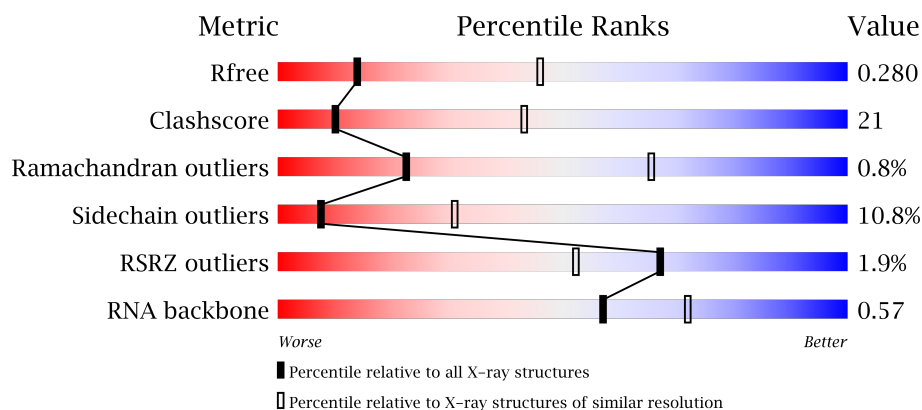
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)
RNA backbone	2435	1045 (3.60-2.80)

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	O	50	
2	P	50	
3	Q	4	
4	A	350	

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Mol	Chain	Length	Quality of chain
4	B	350	
5	C	1169	
6	D	1317	
7	E	107	
8	F	466	
9	J	114	

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
10	SO4	C	1201	-	-	X	-
10	SO4	F	502	-	-	X	-
11	ZN	D	2001	-	-	-	X

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 26574 atoms, of which 16 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 DNA chain called DNA (49-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	O	49	Total	C	N	O	P	0	0	0
			1009	481	188	292	48			

- Molecule 2 is a DNA chain called DNA (44-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	44	Total	C	N	O	P	0	0	0
			903	430	167	262	44			

- Molecule 3 is a RNA chain called RNA (5'-R(*UP*CP*GP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Q	4	Total	C	N	O	P	0	0	0
			82	38	15	26	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	220	Total	C	N	O	S	0	0	0
			1617	1022	278	315	2			
4	B	233	Total	C	N	O	S	0	0	0
			1660	1050	287	321	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	1113	Total	C	N	O	S	0	0	0
			8138	5103	1427	1573	35			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	238	ASN	GLN	conflict	UNP P60281

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	1238	Total	C	N	O	S	0	0	0
			9391	5885	1699	1767	40			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	663	GLU	ALA	conflict	UNP A0QS66
D	1272	ASN	GLN	conflict	UNP A0QS66

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	76	Total	C	N	O		0	0	0
			592	378	100	114				

- Molecule 8 is a protein called RNA polymerase sigma factor SigA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	314	Total	C	N	O	S	0	0	0
			2461	1542	442	470	7			

- Molecule 9 is a protein called RNA polymerase-binding protein RbpA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	86	Total	C	N	O	S	0	0	0
			663	414	122	125	2			

- Molecule 10 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	C	1	Total	O	S	0	0
			5	4	1		
10	D	1	Total	O	S	0	0
			5	4	1		
10	D	1	Total	O	S	0	0
			5	4	1		
10	D	1	Total	O	S	0	0
			5	4	1		
10	F	1	Total	O	S	0	0
			5	4	1		
10	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 12 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



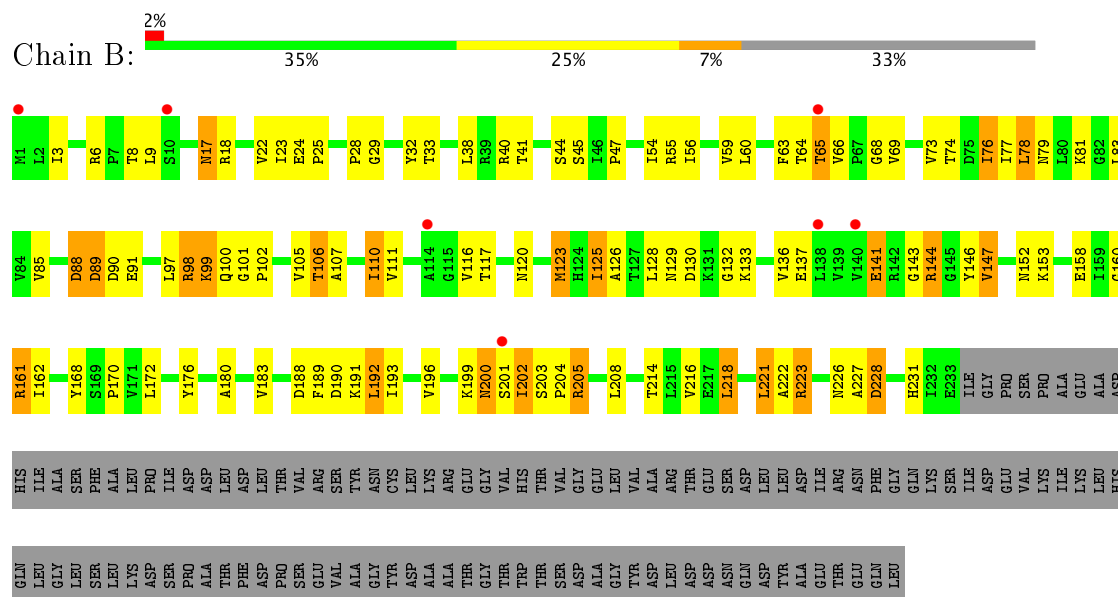
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	D	1	Total	C	H	O	0	0
			10	2	6	2		
12	F	1	Total	C	H	O	0	0
			10	2	6	2		

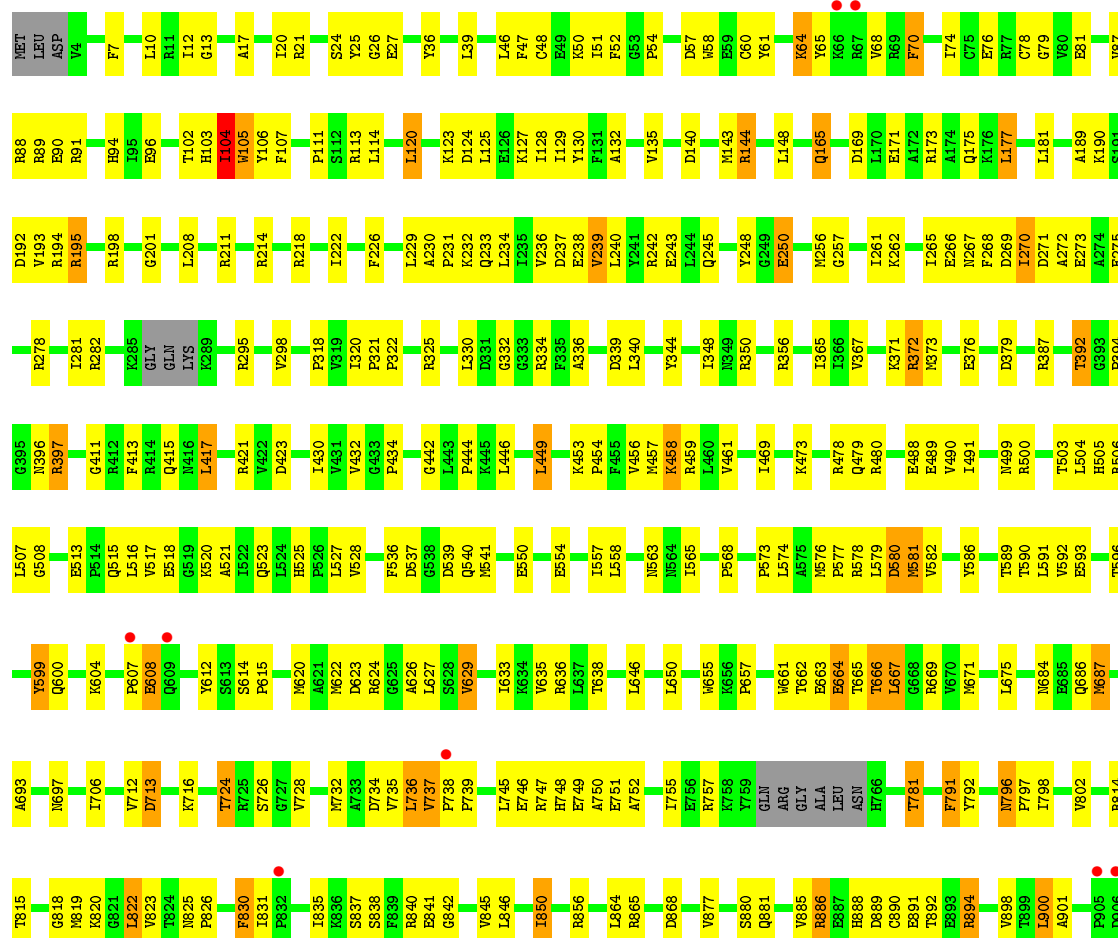
- Molecule 13 is water.

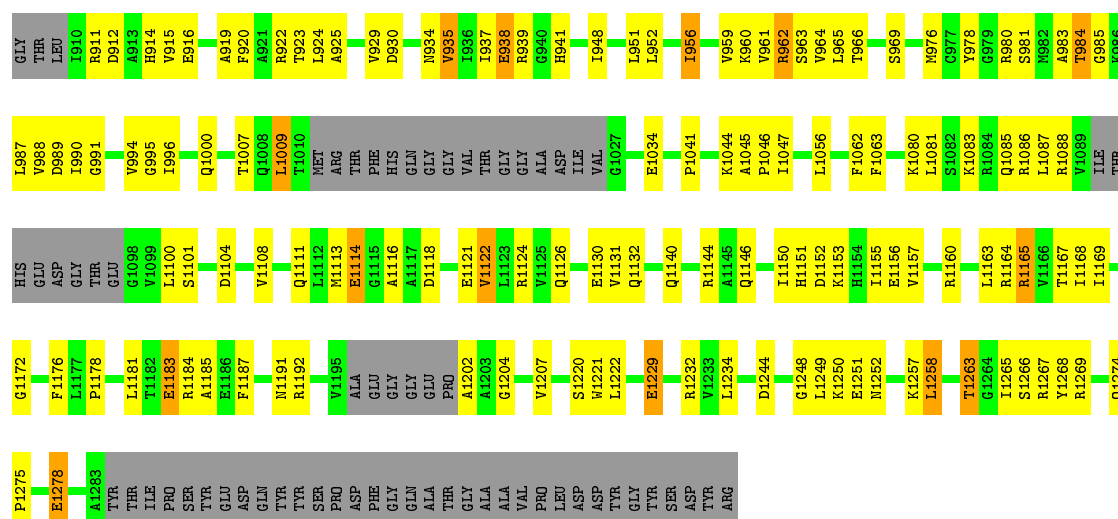
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	H	O	0	0
			3	2	1		
13	D	1	Total	H	O	0	0
			3	2	1		

PHE
ASP
PRO
SER
GLU
VAL
ALA
GLY
TYR
ASP
ALA
ALA
THR
GLY
TRP
THR
SER
THR
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ASN
GLN
ASP
TYR
ALA
GLU
THR
GLN
LEU

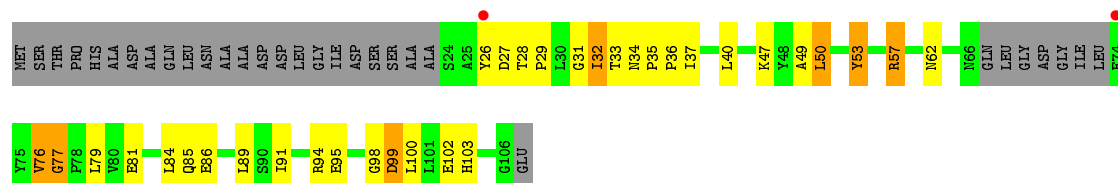
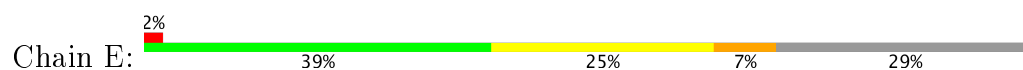
• Molecule 4: DNA-directed RNA polymerase subunit alpha



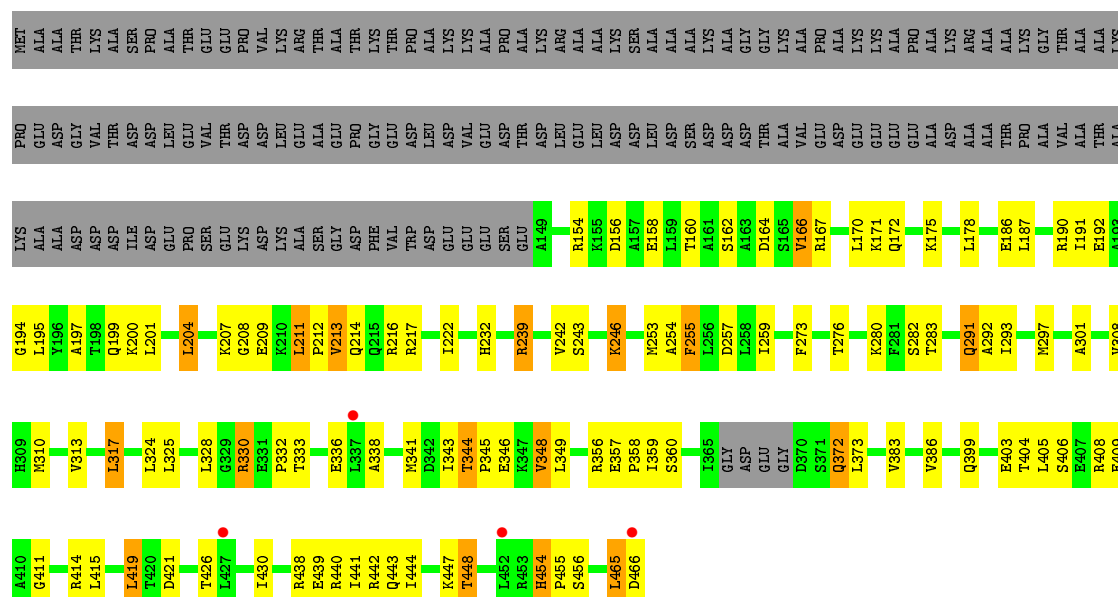
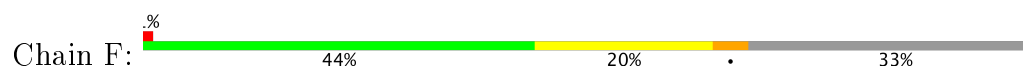




• Molecule 7: DNA-directed RNA polymerase subunit omega

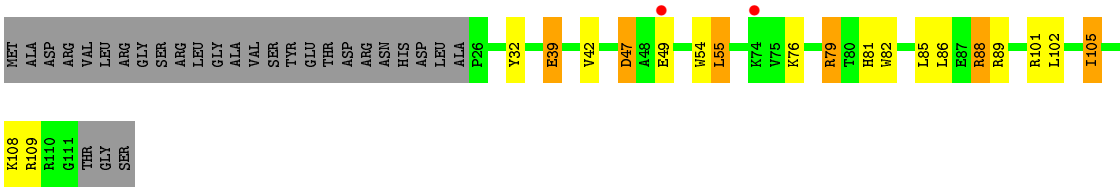


• Molecule 8: RNA polymerase sigma factor SigA



• Molecule 9: RNA polymerase-binding protein RbpA





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	132.06 Å 163.56 Å 139.96 Å 90.00° 107.90° 90.00°	Depositor
Resolution (Å)	50.02 – 3.20 50.01 – 3.20	Depositor EDS
% Data completeness (in resolution range)	93.5 (50.02-3.20) 93.5 (50.01-3.20)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 3.19 Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.253 , 0.280 0.252 , 0.280	Depositor DCC
R_{free} test set	1978 reflections (2.26%)	DCC
Wilson B-factor (Å ²)	85.8	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	26574	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4, EDO

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	O	0.51	0/1133	0.92	0/1749
2	P	0.51	0/1012	0.89	0/1557
3	Q	0.11	0/91	0.60	0/140
4	A	0.23	0/1643	0.45	0/2242
4	B	0.23	0/1686	0.44	0/2308
5	C	0.26	0/8285	0.44	1/11285 (0.0%)
6	D	0.24	0/9540	0.41	0/12930
7	E	0.23	0/604	0.41	0/822
8	F	0.25	0/2491	0.40	0/3365
9	J	0.23	0/677	0.39	0/920
All	All	0.28	0/27162	0.48	1/37318 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	67	ASP	CB-CG-OD2	5.17	122.95	118.30

There are no chirality outliers.

There are no planarity outliers.

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	O	1009	0	554	84	0
2	P	903	0	497	29	0
3	Q	82	0	45	1	0
4	A	1617	0	1616	85	0
4	B	1660	0	1624	97	0
5	C	8138	0	7718	388	1
6	D	9391	0	9221	376	1
7	E	592	0	583	31	0
8	F	2461	0	2467	92	0
9	J	663	0	619	17	0
10	C	5	0	0	2	0
10	D	15	0	0	1	0
10	F	10	0	0	3	0
11	D	2	0	0	0	0
12	D	4	6	6	3	0
12	F	4	6	6	0	0
13	C	1	2	0	1	0
13	D	1	2	0	0	0
All	All	26558	16	24956	1084	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (1084) 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)
6:D:732:MET:O	6:D:840:ARG:NH1	1.85	1.10
6:D:981:SER:HB3	6:D:984:THR:OG1	1.53	1.08
4:A:48:GLY:HA2	4:A:49:ALA:HB3	1.39	1.04
5:C:935:TRP:CH2	5:C:954:LEU:CD2	2.40	1.04
5:C:935:TRP:HH2	5:C:954:LEU:HD22	1.18	1.03
1:O:40:DT:H2''	1:O:41:DC:H5'	1.34	1.02
4:B:55:ARG:NH1	4:B:160:GLY:O	1.91	1.02
5:C:763:ASP:O	5:C:821:ARG:NH1	1.92	1.00
8:F:330:ARG:NH1	8:F:336:GLU:OE2	1.95	0.98
8:F:414:ARG:HA	8:F:419:LEU:HD12	1.46	0.97
6:D:111:PRO:O	6:D:113:ARG:NH1	2.00	0.95
5:C:154:LYS:O	5:C:443:LYS:NZ	1.99	0.94
5:C:935:TRP:HH2	5:C:954:LEU:CD2	1.78	0.94
1:O:13:DT:H3	2:P:37:DA:H61	0.93	0.93
8:F:357:GLU:HG3	8:F:358:PRO:HD2	1.51	0.92
5:C:215:VAL:HG21	5:C:225:VAL:HA	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:935:TRP:CH2	5:C:954:LEU:HD22	2.03	0.91
5:C:572:VAL:HG22	5:C:576:GLN:HE21	1.32	0.90
1:O:12:DG:H2''	1:O:13:DT:H5'	1.54	0.89
5:C:895:MET:HG3	5:C:896:PRO:HD2	1.55	0.89
5:C:534:GLN:HE21	5:C:536:ASN:H	1.21	0.86
6:D:47:PHE:O	6:D:88:ARG:NH2	2.10	0.84
5:C:641:ILE:HD11	5:C:687:VAL:HG13	1.58	0.84
6:D:981:SER:HB3	6:D:984:THR:HG1	1.42	0.84
5:C:751:ARG:HD2	6:D:332:GLY:HA3	1.60	0.84
5:C:935:TRP:CZ2	5:C:954:LEU:CD2	2.60	0.83
5:C:751:ARG:HG2	5:C:856:VAL:HG12	1.58	0.83
6:D:622:MET:HE1	6:D:629:VAL:HG13	1.59	0.83
1:O:38:DC:H1'	1:O:39:DG:H5''	1.60	0.82
5:C:379:GLN:HG2	5:C:421:PHE:HB2	1.62	0.82
8:F:211:LEU:H	8:F:211:LEU:HD23	1.44	0.82
9:J:47:ASP:OD2	9:J:47:ASP:N	2.13	0.81
6:D:488:GLU:HG2	6:D:516:LEU:HD12	1.61	0.81
5:C:708:LYS:NZ	5:C:737:VAL:O	2.13	0.81
1:O:32:DG:N7	8:F:239:ARG:NH1	2.28	0.81
4:B:24:GLU:HG2	4:B:191:LYS:HB2	1.63	0.80
4:A:177:LYS:HG3	4:A:193:ILE:HG23	1.62	0.80
6:D:892:THR:OG1	6:D:894:ARG:NH1	2.13	0.80
5:C:1040:TYR:HE2	5:C:1090:ARG:HD2	1.45	0.80
1:O:4:DT:O4	2:P:46:DA:N6	2.16	0.79
4:B:97:LEU:HB3	4:B:136:VAL:HG13	1.65	0.79
2:P:17:DG:H2''	5:C:430:PHE:CZ	2.18	0.79
6:D:432:VAL:HG22	6:D:434:PRO:HD3	1.63	0.78
6:D:47:PHE:HD1	6:D:322:PRO:HB3	1.47	0.78
5:C:538:PRO:HB2	5:C:546:THR:HB	1.66	0.78
4:A:48:GLY:CA	4:A:49:ALA:HB3	2.13	0.77
8:F:158:GLU:O	8:F:171:LYS:NZ	2.12	0.77
1:O:19:DA:H2''	1:O:20:DT:O5'	1.83	0.77
6:D:981:SER:CB	6:D:984:THR:OG1	2.32	0.77
4:B:6:ARG:O	4:B:25:PRO:HD2	1.84	0.77
4:B:55:ARG:HH11	4:B:160:GLY:C	1.88	0.77
6:D:822:LEU:H	6:D:822:LEU:HD12	1.48	0.77
1:O:32:DG:C8	8:F:239:ARG:HD3	2.20	0.76
6:D:507:LEU:HD23	6:D:574:LEU:HD23	1.66	0.76
6:D:889:ASP:OD2	6:D:891:GLU:N	2.15	0.76
8:F:465:LEU:HD13	8:F:466:ASP:H	1.49	0.75
4:A:48:GLY:HA2	4:A:49:ALA:CB	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:102:ARG:HB2	5:C:125:PHE:HB2	1.69	0.75
6:D:978:TYR:CE1	6:D:994:VAL:HG11	2.22	0.75
5:C:306:LYS:NZ	5:C:366:ASN:OD1	2.20	0.75
5:C:624:ARG:NH1	5:C:628:ASP:OD2	2.20	0.75
5:C:38:PRO:HG3	5:C:508:ARG:HD2	1.67	0.75
5:C:313:LEU:HD12	5:C:327:GLU:OE2	1.87	0.74
5:C:916:ARG:NH2	10:C:1201:SO4:O4	2.20	0.74
6:D:20:ILE:HD13	6:D:318:PRO:HD3	1.68	0.74
5:C:788:ARG:N	5:C:791:ASP:OD2	2.21	0.74
5:C:852:LEU:HB3	5:C:856:VAL:HG23	1.68	0.74
6:D:190:LYS:NZ	6:D:192:ASP:HB3	2.03	0.74
8:F:454:HIS:NE2	8:F:456:SER:OG	2.21	0.74
1:O:38:DC:H2'	1:O:38:DC:O2	1.87	0.74
5:C:954:LEU:HD23	5:C:954:LEU:O	1.86	0.74
1:O:31:DT:H5'	1:O:31:DT:H6	1.51	0.73
5:C:773:ALA:O	5:C:782:ARG:NH2	2.21	0.73
1:O:46:DA:H61	2:P:4:DT:H3	1.33	0.73
5:C:434:ASN:OD1	5:C:1025:HIS:ND1	2.14	0.73
4:B:99:LYS:NZ	4:B:100:GLN:H	1.85	0.73
5:C:41:VAL:O	5:C:624:ARG:NH2	2.20	0.73
5:C:758:GLU:HG2	5:C:798:THR:HG22	1.68	0.73
1:O:32:DG:H2''	1:O:33:DG:OP2	1.87	0.73
6:D:865:ARG:NH1	6:D:1007:THR:O	2.22	0.73
1:O:40:DT:C2'	1:O:41:DC:H5'	2.14	0.73
5:C:680:ILE:HG12	5:C:693:ILE:O	1.89	0.73
6:D:1087:LEU:HD23	6:D:1113:MET:HG2	1.70	0.73
5:C:636:ASP:N	5:C:636:ASP:OD1	2.21	0.72
6:D:128:ILE:HD12	6:D:135:VAL:HB	1.71	0.72
1:O:40:DT:H6	1:O:40:DT:H5''	1.53	0.72
5:C:1108:ILE:HD13	5:C:1108:ILE:H	1.53	0.72
2:P:14:DG:OP2	6:D:421:ARG:NH2	2.22	0.72
4:A:105:VAL:HG23	4:A:128:LEU:HD11	1.72	0.72
6:D:525:HIS:HE1	6:D:527:LEU:HD12	1.52	0.72
7:E:84:LEU:H	7:E:84:LEU:HD12	1.53	0.72
5:C:714:ILE:HG22	5:C:910:THR:HG22	1.69	0.72
6:D:1140:GLN:HG2	6:D:1155:ILE:HD12	1.70	0.72
5:C:809:GLU:OE1	5:C:810:ARG:N	2.23	0.72
8:F:232:HIS:ND1	10:F:502:SO4:O2	2.23	0.72
5:C:935:TRP:CH2	5:C:954:LEU:HD23	2.24	0.71
5:C:1045:GLN:HG2	5:C:1087:THR:HG22	1.71	0.71
5:C:1140:ASP:OD1	6:D:25:TYR:OH	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:1027:LEU:O	5:C:1031:LYS:HG3	1.91	0.71
5:C:800:LYS:HG2	5:C:822:GLU:O	1.90	0.71
6:D:47:PHE:CD1	6:D:322:PRO:HB3	2.25	0.71
6:D:781:THR:HG22	6:D:814:ARG:HD2	1.72	0.71
5:C:1031:LYS:NZ	13:C:1301:HOH:O	2.24	0.71
5:C:23:VAL:HG13	5:C:24:PRO:HD2	1.73	0.71
1:O:37:DC:H2''	1:O:38:DC:O5'	1.89	0.71
4:A:56:ILE:HB	4:A:59:VAL:HG22	1.71	0.71
1:O:13:DT:H3	2:P:37:DA:N6	1.79	0.70
4:B:68:GLY:O	4:B:129:ASN:N	2.21	0.70
5:C:1043:ILE:HD12	5:C:1044:THR:H	1.57	0.70
5:C:535:ALA:HB2	5:C:571:ASP:HB2	1.72	0.70
4:A:26:LEU:HB2	4:A:190:ASP:O	1.92	0.70
5:C:880:HIS:NE2	5:C:924:GLU:OE2	2.23	0.70
5:C:562:VAL:HG22	5:C:563:SER:H	1.56	0.70
6:D:880:SER:O	6:D:995:GLY:HA3	1.91	0.70
5:C:1072:ALA:HB1	6:D:554:GLU:OE2	1.92	0.69
8:F:213:VAL:O	8:F:217:ARG:HG2	1.92	0.69
4:A:48:GLY:O	4:A:143:GLY:N	2.24	0.69
4:A:60:LEU:H	4:A:60:LEU:HD12	1.57	0.69
6:D:189:ALA:HB1	6:D:194:ARG:NH1	2.08	0.69
6:D:365:ILE:HD12	6:D:365:ILE:H	1.57	0.69
5:C:1129:LEU:HA	5:C:1135:ALA:HA	1.74	0.69
6:D:344:TYR:O	6:D:348:ILE:HG22	1.92	0.69
5:C:473:ARG:NH1	5:C:524:ALA:H	1.90	0.69
6:D:411:GLY:O	6:D:415:GLN:HB3	1.93	0.69
6:D:846:LEU:HD12	6:D:846:LEU:H	1.58	0.68
4:A:21:PHE:HB2	4:A:194:ILE:HG22	1.74	0.68
6:D:165:GLN:NE2	6:D:169:ASP:OD2	2.26	0.68
1:O:11:DA:H2''	1:O:12:DG:H5''	1.73	0.68
5:C:952:GLU:OE1	5:C:953:GLU:N	2.27	0.68
5:C:766:ASN:ND2	8:F:466:ASP:OD2	2.27	0.68
1:O:48:DG:OP1	6:D:123:LYS:HG2	1.94	0.68
5:C:1049:GLY:O	5:C:1053:GLN:NE2	2.25	0.68
5:C:478:GLU:OE2	5:C:604:ARG:NH2	2.27	0.68
5:C:70:GLU:HG2	5:C:72:ASN:H	1.58	0.68
4:B:102:PRO:HG3	4:B:130:ASP:HA	1.75	0.67
8:F:344:THR:OG1	8:F:346:GLU:HG2	1.94	0.67
4:A:20:ARG:HB3	4:A:193:ILE:HD11	1.76	0.67
5:C:789:ASP:HA	5:C:830:VAL:HG22	1.76	0.67
5:C:947:ALA:HB1	5:C:950:LEU:CB	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:231:PRO:O	6:D:232:LYS:HB2	1.95	0.67
4:B:65:THR:O	4:B:66:VAL:HG23	1.94	0.67
5:C:685:GLN:HG2	5:C:686:ARG:H	1.60	0.67
1:O:32:DG:H5'	8:F:239:ARG:CG	2.25	0.67
1:O:37:DC:H2''	1:O:38:DC:C5'	2.25	0.67
5:C:939:VAL:HG13	5:C:943:VAL:HG22	1.75	0.67
6:D:444:PRO:HG3	6:D:521:ALA:O	1.95	0.67
5:C:608:PRO:HA	5:C:698:CYS:SG	2.35	0.66
1:O:32:DG:H8	8:F:239:ARG:HD3	1.60	0.66
2:P:34:DA:H4'	2:P:35:DA:OP1	1.94	0.66
8:F:190:ARG:NH1	10:F:502:SO4:O3	2.28	0.66
6:D:981:SER:CB	6:D:984:THR:HG1	2.07	0.66
5:C:231:ALA:HA	5:C:265:LEU:HD22	1.77	0.66
5:C:708:LYS:HG3	5:C:737:VAL:HG23	1.77	0.66
6:D:1275:PRO:HG3	7:E:76:VAL:HG21	1.75	0.66
6:D:1183:GLU:OE1	6:D:1185:ALA:N	2.29	0.66
5:C:1047:PRO:HD2	6:D:421:ARG:O	1.96	0.66
5:C:896:PRO:HB2	5:C:1001:LEU:HD13	1.78	0.65
5:C:235:THR:OG1	5:C:238:ASN:OD1	2.11	0.65
8:F:243:SER:HA	8:F:246:LYS:HD2	1.78	0.65
5:C:724:ASP:OD1	5:C:916:ARG:NH1	2.30	0.65
6:D:991:GLY:HA2	6:D:1265:ILE:HD11	1.77	0.65
5:C:454:LEU:HD13	5:C:459:ALA:HB2	1.79	0.65
8:F:444:ILE:O	8:F:448:THR:OG1	2.14	0.65
1:O:32:DG:H5'	8:F:239:ARG:HG2	1.79	0.65
5:C:551:MET:O	5:C:552:VAL:HG13	1.97	0.65
6:D:1086:ARG:O	6:D:1087:LEU:HD23	1.96	0.65
4:A:40:ARG:HH12	4:B:32:TYR:HB2	1.62	0.65
5:C:531:VAL:HG12	5:C:568:ASP:OD1	1.97	0.65
4:A:146:TYR:HD2	4:A:167:ILE:HG12	1.61	0.64
5:C:766:ASN:O	5:C:767:VAL:HG13	1.97	0.64
5:C:728:LEU:HD11	5:C:886:ILE:HD13	1.78	0.64
6:D:190:LYS:HZ3	6:D:192:ASP:HB3	1.60	0.64
1:O:38:DC:C1'	1:O:39:DG:H5''	2.26	0.64
4:A:46:ILE:HG22	4:A:170:PRO:HG2	1.78	0.64
6:D:103:HIS:O	6:D:104:ILE:HG22	1.97	0.64
8:F:211:LEU:HB2	8:F:212:PRO:HD2	1.79	0.64
6:D:65:TYR:HB3	6:D:70:PHE:CE2	2.33	0.64
5:C:583:ALA:O	5:C:619:THR:HG21	1.98	0.64
6:D:268:PHE:CZ	6:D:273:GLU:HG3	2.33	0.64
6:D:925:ALA:O	6:D:939:ARG:HD2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:454:HIS:CD2	8:F:456:SER:HG	2.15	0.64
4:B:29:GLY:HA2	4:B:190:ASP:OD2	1.97	0.64
6:D:1249:LEU:HD12	6:D:1250:LYS:N	2.13	0.64
6:D:237:ASP:O	6:D:238:GLU:HB3	1.96	0.64
5:C:935:TRP:CZ2	5:C:954:LEU:HD21	2.31	0.64
5:C:952:GLU:OE1	5:C:953:GLU:HB2	1.96	0.64
6:D:270:ILE:H	6:D:270:ILE:HD13	1.63	0.64
4:A:9:LEU:HB2	4:A:23:ILE:HG12	1.78	0.64
4:A:50:ALA:HB3	4:A:168:TYR:CD1	2.32	0.64
7:E:40:LEU:HB3	7:E:50:LEU:HD11	1.79	0.64
6:D:1047:ILE:HD13	6:D:1122:VAL:HG12	1.78	0.64
6:D:1034:GLU:OE2	6:D:1041:PRO:HA	1.98	0.63
6:D:796:ASN:HD21	6:D:798:ILE:HG23	1.63	0.63
6:D:901:ALA:HA	6:D:911:ARG:C	2.18	0.63
4:A:97:LEU:HB2	4:A:110:ILE:HG23	1.80	0.63
5:C:568:ASP:N	5:C:568:ASP:OD1	2.29	0.63
6:D:706:ILE:HG13	7:E:36:PRO:HB3	1.79	0.63
5:C:306:LYS:O	5:C:310:LYS:HB3	1.98	0.63
6:D:12:ILE:HG12	6:D:13:GLY:H	1.64	0.63
5:C:117:ASP:HA	5:C:161:GLY:HA3	1.81	0.63
4:B:22:VAL:HG12	4:B:193:ILE:HG12	1.80	0.63
5:C:482:GLY:O	5:C:485:ILE:HG13	1.98	0.63
5:C:916:ARG:NH2	10:C:1201:SO4:S	2.72	0.63
6:D:1121:GLU:OE2	6:D:1124:ARG:NH2	2.32	0.63
4:B:200:ASN:OD1	4:B:200:ASN:N	2.24	0.63
5:C:664:ARG:NH1	5:C:675:ALA:HB1	2.14	0.63
6:D:1266:SER:HA	6:D:1269:ARG:NH1	2.14	0.63
1:O:6:DA:H2"	1:O:7:DC:H5'	1.80	0.63
6:D:242:ARG:NH1	6:D:245:GLN:OE1	2.31	0.62
4:A:176:TYR:HB3	4:A:194:ILE:HG13	1.81	0.62
5:C:476:PRO:HG2	5:C:477:ILE:HD12	1.81	0.62
6:D:1046:PRO:HG2	6:D:1081:LEU:HD21	1.81	0.62
6:D:1088:ARG:HH11	6:D:1111:GLN:HB3	1.62	0.62
6:D:1118:ASP:HB3	6:D:1121:GLU:HB2	1.80	0.62
6:D:713:ASP:OD1	6:D:716:LYS:NZ	2.32	0.62
2:P:43:DG:O6	8:F:438:ARG:NH1	2.32	0.62
1:O:33:DG:H5"	8:F:246:LYS:HE2	1.80	0.62
5:C:467:HIS:CG	5:C:468:PRO:HD2	2.35	0.62
5:C:618:GLY:O	5:C:964:ALA:HA	1.99	0.62
4:B:172:LEU:HA	6:D:620:MET:HE2	1.81	0.62
8:F:345:PRO:O	8:F:348:VAL:HG13	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:206:ASP:OD1	4:B:226:ASN:ND2	2.33	0.62
6:D:446:LEU:HD12	6:D:446:LEU:H	1.63	0.62
5:C:480:PRO:O	5:C:485:ILE:HG12	2.00	0.62
5:C:824:ARG:HE	5:C:825:ASP:H	1.48	0.62
6:D:1172:GLY:HA2	6:D:1202:ALA:HB2	1.82	0.62
5:C:145:MET:O	5:C:411:ILE:HD12	2.00	0.62
5:C:752:ASP:OD1	5:C:857:ASN:ND2	2.33	0.62
6:D:237:ASP:OD1	6:D:239:VAL:HG13	1.99	0.61
4:B:41:THR:O	4:B:45:SER:HB3	2.00	0.61
6:D:978:TYR:CD2	6:D:988:VAL:HG21	2.35	0.61
5:C:178:PHE:CE1	5:C:193:VAL:HG13	2.34	0.61
6:D:189:ALA:HB1	6:D:194:ARG:HH11	1.64	0.61
1:O:32:DG:C5'	8:F:239:ARG:HG2	2.30	0.61
2:P:43:DG:OP2	8:F:426:THR:OG1	2.15	0.61
5:C:935:TRP:HZ2	5:C:954:LEU:HD21	1.66	0.61
5:C:473:ARG:HH11	5:C:524:ALA:H	1.46	0.61
5:C:216:ARG:HG3	5:C:220:LYS:O	2.01	0.61
4:B:101:GLY:N	4:B:132:GLY:O	2.30	0.61
6:D:589:THR:HG21	6:D:687:MET:SD	2.41	0.61
5:C:1043:ILE:O	6:D:89:ARG:NH2	2.34	0.61
5:C:935:TRP:CB	5:C:982:SER:HB2	2.31	0.60
2:P:34:DA:H2''	2:P:35:DA:O5'	2.01	0.60
5:C:710:LEU:HD13	5:C:1021:ILE:HD11	1.83	0.60
4:B:56:ILE:HG13	4:B:136:VAL:HB	1.83	0.60
4:B:17:ASN:OD1	4:B:17:ASN:N	2.33	0.60
4:B:66:VAL:HG12	4:B:69:VAL:HG22	1.83	0.60
6:D:951:LEU:HB3	6:D:956:ILE:HD11	1.82	0.60
1:O:18:DA:H2''	1:O:19:DA:C8	2.36	0.60
5:C:1040:TYR:CE2	5:C:1090:ARG:HD2	2.32	0.60
9:J:108:LYS:HD3	9:J:108:LYS:O	2.01	0.60
1:O:43:DC:H2''	1:O:44:DG:OP2	2.01	0.60
4:A:12:GLU:O	4:A:19:SER:HB2	2.01	0.60
4:B:88:ASP:N	4:B:88:ASP:OD2	2.32	0.60
6:D:894:ARG:HB2	6:D:894:ARG:HH11	1.66	0.60
4:B:158:GLU:OE1	4:B:161:ARG:NH1	2.35	0.60
6:D:748:HIS:HA	6:D:751:GLU:HG2	1.84	0.60
6:D:796:ASN:OD1	6:D:798:ILE:HG22	2.01	0.60
8:F:194:GLY:HA2	8:F:222:ILE:HG22	1.84	0.60
1:O:44:DG:H2''	1:O:45:DG:OP2	2.01	0.60
5:C:144:PHE:CZ	5:C:146:GLY:HA2	2.37	0.60
1:O:19:DA:H4'	1:O:20:DT:OP1	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:46:ILE:HB	4:A:170:PRO:HD2	1.84	0.59
5:C:796:LYS:HB3	5:C:826:THR:O	2.02	0.59
1:O:2:DC:H2"	1:O:3:DT:O5'	2.02	0.59
4:A:159:ILE:H	4:A:159:ILE:HD12	1.67	0.59
5:C:423:GLY:O	5:C:424:THR:OG1	2.14	0.59
5:C:698:CYS:O	5:C:699:THR:HG23	2.01	0.59
5:C:572:VAL:HG22	5:C:576:GLN:NE2	2.11	0.59
6:D:230:ALA:HB1	6:D:231:PRO:HD2	1.84	0.59
6:D:397:ARG:HB2	6:D:397:ARG:HH11	1.67	0.59
6:D:64:LYS:NZ	6:D:64:LYS:HB3	2.17	0.59
5:C:429:GLN:OE1	5:C:442:HIS:NE2	2.28	0.59
5:C:675:ALA:HA	5:C:697:PRO:HG3	1.83	0.59
6:D:181:LEU:O	6:D:181:LEU:HD23	2.01	0.59
5:C:574:PRO:O	5:C:575:ARG:HG2	2.02	0.59
5:C:1041:SER:HB3	5:C:1044:THR:O	2.03	0.59
5:C:193:VAL:HB	5:C:205:PHE:HB2	1.84	0.59
5:C:853:PRO:O	5:C:856:VAL:HG22	2.02	0.59
1:O:31:DT:C6	1:O:31:DT:H5'	2.37	0.59
4:A:177:LYS:CG	4:A:193:ILE:HG23	2.33	0.59
4:B:170:PRO:HA	4:B:199:LYS:HE2	1.84	0.59
5:C:464:ARG:HD3	5:C:485:ILE:O	2.03	0.59
5:C:967:VAL:HG23	5:C:968:PHE:H	1.67	0.59
5:C:1073:ALA:H	6:D:1263:THR:HG23	1.67	0.59
6:D:104:ILE:HD12	6:D:379:ASP:HB3	1.84	0.59
6:D:339:ASP:OD1	8:F:360:SER:OG	2.20	0.59
8:F:409:GLU:HB3	8:F:448:THR:HG21	1.84	0.59
1:O:12:DG:C2'	1:O:13:DT:H5'	2.30	0.59
7:E:29:PRO:HB2	7:E:33:THR:HG23	1.84	0.58
6:D:525:HIS:CE1	6:D:527:LEU:HD12	2.36	0.58
5:C:507:TYR:OH	5:C:553:ARG:NH2	2.36	0.58
6:D:1088:ARG:NH1	6:D:1111:GLN:H	2.01	0.58
6:D:106:TYR:HB3	6:D:113:ARG:HB2	1.85	0.58
5:C:458:ARG:O	5:C:458:ARG:HG3	2.03	0.58
6:D:666:THR:HG23	6:D:669:ARG:HD2	1.84	0.58
5:C:154:LYS:HB3	5:C:154:LYS:NZ	2.18	0.58
8:F:254:ALA:HB3	8:F:257:ASP:OD2	2.04	0.58
5:C:812:LEU:HA	5:C:815:ILE:HG23	1.84	0.58
6:D:818:GLY:O	6:D:838:SER:HB3	2.03	0.58
6:D:24:SER:HB2	6:D:94:HIS:HB3	1.85	0.58
8:F:465:LEU:HD22	8:F:466:ASP:N	2.18	0.58
5:C:574:PRO:HB2	5:C:968:PHE:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:103:HIS:ND1	6:D:105:TRP:HB2	2.18	0.58
7:E:76:VAL:O	7:E:77:GLY:O	2.21	0.58
5:C:986:ASN:C	5:C:988:ASP:H	2.07	0.58
6:D:1267:ARG:HG3	6:D:1268:TYR:N	2.19	0.58
5:C:1139:ARG:HG2	6:D:90:GLU:OE2	2.04	0.58
6:D:796:ASN:HD21	6:D:798:ILE:CG2	2.17	0.57
4:B:9:LEU:HD21	4:B:208:LEU:HD21	1.87	0.57
6:D:892:THR:HG1	6:D:894:ARG:HH12	1.44	0.57
6:D:1087:LEU:HA	6:D:1113:MET:HA	1.85	0.57
6:D:978:TYR:CZ	6:D:994:VAL:HG11	2.39	0.57
1:O:35:DA:H2''	1:O:36:DG:C4'	2.34	0.57
5:C:196:ILE:O	5:C:196:ILE:HG23	2.04	0.57
5:C:454:LEU:O	5:C:454:LEU:HD12	2.05	0.57
5:C:611:ARG:O	5:C:708:LYS:HE2	2.04	0.57
5:C:25:GLY:HA3	5:C:691:GLN:HG3	1.86	0.57
6:D:737:VAL:HG13	6:D:840:ARG:CD	2.35	0.57
8:F:454:HIS:ND1	8:F:455:PRO:HD2	2.19	0.57
4:A:3:ILE:HD12	4:A:3:ILE:O	2.04	0.57
6:D:1140:GLN:HG2	6:D:1155:ILE:CD1	2.34	0.57
1:O:39:DG:H8	1:O:39:DG:O5'	1.87	0.57
4:B:141:GLU:OE2	4:B:168:TYR:OH	2.21	0.57
5:C:394:ARG:CB	5:C:408:LEU:HD23	2.34	0.57
1:O:35:DA:H2''	1:O:36:DG:O4'	2.04	0.57
6:D:728:VAL:HG23	6:D:797:PRO:HB3	1.84	0.57
5:C:273:ARG:O	5:C:275:GLY:N	2.38	0.57
6:D:963:SER:OG	6:D:1156:GLU:OE1	2.20	0.57
6:D:459:ARG:NE	6:D:489:GLU:OE2	2.37	0.57
4:A:42:LEU:O	4:A:171:VAL:HG11	2.04	0.57
5:C:1019:MET:HG2	5:C:1020:TYR:H	1.70	0.57
8:F:186:GLU:OE2	9:J:101:ARG:NH2	2.31	0.57
3:Q:4:A:OP1	5:C:883:LYS:NZ	2.25	0.57
4:B:152:ASN:O	4:B:153:LYS:HB2	2.05	0.56
4:B:221:LEU:HD12	4:B:222:ALA:N	2.20	0.56
6:D:453:LYS:HB3	6:D:454:PRO:HD3	1.86	0.56
2:P:3:DA:H2''	2:P:4:DT:C5	2.40	0.56
4:A:130:ASP:OD1	4:A:130:ASP:N	2.32	0.56
5:C:1048:LEU:HD12	5:C:1053:GLN:HB3	1.86	0.56
5:C:491:LEU:HD23	5:C:492:SER:N	2.21	0.56
5:C:216:ARG:HE	5:C:221:ARG:HA	1.70	0.56
7:E:31:GLY:O	7:E:33:THR:N	2.33	0.56
6:D:922:ARG:NH2	6:D:1156:GLU:OE2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:64:THR:O	4:B:65:THR:HG22	2.06	0.56
7:E:35:PRO:HG2	7:E:40:LEU:HD11	1.86	0.56
6:D:114:LEU:HD21	6:D:265:ILE:HD11	1.87	0.56
6:D:1251:GLU:OE1	6:D:1251:GLU:N	2.39	0.56
5:C:913:VAL:HB	5:C:914:PRO:HD3	1.87	0.55
6:D:747:ARG:O	6:D:751:GLU:HG2	2.05	0.55
5:C:762:ARG:HG2	5:C:762:ARG:O	2.06	0.55
5:C:752:ASP:N	5:C:855:GLY:O	2.34	0.55
6:D:1221:TRP:CD1	6:D:1244:ASP:HB2	2.41	0.55
6:D:612:TYR:HD1	6:D:633:ILE:HD13	1.70	0.55
6:D:663:GLU:HG2	6:D:664:GLU:H	1.70	0.55
5:C:167:VAL:HG22	5:C:168:SER:H	1.70	0.55
5:C:950:LEU:CB	5:C:951:PRO:HD2	2.37	0.55
6:D:148:LEU:HD13	6:D:148:LEU:O	2.06	0.55
6:D:500:ARG:NH2	6:D:539:ASP:OD2	2.30	0.55
4:A:210:SER:OG	4:B:228:ASP:OD1	2.25	0.55
5:C:125:PHE:HE1	5:C:144:PHE:HB2	1.71	0.55
6:D:1257:LYS:HG2	6:D:1258:LEU:H	1.72	0.55
6:D:646:LEU:HD23	6:D:646:LEU:O	2.07	0.55
5:C:852:LEU:HB3	5:C:856:VAL:CG2	2.36	0.55
6:D:124:ASP:HB3	6:D:234:LEU:CD1	2.37	0.55
6:D:593:GLU:N	6:D:593:GLU:OE1	2.35	0.55
6:D:74:ILE:HD12	9:J:42:VAL:HG13	1.88	0.55
6:D:1248:GLY:O	6:D:1252:ASN:ND2	2.38	0.55
1:O:35:DA:O3'	1:O:36:DG:H4'	2.07	0.55
4:A:152:ASN:N	4:A:152:ASN:OD1	2.40	0.55
5:C:1139:ARG:HG2	6:D:90:GLU:CD	2.27	0.55
5:C:70:GLU:OE1	5:C:72:ASN:HB3	2.06	0.55
5:C:728:LEU:HD11	5:C:886:ILE:CD1	2.37	0.55
5:C:947:ALA:CA	5:C:950:LEU:CB	2.84	0.55
6:D:442:GLY:HA3	6:D:523:GLN:HB2	1.87	0.55
5:C:533:ALA:HB3	5:C:570:MET:HB2	1.89	0.55
5:C:797:VAL:HG13	5:C:823:VAL:HB	1.89	0.55
6:D:592:VAL:HG21	12:D:2006:EDO:H12	1.89	0.55
5:C:518:GLN:O	5:C:519:ILE:HD12	2.06	0.55
4:B:170:PRO:HB2	4:B:202:ILE:HD12	1.89	0.55
4:B:214:THR:O	4:B:218:LEU:HB2	2.06	0.55
5:C:1040:TYR:HE2	5:C:1090:ARG:CD	2.19	0.55
6:D:825:ASN:CB	6:D:826:PRO:HD2	2.37	0.55
7:E:49:ALA:O	7:E:53:TYR:HB2	2.07	0.55
1:O:39:DG:OP1	5:C:458:ARG:HD2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:1167:THR:O	6:D:1204:GLY:HA3	2.07	0.54
6:D:751:GLU:O	6:D:755:ILE:HG13	2.06	0.54
7:E:26:TYR:HB3	7:E:29:PRO:HD3	1.90	0.54
4:B:89:ASP:O	4:B:90:ASP:HB2	2.07	0.54
5:C:1087:THR:HA	5:C:1090:ARG:NE	2.22	0.54
8:F:253:MET:HG2	8:F:301:ALA:HB2	1.89	0.54
1:O:21:DT:OP2	6:D:36:TYR:OH	2.23	0.54
5:C:788:ARG:HG2	5:C:789:ASP:OD1	2.08	0.54
5:C:932:LYS:O	5:C:960:ASP:N	2.35	0.54
5:C:174:PRO:HA	5:C:196:ILE:HG23	1.90	0.54
5:C:947:ALA:HA	5:C:950:LEU:CB	2.37	0.54
5:C:718:GLU:H	6:D:724:THR:CG2	2.20	0.54
2:P:11:DG:H2''	2:P:12:DT:H5'	1.88	0.54
5:C:947:ALA:CB	5:C:950:LEU:CB	2.86	0.54
6:D:1009:LEU:HD12	6:D:1146:GLN:HG3	1.89	0.54
6:D:124:ASP:HB3	6:D:234:LEU:HD13	1.89	0.54
6:D:911:ARG:HG2	6:D:912:ASP:H	1.72	0.54
7:E:31:GLY:C	7:E:33:THR:H	2.10	0.54
4:B:221:LEU:HD12	4:B:222:ALA:H	1.73	0.54
6:D:60:CYS:HB2	6:D:78:CYS:SG	2.48	0.54
6:D:1183:GLU:OE1	6:D:1184:ARG:N	2.41	0.53
1:O:6:DA:H2''	1:O:7:DC:OP2	2.07	0.53
4:B:100:GLN:HA	4:B:133:LYS:HA	1.90	0.53
6:D:190:LYS:HB3	6:D:193:VAL:HG12	1.90	0.53
1:O:40:DT:OP1	5:C:458:ARG:NH1	2.34	0.53
4:B:170:PRO:HB3	4:B:201:SER:HB2	1.90	0.53
5:C:572:VAL:H	5:C:576:GLN:NE2	2.06	0.53
6:D:978:TYR:CZ	6:D:1153:LYS:HD3	2.43	0.53
4:A:48:GLY:HA3	4:A:168:TYR:HB3	1.90	0.53
5:C:504:GLU:HG2	5:C:523:THR:HB	1.90	0.53
5:C:626:ALA:HB2	5:C:704:MET:HG2	1.90	0.53
5:C:796:LYS:HG2	5:C:797:VAL:H	1.74	0.53
6:D:195:ARG:HH21	6:D:198:ARG:HD2	1.73	0.53
8:F:406:SER:HB3	8:F:409:GLU:HG3	1.88	0.53
5:C:939:VAL:CG1	5:C:943:VAL:HG22	2.37	0.53
6:D:48:CYS:SG	6:D:50:LYS:HB3	2.49	0.53
5:C:968:PHE:CG	6:D:845:VAL:HG22	2.43	0.53
6:D:336:ALA:HA	8:F:359:ILE:O	2.07	0.53
5:C:742:HIS:CD2	5:C:868:ARG:HG3	2.44	0.53
5:C:102:ARG:NH2	5:C:142:THR:HG23	2.24	0.53
6:D:1087:LEU:CD2	6:D:1113:MET:HG2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:404:THR:O	8:F:405:LEU:HG	2.09	0.53
1:O:38:DC:C2'	1:O:39:DG:H5"	2.38	0.53
1:O:45:DG:H2"	1:O:46:DA:C8	2.44	0.53
4:A:40:ARG:HH12	4:B:32:TYR:CB	2.21	0.53
4:B:63:PHE:HE2	6:D:604:LYS:H	1.55	0.53
5:C:103:PHE:CZ	5:C:124:LEU:HG	2.44	0.53
5:C:1139:ARG:NE	5:C:1139:ARG:HA	2.23	0.53
5:C:509:LYS:O	5:C:516:THR:OG1	2.12	0.53
6:D:894:ARG:HB3	6:D:966:THR:HB	1.91	0.53
5:C:721:ASN:HB3	5:C:727:ILE:HG13	1.91	0.53
4:B:78:LEU:HD13	6:D:636:ARG:HE	1.74	0.53
6:D:1150:ILE:HG22	6:D:1151:HIS:H	1.73	0.53
6:D:1165:ARG:HG2	6:D:1181:LEU:HB3	1.90	0.53
6:D:573:PRO:HG2	6:D:576:MET:CE	2.39	0.53
6:D:881:GLN:OE1	6:D:1250:LYS:HE2	2.09	0.53
2:P:48:DG:H2"	2:P:49:DC:OP2	2.09	0.53
4:A:30:PHE:HE1	4:B:44:SER:HB3	1.74	0.52
6:D:130:TYR:CZ	6:D:387:ARG:NH1	2.77	0.52
6:D:457:MET:O	6:D:461:VAL:HG23	2.08	0.52
6:D:573:PRO:HG2	6:D:576:MET:HE2	1.91	0.52
6:D:599:TYR:HB3	6:D:633:ILE:HA	1.91	0.52
4:A:70:LYS:HG3	5:C:679:PRO:HG2	1.90	0.52
5:C:696:GLY:N	5:C:699:THR:OG1	2.42	0.52
6:D:1044:LYS:HG2	6:D:1045:ALA:H	1.74	0.52
8:F:207:LYS:O	8:F:209:GLU:HG3	2.09	0.52
5:C:1116:LEU:O	5:C:1120:GLN:HG3	2.09	0.52
5:C:432:ASP:OD2	5:C:438:SER:HB2	2.09	0.52
6:D:1101:SER:N	6:D:1104:ASP:OD2	2.32	0.52
6:D:1222:LEU:HD23	6:D:1244:ASP:OD2	2.08	0.52
8:F:406:SER:HB3	8:F:409:GLU:CG	2.39	0.52
5:C:325:THR:HG23	5:C:326:GLU:H	1.74	0.52
5:C:494:TYR:HB3	5:C:506:PRO:HG3	1.90	0.52
8:F:164:ASP:OD1	8:F:166:VAL:HG13	2.10	0.52
4:A:212:GLY:O	4:A:215:LEU:HD12	2.09	0.52
8:F:171:LYS:O	8:F:175:LYS:HG3	2.10	0.52
8:F:204:LEU:O	8:F:208:GLY:N	2.43	0.52
5:C:173:SER:O	5:C:177:TYR:OH	2.19	0.52
5:C:534:GLN:NE2	5:C:536:ASN:H	1.98	0.52
5:C:728:LEU:HD23	5:C:906:ILE:HG22	1.90	0.52
5:C:946:TRP:C	5:C:946:TRP:CD1	2.83	0.52
6:D:130:TYR:OH	6:D:379:ASP:OD2	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:440:ARG:NH1	8:F:443:GLN:OE1	2.38	0.52
4:A:14:VAL:HG13	4:A:18:ARG:HG3	1.90	0.52
4:A:46:ILE:CG2	4:A:170:PRO:HG2	2.39	0.52
5:C:1003:ASP:OD2	5:C:1005:ARG:N	2.43	0.52
5:C:1021:ILE:N	5:C:1021:ILE:HD13	2.25	0.52
6:D:912:ASP:HB3	6:D:915:VAL:HG13	1.90	0.52
8:F:399:GLN:O	8:F:403:GLU:HB2	2.10	0.52
1:O:39:DG:OP1	1:O:39:DG:H3'	2.10	0.52
4:B:97:LEU:HD13	4:B:110:ILE:HG22	1.92	0.52
5:C:1021:ILE:HD13	5:C:1021:ILE:H	1.75	0.52
5:C:102:ARG:NH2	5:C:126:VAL:O	2.42	0.52
5:C:56:VAL:O	5:C:58:SER:N	2.42	0.52
4:B:76:ILE:HD11	4:B:126:ALA:HB2	1.92	0.51
5:C:403:ILE:HB	5:C:407:THR:CB	2.40	0.51
5:C:728:LEU:CD1	5:C:886:ILE:HD13	2.39	0.51
1:O:31:DT:H2''	8:F:239:ARG:HD2	1.90	0.51
1:O:34:DG:H4'	1:O:35:DA:H5'	1.92	0.51
1:O:38:DC:H2''	1:O:39:DG:C5'	2.39	0.51
2:P:16:DG:OP2	2:P:16:DG:H8	1.93	0.51
4:A:14:VAL:HG13	4:A:15:ALA:H	1.75	0.51
5:C:1031:LYS:HB3	6:D:540:GLN:NE2	2.25	0.51
5:C:178:PHE:O	5:C:358:VAL:HG22	2.10	0.51
6:D:226:PHE:CE1	6:D:248:TYR:HB3	2.45	0.51
1:O:19:DA:H2'	1:O:20:DT:C6	2.46	0.51
6:D:586:TYR:O	6:D:590:THR:HG23	2.11	0.51
1:O:41:DC:H2''	1:O:42:DA:OP2	2.11	0.51
5:C:811:LEU:HD23	5:C:811:LEU:O	2.11	0.51
5:C:853:PRO:HD2	5:C:856:VAL:HG21	1.92	0.51
6:D:127:LYS:HA	6:D:132:ALA:HB3	1.93	0.51
6:D:667:LEU:O	6:D:671:MET:HG3	2.10	0.51
4:A:18:ARG:HB3	4:A:197:GLU:HB2	1.92	0.51
5:C:1087:THR:HA	5:C:1090:ARG:HE	1.74	0.51
5:C:156:THR:HG21	5:C:163:GLU:OE2	2.10	0.51
6:D:1085:GLN:HB2	6:D:1113:MET:CE	2.41	0.51
6:D:269:ASP:HB3	6:D:272:ALA:HB3	1.93	0.51
4:A:49:ALA:HB1	4:A:85:VAL:O	2.10	0.51
4:B:99:LYS:HZ3	4:B:100:GLN:H	1.56	0.51
5:C:535:ALA:HB2	5:C:571:ASP:CB	2.38	0.51
1:O:45:DG:H2''	1:O:46:DA:H8	1.75	0.51
6:D:693:ALA:O	6:D:697:ASN:HB2	2.11	0.51
4:A:2:LEU:O	4:A:2:LEU:HD22	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:1078:GLU:HG3	5:C:1082:ILE:HD11	1.93	0.51
5:C:427:LEU:HD21	5:C:451:PRO:HD2	1.93	0.51
6:D:140:ASP:OD2	6:D:143:MET:HB2	2.10	0.51
5:C:102:ARG:HH22	5:C:142:THR:HG23	1.75	0.51
5:C:439:GLY:O	5:C:443:LYS:HG3	2.11	0.51
6:D:144:ARG:NH2	6:D:229:LEU:O	2.30	0.51
6:D:46:LEU:HB3	6:D:325:ARG:HH12	1.75	0.51
7:E:28:THR:HG23	7:E:28:THR:O	2.10	0.51
7:E:99:ASP:OD2	7:E:99:ASP:N	2.44	0.51
1:O:30:DC:OP2	8:F:282:SER:OG	2.27	0.51
1:O:6:DA:C2'	1:O:7:DC:H5'	2.40	0.51
4:A:199:LYS:O	4:A:200:ASN:HB2	2.12	0.50
6:D:190:LYS:HD2	6:D:192:ASP:H	1.76	0.50
5:C:203:LEU:HA	5:C:217:ILE:HA	1.93	0.50
5:C:749:ASP:HB3	5:C:859:LEU:HD23	1.93	0.50
5:C:736:ASP:OD1	5:C:869:LYS:HE2	2.11	0.50
6:D:965:LEU:HD22	6:D:1132:GLN:OE1	2.11	0.50
5:C:112:GLU:HG2	5:C:116:LYS:HD2	1.94	0.50
6:D:888:HIS:N	10:D:2004:SO4:O2	2.42	0.50
6:D:76:GLU:H	6:D:76:GLU:CD	2.15	0.50
1:O:23:DT:H71	8:F:308:VAL:HG21	1.92	0.50
4:B:68:GLY:O	4:B:128:LEU:HD12	2.11	0.50
4:B:143:GLY:HA3	4:B:168:TYR:CD1	2.45	0.50
4:B:28:PRO:HA	4:B:190:ASP:OD2	2.11	0.50
6:D:230:ALA:N	6:D:233:GLN:OE1	2.44	0.50
6:D:340:LEU:H	6:D:340:LEU:HD22	1.75	0.50
7:E:86:GLU:OE1	7:E:91:ILE:HG12	2.12	0.50
5:C:1036:SER:O	6:D:423:ASP:HB3	2.10	0.50
5:C:685:GLN:HG2	5:C:686:ARG:N	2.26	0.50
6:D:901:ALA:HA	6:D:911:ARG:O	2.10	0.50
6:D:938:GLU:OE1	6:D:938:GLU:N	2.45	0.50
2:P:31:DT:H2''	2:P:32:DT:C6	2.46	0.50
5:C:935:TRP:CZ2	5:C:954:LEU:HD23	2.41	0.50
6:D:1152:ASP:O	6:D:1156:GLU:HG3	2.12	0.50
6:D:1267:ARG:HG3	6:D:1268:TYR:H	1.77	0.50
6:D:557:ILE:HG22	6:D:558:LEU:HD12	1.94	0.50
5:C:176:VAL:HG22	5:C:307:VAL:HG12	1.93	0.50
5:C:435:ASN:HB2	5:C:436:PRO:HD2	1.93	0.50
5:C:762:ARG:NH1	5:C:775:LEU:O	2.40	0.50
8:F:273:PHE:O	9:J:88:ARG:NH2	2.44	0.50
5:C:711:LEU:HD23	5:C:904:VAL:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:568:PRO:HB3	6:D:983:ALA:HB2	1.93	0.50
6:D:578:ARG:HA	6:D:582:VAL:HG23	1.91	0.50
6:D:748:HIS:O	6:D:752:ALA:N	2.29	0.50
4:B:120:ASN:ND2	4:B:123:MET:SD	2.85	0.50
5:C:102:ARG:HB2	5:C:125:PHE:CB	2.41	0.50
8:F:338:ALA:HB1	8:F:343:ILE:O	2.11	0.50
1:O:14:DG:H2"	1:O:15:DT:OP2	2.12	0.50
1:O:30:DC:OP2	8:F:280:LYS:HG2	2.11	0.50
4:A:159:ILE:N	4:A:159:ILE:HD12	2.27	0.49
6:D:1140:GLN:O	6:D:1144:ARG:HG3	2.12	0.49
6:D:736:LEU:N	6:D:792:TYR:OH	2.39	0.49
8:F:156:ASP:O	8:F:160:THR:HG23	2.12	0.49
4:B:73:VAL:O	4:B:77:ILE:HG12	2.12	0.49
5:C:229:LEU:HD22	5:C:229:LEU:H	1.77	0.49
6:D:102:THR:HG21	6:D:129:ILE:HG21	1.93	0.49
4:A:21:PHE:O	4:A:193:ILE:HD12	2.13	0.49
5:C:534:GLN:NE2	5:C:535:ALA:N	2.60	0.49
6:D:1151:HIS:ND1	6:D:1153:LYS:HG2	2.27	0.49
6:D:577:PRO:HA	6:D:581:MET:CE	2.42	0.49
6:D:633:ILE:HD12	6:D:635:VAL:HG22	1.94	0.49
8:F:211:LEU:H	8:F:211:LEU:CD2	2.21	0.49
4:B:47:PRO:HA	4:B:144:ARG:HG3	1.93	0.49
9:J:85:LEU:HD13	9:J:88:ARG:NH1	2.27	0.49
1:O:5:DG:H2"	1:O:6:DA:OP2	2.12	0.49
4:A:2:LEU:N	4:A:2:LEU:HD13	2.28	0.49
4:A:40:ARG:HD3	4:B:33:THR:HG22	1.94	0.49
5:C:1075:THR:O	5:C:1079:LEU:HG	2.12	0.49
5:C:765:PRO:HB3	5:C:821:ARG:HD2	1.93	0.49
6:D:1062:PHE:CE1	6:D:1080:LYS:HB3	2.46	0.49
5:C:809:GLU:O	5:C:810:ARG:CB	2.60	0.49
6:D:1172:GLY:HA3	6:D:1176:PHE:HB2	1.95	0.49
6:D:507:LEU:CD2	6:D:574:LEU:HD23	2.41	0.49
7:E:98:GLY:C	7:E:100:LEU:HD12	2.32	0.49
5:C:277:PRO:HB3	8:F:154:ARG:HA	1.95	0.49
9:J:88:ARG:O	9:J:89:ARG:NH1	2.38	0.49
2:P:17:DG:H8	2:P:17:DG:OP2	1.96	0.49
4:B:106:THR:OG1	4:B:107:ALA:N	2.45	0.49
4:B:228:ASP:N	4:B:228:ASP:OD2	2.43	0.49
5:C:190:LEU:C	5:C:191:HIS:HD1	2.15	0.49
5:C:466:VAL:HG12	6:D:856:ARG:CZ	2.42	0.49
5:C:334:GLU:O	5:C:338:ARG:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:214:ARG:O	6:D:218:ARG:HG3	2.12	0.49
6:D:26:GLY:HA3	6:D:51:ILE:HG21	1.95	0.49
5:C:1019:MET:HG2	5:C:1020:TYR:N	2.27	0.49
5:C:264:ALA:O	5:C:268:ILE:HG22	2.12	0.49
5:C:34:LYS:HD3	5:C:34:LYS:N	2.27	0.49
7:E:26:TYR:CZ	7:E:36:PRO:HG2	2.48	0.49
1:O:47:DT:H2''	1:O:48:DG:C8	2.48	0.49
5:C:437:LEU:O	5:C:441:THR:OG1	2.30	0.49
5:C:641:ILE:H	5:C:641:ILE:HD12	1.77	0.49
8:F:211:LEU:HG	8:F:216:ARG:HB2	1.94	0.49
5:C:975:GLU:O	5:C:979:LEU:HG	2.13	0.48
6:D:218:ARG:O	6:D:222:ILE:HG13	2.13	0.48
1:O:25:DC:OP1	9:J:79:ARG:NH2	2.46	0.48
4:A:107:ALA:HB2	4:A:123:MET:HB3	1.94	0.48
5:C:540:ASP:OD2	5:C:543:GLY:N	2.44	0.48
6:D:130:TYR:HE1	6:D:376:GLU:HG2	1.78	0.48
6:D:527:LEU:HD13	6:D:712:VAL:HG12	1.95	0.48
6:D:589:THR:OG1	6:D:686:GLN:HA	2.12	0.48
6:D:819:MET:HB2	6:D:835:ILE:O	2.13	0.48
6:D:901:ALA:CB	6:D:911:ARG:HA	2.43	0.48
7:E:26:TYR:O	7:E:27:ASP:HB2	2.13	0.48
5:C:178:PHE:CG	5:C:193:VAL:HG22	2.48	0.48
4:A:197:GLU:OE1	5:C:987:ARG:NH1	2.45	0.48
5:C:1069:ALA:HB3	6:D:506:ARG:HB3	1.94	0.48
1:O:32:DG:H5'	8:F:239:ARG:CD	2.42	0.48
5:C:271:LYS:O	5:C:274:PRO:HD3	2.13	0.48
5:C:33:ALA:HB2	5:C:966:PRO:HG2	1.95	0.48
5:C:437:LEU:HD12	5:C:706:LEU:HD11	1.95	0.48
5:C:722:TYR:H	5:C:725:ALA:HB3	1.78	0.48
5:C:984:LEU:CB	5:C:991:VAL:HG23	2.43	0.48
6:D:922:ARG:HH22	6:D:1156:GLU:CD	2.15	0.48
5:C:464:ARG:O	6:D:856:ARG:NH1	2.45	0.48
8:F:373:LEU:HD23	8:F:373:LEU:C	2.34	0.48
4:A:84:VAL:HG22	4:A:120:ASN:ND2	2.29	0.48
4:B:55:ARG:HE	4:B:56:ILE:N	2.11	0.48
6:D:1044:LYS:O	6:D:1085:GLN:NE2	2.40	0.48
6:D:111:PRO:HD2	6:D:1232:ARG:HH12	1.79	0.48
6:D:746:GLU:O	6:D:750:ALA:HB3	2.13	0.48
7:E:79:LEU:HB2	7:E:95:GLU:HG2	1.95	0.48
4:A:216:VAL:HG13	4:B:216:VAL:HG23	1.96	0.48
5:C:609:LEU:HD13	5:C:708:LYS:HE3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:768:SER:O	5:C:771:VAL:HG22	2.13	0.48
5:C:930:VAL:HG11	5:C:979:LEU:HB3	1.96	0.48
6:D:737:VAL:HG13	6:D:840:ARG:HD3	1.96	0.48
4:A:177:LYS:HG3	4:A:193:ILE:CG2	2.39	0.48
4:B:69:VAL:HG12	4:B:128:LEU:HA	1.94	0.48
5:C:125:PHE:CE1	5:C:144:PHE:HB2	2.48	0.48
5:C:357:GLU:HG2	5:C:358:VAL:N	2.28	0.48
5:C:534:GLN:HE21	5:C:536:ASN:N	2.00	0.48
6:D:898:VAL:HG11	6:D:919:ALA:HB2	1.96	0.48
5:C:178:PHE:CD1	5:C:193:VAL:HG22	2.49	0.48
5:C:79:GLU:O	5:C:83:GLU:HG3	2.14	0.48
6:D:114:LEU:HB3	6:D:125:LEU:HD21	1.95	0.48
6:D:372:ARG:HG3	6:D:373:MET:N	2.28	0.48
5:C:193:VAL:CG2	5:C:336:LEU:HG	2.44	0.48
5:C:231:ALA:HA	5:C:265:LEU:CD2	2.43	0.48
6:D:190:LYS:HZ2	6:D:192:ASP:HB3	1.76	0.48
6:D:925:ALA:HB3	6:D:960:LYS:HG2	1.95	0.48
6:D:661:TRP:CZ3	6:D:663:GLU:HB2	2.49	0.48
1:O:6:DA:H1'	1:O:7:DC:H5'	1.96	0.47
5:C:780:ILE:HD12	5:C:841:ILE:HG21	1.97	0.47
2:P:15:DA:P	5:C:1050:GLY:HA2	2.54	0.47
5:C:609:LEU:CD1	5:C:708:LYS:HE3	2.44	0.47
6:D:1278:GLU:HG3	6:D:1278:GLU:H	1.40	0.47
6:D:592:VAL:HG11	12:D:2006:EDO:H11	1.95	0.47
6:D:815:THR:HA	6:D:820:LYS:HA	1.96	0.47
1:O:40:DT:C6	1:O:40:DT:H5''	2.43	0.47
4:B:55:ARG:HH11	4:B:160:GLY:CA	2.27	0.47
5:C:204:GLU:O	5:C:216:ARG:N	2.47	0.47
5:C:498:ASN:HB2	5:C:502:PHE:O	2.14	0.47
5:C:556:GLY:N	5:C:557:GLY:HA2	2.28	0.47
6:D:64:LYS:HB3	6:D:64:LYS:HZ3	1.78	0.47
6:D:822:LEU:HB2	6:D:830:PHE:CE1	2.50	0.47
6:D:916:GLU:HA	6:D:920:PHE:HB2	1.95	0.47
4:A:100:GLN:HG3	4:A:101:GLY:N	2.29	0.47
5:C:1126:VAL:HG12	6:D:12:ILE:HG13	1.95	0.47
6:D:51:ILE:HG13	6:D:52:PHE:H	1.79	0.47
6:D:473:LYS:HD2	8:F:386:VAL:HG21	1.97	0.47
1:O:38:DC:H1'	1:O:39:DG:C5'	2.39	0.47
4:B:170:PRO:HB2	4:B:202:ILE:CD1	2.44	0.47
4:B:40:ARG:HH22	6:D:623:ASP:HB3	1.79	0.47
5:C:1086:ASP:O	5:C:1090:ARG:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:365:GLY:HA3	5:C:525:ASP:OD1	2.15	0.47
5:C:935:TRP:HA	5:C:983:THR:HG23	1.96	0.47
6:D:392:THR:OG1	6:D:396:ASN:HA	2.13	0.47
5:C:786:GLU:O	5:C:787:VAL:HG13	2.15	0.47
6:D:12:ILE:HG12	6:D:13:GLY:N	2.29	0.47
6:D:87:VAL:O	6:D:91:ARG:HG3	2.14	0.47
5:C:589:GLU:OE1	5:C:589:GLU:N	2.30	0.47
5:C:939:VAL:HA	5:C:944:PRO:HD3	1.96	0.47
6:D:550:GLU:O	6:D:554:GLU:HG3	2.15	0.47
1:O:38:DC:N4	5:C:202:TRP:CB	2.78	0.47
1:O:38:DC:N4	5:C:202:TRP:HB2	2.30	0.47
4:A:94:THR:HG22	4:A:139:VAL:HG22	1.97	0.47
5:C:986:ASN:O	5:C:988:ASP:N	2.45	0.47
4:B:99:LYS:HB3	4:B:99:LYS:HZ2	1.80	0.47
5:C:175:GLY:O	5:C:196:ILE:HG22	2.14	0.47
5:C:335:TYR:CE1	5:C:356:VAL:HG13	2.49	0.47
6:D:580:ASP:N	6:D:580:ASP:OD1	2.48	0.47
6:D:735:VAL:O	6:D:840:ARG:NH1	2.48	0.47
6:D:930:ASP:OD2	6:D:934:ASN:N	2.31	0.47
6:D:513:GLU:OE1	7:E:32:ILE:HB	2.15	0.47
6:D:334:ARG:HD3	8:F:356:ARG:NH2	2.30	0.47
8:F:465:LEU:O	8:F:466:ASP:HB2	2.14	0.47
4:A:147:VAL:CG1	4:A:166:SER:HB2	2.45	0.46
2:P:17:DG:H2"	5:C:430:PHE:CE2	2.50	0.46
5:C:597:LEU:HD23	5:C:598:MET:N	2.30	0.46
6:D:503:THR:HG23	6:D:508:GLY:HA3	1.97	0.46
6:D:661:TRP:HZ3	6:D:663:GLU:HB2	1.80	0.46
1:O:45:DG:H8	1:O:45:DG:OP2	1.98	0.46
4:A:38:LEU:HD13	4:A:208:LEU:HD11	1.97	0.46
4:B:55:ARG:O	4:B:137:GLU:N	2.34	0.46
4:B:76:ILE:HA	4:B:79:ASN:HB2	1.97	0.46
5:C:873:GLY:HA3	5:C:1028:VAL:HG11	1.96	0.46
5:C:534:GLN:NE2	5:C:535:ALA:H	2.13	0.46
6:D:515:GLN:O	6:D:517:VAL:HG23	2.15	0.46
6:D:948:ILE:O	6:D:952:LEU:HD13	2.15	0.46
1:O:46:DA:N6	2:P:4:DT:H3	2.08	0.46
4:B:101:GLY:O	4:B:128:LEU:HD23	2.14	0.46
6:D:17:ALA:O	6:D:21:ARG:HG3	2.15	0.46
6:D:350:ARG:HD3	6:D:373:MET:HB3	1.97	0.46
6:D:624:ARG:HE	6:D:624:ARG:HB3	1.52	0.46
6:D:622:MET:CE	6:D:629:VAL:HG22	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:28:PRO:HA	4:B:29:GLY:HA2	1.47	0.46
5:C:718:GLU:H	6:D:724:THR:HG21	1.80	0.46
5:C:951:PRO:CB	5:C:954:LEU:HD13	2.45	0.46
6:D:1062:PHE:H	6:D:1083:LYS:HE3	1.79	0.46
6:D:1168:ILE:O	6:D:1178:PRO:HA	2.16	0.46
6:D:557:ILE:O	6:D:563:ASN:ND2	2.42	0.46
6:D:58:TRP:CD2	6:D:68:VAL:HG12	2.51	0.46
4:A:113:PRO:HD2	4:A:116:VAL:HG21	1.96	0.46
5:C:751:ARG:CG	5:C:856:VAL:HG12	2.37	0.46
6:D:929:VAL:HG12	6:D:935:VAL:HG22	1.96	0.46
4:B:180:ALA:HB1	4:B:188:ASP:HA	1.97	0.46
5:C:80:VAL:HG12	5:C:384:LEU:HD12	1.98	0.46
6:D:432:VAL:HG13	6:D:434:PRO:HD3	1.97	0.46
8:F:439:GLU:OE1	8:F:442:ARG:NH2	2.47	0.46
8:F:408:ARG:HH21	8:F:444:ILE:HD11	1.80	0.46
5:C:921:GLN:O	5:C:925:THR:OG1	2.26	0.46
4:A:19:SER:OG	4:A:204:PRO:HB2	2.16	0.46
4:B:55:ARG:HD3	4:B:160:GLY:HA3	1.98	0.46
5:C:154:LYS:HB3	5:C:154:LYS:HZ3	1.79	0.46
6:D:1088:ARG:HD3	6:D:1111:GLN:HB3	1.97	0.46
6:D:1153:LYS:O	6:D:1157:VAL:HG23	2.16	0.46
6:D:478:ARG:HH11	6:D:480:ARG:HG2	1.80	0.46
5:C:998:LYS:NZ	6:D:734:ASP:OD1	2.48	0.46
4:A:40:ARG:HD2	5:C:1004:GLY:O	2.16	0.46
4:B:205:ARG:HB2	4:B:205:ARG:NH2	2.32	0.46
5:C:1079:LEU:HA	5:C:1083:LYS:HG3	1.97	0.46
5:C:518:GLN:C	5:C:519:ILE:HD12	2.35	0.46
6:D:413:PHE:HA	6:D:417:LEU:HB2	1.97	0.46
5:C:505:THR:HG22	5:C:506:PRO:HD2	1.97	0.45
5:C:884:GLY:HA2	6:D:537:ASP:HA	1.98	0.45
4:A:84:VAL:O	4:A:84:VAL:HG23	2.16	0.45
5:C:159:ILE:HB	5:C:164:ARG:HD2	1.99	0.45
5:C:37:GLU:OE1	5:C:494:TYR:OH	2.33	0.45
6:D:469:ILE:HG12	6:D:469:ILE:O	2.16	0.45
6:D:739:PRO:HD3	6:D:791:PHE:HE2	1.81	0.45
6:D:831:ILE:HG13	6:D:831:ILE:O	2.14	0.45
6:D:877:VAL:HG13	6:D:996:ILE:HG23	1.99	0.45
2:P:15:DA:OP2	5:C:1050:GLY:HA2	2.15	0.45
5:C:357:GLU:HG2	5:C:358:VAL:O	2.16	0.45
5:C:601:ASN:O	5:C:604:ARG:HG2	2.16	0.45
6:D:50:LYS:O	6:D:50:LYS:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:823:VAL:O	6:D:831:ILE:HG12	2.17	0.45
6:D:837:SER:HB3	6:D:842:GLY:O	2.17	0.45
6:D:962:ARG:HH21	6:D:976:MET:CB	2.29	0.45
4:B:8:THR:O	4:B:23:ILE:HA	2.15	0.45
5:C:301:ARG:HD2	5:C:302:VAL:N	2.32	0.45
5:C:587:PHE:HZ	5:C:927:LEU:HD12	1.82	0.45
6:D:1252:ASN:OD1	6:D:1257:LYS:HD3	2.17	0.45
6:D:104:ILE:HG13	6:D:379:ASP:OD2	2.16	0.45
7:E:89:LEU:O	7:E:89:LEU:HD23	2.16	0.45
5:C:754:LYS:HD3	6:D:39:LEU:HD12	1.98	0.45
6:D:1081:LEU:HD22	6:D:1113:MET:SD	2.56	0.45
6:D:60:CYS:SG	6:D:64:LYS:N	2.90	0.45
8:F:197:ALA:O	8:F:201:LEU:HG	2.16	0.45
5:C:449:LEU:O	5:C:449:LEU:HD12	2.16	0.45
6:D:271:ASP:O	6:D:275:GLU:HG3	2.16	0.45
6:D:663:GLU:HG2	6:D:664:GLU:N	2.30	0.45
5:C:641:ILE:N	5:C:641:ILE:HD12	2.32	0.45
6:D:282:ARG:HA	6:D:282:ARG:HD3	1.86	0.45
6:D:50:LYS:HZ1	9:J:55:LEU:HD22	1.82	0.45
4:B:203:SER:HB2	4:B:204:PRO:HD2	1.98	0.45
5:C:106:VAL:HG11	5:C:120:TYR:CZ	2.51	0.45
5:C:216:ARG:NE	5:C:221:ARG:HA	2.32	0.45
5:C:87:ILE:HB	5:C:96:LEU:HB3	1.99	0.45
6:D:1114:GLU:OE1	6:D:1114:GLU:HA	2.17	0.45
6:D:54:PRO:HG3	6:D:81:GLU:O	2.17	0.45
4:A:109:ASP:N	4:A:109:ASP:OD2	2.49	0.45
5:C:102:ARG:N	5:C:125:PHE:O	2.38	0.45
6:D:129:ILE:HA	6:D:257:GLY:HA2	1.98	0.45
8:F:447:LYS:HD3	8:F:447:LYS:HA	1.71	0.45
5:C:753:THR:HG23	5:C:756:GLY:O	2.16	0.45
6:D:129:ILE:HG22	6:D:261:ILE:HG13	1.99	0.45
2:P:2:DC:H2"	2:P:3:DA:C8	2.52	0.45
2:P:6:DC:H2"	2:P:7:DG:C8	2.52	0.45
4:A:4:SER:O	4:A:5:GLN:HG3	2.17	0.44
5:C:397:THR:O	5:C:397:THR:OG1	2.34	0.44
5:C:368:ARG:HB3	5:C:502:PHE:CE1	2.51	0.44
5:C:610:VAL:HG23	5:C:611:ARG:H	1.82	0.44
5:C:635:ALA:HB2	5:C:693:ILE:HD11	1.99	0.44
6:D:459:ARG:NH2	6:D:489:GLU:OE2	2.50	0.44
6:D:738:PRO:HA	6:D:739:PRO:HD3	1.91	0.44
4:A:152:ASN:HB3	4:A:157:ALA:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:751:ARG:HA	5:C:856:VAL:HA	2.00	0.44
5:C:1065:TRP:HB3	6:D:1000:GLN:HE21	1.82	0.44
5:C:171:VAL:HG21	5:C:370:ARG:NE	2.33	0.44
6:D:1132:GLN:HG2	6:D:1163:LEU:CD1	2.47	0.44
6:D:1132:GLN:HG2	6:D:1163:LEU:HD13	1.99	0.44
6:D:1258:LEU:HA	6:D:1258:LEU:HD12	1.74	0.44
5:C:798:THR:HG23	5:C:826:THR:HG21	1.99	0.44
6:D:527:LEU:CD1	6:D:712:VAL:HG12	2.48	0.44
7:E:98:GLY:O	7:E:100:LEU:HD12	2.17	0.44
8:F:310:MET:O	8:F:313:VAL:HG22	2.18	0.44
1:O:39:DG:C8	1:O:39:DG:O5'	2.68	0.44
4:B:77:ILE:O	4:B:81:LYS:HG3	2.17	0.44
5:C:1138:MET:H	5:C:1138:MET:HG2	1.50	0.44
5:C:942:GLY:O	5:C:943:VAL:HB	2.18	0.44
6:D:234:LEU:CD2	6:D:236:VAL:HG22	2.48	0.44
6:D:27:GLU:OE2	6:D:96:GLU:HB2	2.17	0.44
6:D:57:ASP:HB3	6:D:58:TRP:CE3	2.53	0.44
6:D:577:PRO:HA	6:D:581:MET:HE1	1.99	0.44
8:F:191:ILE:O	8:F:195:LEU:HD13	2.17	0.44
1:O:32:DG:H5''	8:F:239:ARG:HG2	1.99	0.44
4:B:55:ARG:NH2	4:B:59:VAL:HB	2.32	0.44
6:D:120:LEU:HD13	6:D:120:LEU:HA	1.81	0.44
6:D:1221:TRP:NE1	6:D:1244:ASP:HB2	2.32	0.44
6:D:846:LEU:O	6:D:850:ILE:HG12	2.17	0.44
9:J:32:TYR:O	9:J:39:GLU:HA	2.17	0.44
4:B:110:ILE:HD12	4:B:111:VAL:N	2.32	0.44
5:C:1064:CYS:O	5:C:1068:GLN:HG3	2.17	0.44
8:F:317:LEU:HD23	8:F:317:LEU:HA	1.85	0.44
4:A:172:LEU:HB3	4:A:197:GLU:HG2	1.99	0.44
5:C:751:ARG:HD2	6:D:332:GLY:CA	2.39	0.44
6:D:1041:PRO:HB3	6:D:1116:ALA:HB3	1.99	0.44
6:D:1062:PHE:N	6:D:1083:LYS:HE3	2.32	0.44
6:D:614:SER:HB2	6:D:615:PRO:HD2	1.98	0.44
1:O:33:DG:C5'	8:F:246:LYS:HE2	2.46	0.44
8:F:372:GLN:H	8:F:372:GLN:HG2	1.51	0.44
4:B:85:VAL:HG23	4:B:117:THR:O	2.18	0.43
6:D:987:LEU:HG	6:D:988:VAL:H	1.82	0.43
8:F:187:LEU:O	8:F:191:ILE:HG13	2.17	0.43
8:F:214:GLN:OE1	9:J:109:ARG:NH2	2.49	0.43
1:O:29:DA:H8	8:F:283:THR:OG1	2.01	0.43
5:C:710:LEU:HB2	5:C:1021:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:589:THR:CB	6:D:686:GLN:HA	2.48	0.43
2:P:43:DG:P	8:F:426:THR:HG1	2.40	0.43
1:O:5:DG:H2"	1:O:6:DA:C8	2.53	0.43
5:C:753:THR:OG1	5:C:754:LYS:N	2.50	0.43
6:D:1100:LEU:HD23	6:D:1100:LEU:HA	1.81	0.43
6:D:1044:LYS:HE3	6:D:1118:ASP:HB2	2.01	0.43
6:D:1169:ILE:HG13	6:D:1204:GLY:HA2	2.00	0.43
6:D:478:ARG:HG2	6:D:478:ARG:O	2.18	0.43
6:D:650:LEU:HD13	6:D:661:TRP:HB2	1.99	0.43
8:F:324:LEU:HB2	8:F:332:PRO:HG3	1.99	0.43
4:B:32:TYR:HB3	5:C:1005:ARG:HG3	2.00	0.43
4:B:54:ILE:HD11	4:B:77:ILE:HD13	1.99	0.43
5:C:177:TYR:HE1	5:C:306:LYS:HZ3	1.67	0.43
5:C:545:PHE:CE1	5:C:550:VAL:HG11	2.53	0.43
5:C:622:GLU:HB3	5:C:704:MET:H	1.84	0.43
5:C:85:SER:HA	5:C:86:PRO:HA	1.66	0.43
6:D:739:PRO:HD3	6:D:791:PHE:CE2	2.53	0.43
6:D:885:VAL:HG21	6:D:988:VAL:HG11	1.99	0.43
4:A:48:GLY:CA	4:A:49:ALA:CB	2.83	0.43
5:C:313:LEU:HD11	5:C:348:VAL:HG11	1.99	0.43
5:C:926:HIS:O	5:C:930:VAL:HG23	2.18	0.43
6:D:430:ILE:HG21	6:D:541:MET:SD	2.59	0.43
6:D:655:TRP:O	6:D:657:PRO:HD3	2.17	0.43
6:D:757:ARG:CZ	6:D:757:ARG:HB3	2.48	0.43
1:O:14:DG:H1	2:P:36:DC:H42	1.66	0.43
4:A:9:LEU:HD12	4:A:10:SER:N	2.34	0.43
5:C:822:GLU:H	5:C:822:GLU:CD	2.21	0.43
4:A:111:VAL:O	4:A:111:VAL:HG22	2.17	0.43
5:C:196:ILE:O	5:C:196:ILE:CG2	2.67	0.43
5:C:306:LYS:HE3	5:C:306:LYS:HB3	1.93	0.43
5:C:841:ILE:HD12	5:C:862:VAL:HG22	2.01	0.43
5:C:973:GLU:OE2	6:D:841:GLU:HA	2.19	0.43
6:D:877:VAL:O	6:D:881:GLN:HB3	2.18	0.43
7:E:37:ILE:N	7:E:37:ILE:HD12	2.33	0.43
7:E:81:GLU:O	7:E:94:ARG:NH2	2.51	0.43
1:O:48:DG:P	6:D:123:LYS:HG2	2.59	0.43
4:A:84:VAL:HG22	4:A:120:ASN:CG	2.39	0.43
4:B:25:PRO:HG3	4:B:183:VAL:CG2	2.49	0.43
5:C:591:ASP:OD2	5:C:880:HIS:ND1	2.52	0.43
5:C:715:MET:HA	5:C:910:THR:HG23	2.00	0.43
6:D:525:HIS:O	6:D:528:VAL:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:592:VAL:HG21	12:D:2006:EDO:C1	2.49	0.43
6:D:636:ARG:CG	6:D:662:THR:HG22	2.49	0.43
6:D:589:THR:HB	6:D:686:GLN:HA	2.01	0.43
6:D:61:TYR:HB3	6:D:78:CYS:HB2	2.01	0.43
6:D:889:ASP:OD2	6:D:890:CYS:N	2.52	0.43
6:D:900:LEU:HD12	6:D:959:VAL:HG22	2.01	0.43
6:D:996:ILE:H	6:D:996:ILE:HG13	1.62	0.43
4:A:212:GLY:O	4:A:216:VAL:HG23	2.18	0.43
5:C:1098:VAL:HG11	6:D:469:ILE:HD12	2.01	0.43
5:C:1129:LEU:CA	5:C:1135:ALA:HA	2.47	0.43
5:C:156:THR:OG1	5:C:157:PHE:N	2.51	0.43
5:C:531:VAL:HG22	5:C:552:VAL:HB	1.99	0.43
4:A:173:LYS:HD3	5:C:900:ASP:O	2.19	0.43
5:C:932:LYS:HG3	5:C:1018:TYR:CE2	2.54	0.43
5:C:938:ASP:O	5:C:939:VAL:HB	2.19	0.43
6:D:822:LEU:H	6:D:822:LEU:CD1	2.25	0.43
4:A:214:THR:HG23	4:B:231:HIS:CB	2.49	0.43
6:D:1220:SER:OG	6:D:1244:ASP:OD2	2.25	0.43
6:D:124:ASP:O	6:D:128:ILE:HG12	2.19	0.43
6:D:1257:LYS:HG2	6:D:1258:LEU:N	2.34	0.43
6:D:591:LEU:HD12	6:D:666:THR:HG22	2.00	0.43
6:D:924:LEU:HD12	6:D:937:ILE:HG22	2.00	0.43
8:F:255:PHE:O	8:F:259:ILE:HG13	2.18	0.43
4:B:162:ILE:HG23	6:D:607:PRO:HG2	2.00	0.42
5:C:177:TYR:CE1	5:C:366:ASN:HB3	2.54	0.42
5:C:826:THR:O	5:C:826:THR:HG23	2.19	0.42
6:D:278:ARG:O	6:D:281:ILE:HG22	2.19	0.42
6:D:665:THR:HG22	6:D:684:ASN:OD1	2.19	0.42
7:E:31:GLY:O	7:E:33:THR:HG22	2.19	0.42
5:C:261:THR:O	5:C:265:LEU:HD23	2.19	0.42
5:C:714:ILE:HG22	5:C:910:THR:CG2	2.45	0.42
5:C:950:LEU:CB	5:C:951:PRO:CD	2.96	0.42
6:D:320:ILE:HG12	6:D:321:PRO:HD2	2.00	0.42
6:D:655:TRP:C	6:D:657:PRO:HD3	2.39	0.42
6:D:980:ARG:HD3	6:D:985:GLY:HA2	2.01	0.42
8:F:167:ARG:O	8:F:170:LEU:N	2.51	0.42
8:F:328:LEU:HD23	8:F:330:ARG:NH2	2.33	0.42
5:C:574:PRO:O	5:C:575:ARG:CG	2.67	0.42
5:C:788:ARG:HG2	5:C:789:ASP:N	2.35	0.42
6:D:565:ILE:HG22	6:D:565:ILE:O	2.19	0.42
6:D:737:VAL:HG13	6:D:840:ARG:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:57:ARG:NE	7:E:95:GLU:OE1	2.40	0.42
8:F:192:GLU:OE2	9:J:88:ARG:NH2	2.52	0.42
8:F:242:VAL:O	8:F:246:LYS:HG3	2.18	0.42
8:F:430:ILE:HB	8:F:441:ILE:HD13	2.00	0.42
8:F:195:LEU:HD21	9:J:81:HIS:CG	2.54	0.42
4:B:192:LEU:HD12	4:B:193:ILE:N	2.33	0.42
5:C:301:ARG:HD2	5:C:302:VAL:HG23	2.02	0.42
5:C:800:LYS:HD2	5:C:824:ARG:HB2	2.01	0.42
6:D:1113:MET:HE2	6:D:1113:MET:HB3	1.77	0.42
6:D:173:ARG:NH2	6:D:201:GLY:HA2	2.35	0.42
6:D:581:MET:HG2	6:D:716:LYS:HA	2.00	0.42
7:E:31:GLY:O	7:E:32:ILE:HG22	2.19	0.42
4:A:100:GLN:CG	4:A:101:GLY:N	2.83	0.42
4:B:25:PRO:HG3	4:B:183:VAL:HG21	2.00	0.42
6:D:262:LYS:O	6:D:266:GLU:HG3	2.19	0.42
6:D:579:LEU:HD23	6:D:579:LEU:HA	1.95	0.42
6:D:735:VAL:HA	6:D:792:TYR:OH	2.19	0.42
5:C:534:GLN:HG3	5:C:536:ASN:H	1.85	0.42
6:D:1151:HIS:CE1	6:D:1153:LYS:HE3	2.55	0.42
6:D:171:GLU:O	6:D:175:GLN:HG3	2.19	0.42
4:B:74:THR:OG1	6:D:608:GLU:OE1	2.22	0.42
4:A:107:ALA:O	4:A:110:ILE:HG12	2.19	0.42
4:A:59:VAL:HG11	4:A:73:VAL:HG21	2.00	0.42
5:C:427:LEU:HD22	5:C:427:LEU:H	1.85	0.42
5:C:809:GLU:O	5:C:810:ARG:HB3	2.20	0.42
6:D:237:ASP:OD1	6:D:240:LEU:N	2.46	0.42
6:D:449:LEU:HD22	6:D:449:LEU:O	2.20	0.42
7:E:40:LEU:CB	7:E:50:LEU:HD11	2.47	0.42
8:F:276:THR:HG23	9:J:89:ARG:NH2	2.34	0.42
4:A:146:TYR:CD2	4:A:167:ILE:HG12	2.49	0.42
5:C:562:VAL:HG22	5:C:563:SER:N	2.30	0.42
5:C:808:GLU:N	5:C:808:GLU:OE1	2.37	0.42
4:A:97:LEU:HD21	4:A:105:VAL:HG11	2.02	0.42
4:B:223:ARG:O	4:B:223:ARG:HG2	2.20	0.42
4:B:59:VAL:O	4:B:60:LEU:HD23	2.20	0.42
4:B:97:LEU:HD21	4:B:105:VAL:HG11	2.02	0.42
5:C:94:MET:HB3	5:C:132:ASN:ND2	2.34	0.42
5:C:412:ARG:N	5:C:413:PRO:HD2	2.35	0.42
5:C:38:PRO:CG	5:C:508:ARG:HD2	2.44	0.42
6:D:177:LEU:O	6:D:181:LEU:HB2	2.20	0.42
1:O:14:DG:H1	2:P:36:DC:N4	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:1043:ILE:H	5:C:1043:ILE:HG13	1.57	0.42
5:C:288:GLU:O	5:C:293:LYS:N	2.48	0.42
5:C:77:LEU:O	5:C:81:LEU:HD22	2.20	0.42
6:D:633:ILE:CD1	6:D:635:VAL:HG22	2.50	0.42
8:F:409:GLU:HB3	8:F:448:THR:CG2	2.50	0.42
1:O:40:DT:P	5:C:458:ARG:HD3	2.60	0.42
4:B:18:ARG:HA	4:B:196:VAL:O	2.20	0.41
4:A:40:ARG:CD	4:B:33:THR:HG22	2.49	0.41
5:C:433:GLN:HG3	5:C:669:SER:OG	2.19	0.41
6:D:394:PRO:O	6:D:397:ARG:HG2	2.20	0.41
4:B:74:THR:O	4:B:78:LEU:HG	2.19	0.41
5:C:270:ARG:O	5:C:274:PRO:HD3	2.20	0.41
5:C:548:ASP:OD1	5:C:549:ARG:N	2.54	0.41
5:C:786:GLU:HG2	5:C:787:VAL:H	1.85	0.41
5:C:932:LYS:C	5:C:932:LYS:HD3	2.40	0.41
6:D:1187:PHE:O	6:D:1191:ASN:HB2	2.20	0.41
8:F:254:ALA:HA	10:F:501:SO4:O4	2.20	0.41
1:O:34:DG:C4'	1:O:35:DA:H5'	2.50	0.41
4:A:50:ALA:HB3	4:A:168:TYR:CE1	2.55	0.41
5:C:1087:THR:HG22	5:C:1090:ARG:HH21	1.85	0.41
5:C:303:GLY:O	5:C:307:VAL:HG22	2.19	0.41
5:C:761:THR:OG1	5:C:762:ARG:N	2.53	0.41
6:D:26:GLY:HA3	6:D:51:ILE:CG2	2.49	0.41
6:D:51:ILE:HG13	6:D:52:PHE:N	2.35	0.41
6:D:636:ARG:HG3	6:D:662:THR:HG22	2.02	0.41
6:D:79:GLY:HA2	9:J:54:TRP:CH2	2.55	0.41
1:O:38:DC:H5'	1:O:38:DC:O2	2.20	0.41
4:A:57:ASP:OD1	4:A:57:ASP:N	2.53	0.41
4:B:226:ASN:O	4:B:227:ALA:HB3	2.21	0.41
4:B:98:ARG:HB3	4:B:98:ARG:HE	1.65	0.41
5:C:228:LEU:HA	5:C:228:LEU:HD12	1.94	0.41
5:C:811:LEU:O	5:C:815:ILE:HG22	2.21	0.41
5:C:831:PRO:HD2	5:C:834:GLU:OE2	2.20	0.41
5:C:840:GLY:O	5:C:841:ILE:HD13	2.20	0.41
6:D:250:GLU:H	6:D:250:GLU:HG2	1.66	0.41
5:C:1075:THR:OG1	6:D:554:GLU:OE2	2.24	0.41
1:O:43:DC:H2''	1:O:44:DG:C8	2.55	0.41
4:A:46:ILE:HA	4:A:47:PRO:HD3	1.91	0.41
5:C:477:ILE:HD12	5:C:477:ILE:N	2.34	0.41
6:D:726:SER:HB3	6:D:728:VAL:HG12	2.02	0.41
6:D:989:ASP:OD2	7:E:47:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:26:LEU:HD21	4:B:218:LEU:HD21	2.02	0.41
5:C:237:GLU:OE1	5:C:237:GLU:N	2.37	0.41
5:C:24:PRO:HG3	5:C:689:ALA:O	2.21	0.41
5:C:919:ILE:HG13	5:C:919:ILE:O	2.21	0.41
5:C:951:PRO:HG2	5:C:951:PRO:O	2.21	0.41
6:D:1056:LEU:HD11	6:D:1063:PHE:HE1	1.86	0.41
6:D:1126:GLN:OE1	6:D:1130:GLU:HG2	2.20	0.41
6:D:367:VAL:HG12	6:D:371:LYS:HE3	2.03	0.41
6:D:822:LEU:HD23	6:D:831:ILE:O	2.20	0.41
6:D:886:ARG:HD2	6:D:886:ARG:HA	1.54	0.41
8:F:317:LEU:HG	8:F:341:MET:SD	2.61	0.41
9:J:102:LEU:O	9:J:105:ILE:HG23	2.19	0.41
1:O:31:DT:O3'	8:F:239:ARG:HD2	2.19	0.41
4:A:52:THR:HA	4:A:166:SER:OG	2.21	0.41
4:B:144:ARG:HH11	4:B:144:ARG:HB2	1.86	0.41
5:C:205:PHE:CE1	5:C:215:VAL:HG13	2.56	0.41
5:C:387:MET:O	5:C:391:VAL:HG23	2.20	0.41
5:C:434:ASN:O	5:C:608:PRO:HD3	2.20	0.41
6:D:17:ALA:HB1	6:D:21:ARG:NH1	2.36	0.41
6:D:52:PHE:CD2	6:D:322:PRO:HD3	2.55	0.41
8:F:291:GLN:HG3	8:F:292:ALA:N	2.35	0.41
1:O:17:DA:H1'	1:O:18:DA:H5'	2.01	0.41
4:B:105:VAL:HG12	4:B:125:ILE:HG21	2.01	0.41
5:C:1040:TYR:CE2	5:C:1090:ARG:NH1	2.88	0.41
5:C:524:ALA:O	5:C:527:GLU:N	2.52	0.41
5:C:722:TYR:O	6:D:536:PHE:HD1	2.04	0.41
5:C:907:ILE:HD12	5:C:907:ILE:N	2.35	0.41
5:C:947:ALA:O	5:C:950:LEU:CB	2.69	0.41
5:C:935:TRP:HB3	5:C:982:SER:HB2	2.03	0.41
6:D:666:THR:HG23	6:D:669:ARG:CD	2.49	0.41
8:F:200:LYS:O	8:F:204:LEU:HD23	2.21	0.41
1:O:12:DG:N2	2:P:39:DT:O2	2.54	0.41
4:A:146:TYR:CD2	5:C:734:GLU:HG2	2.55	0.41
4:B:146:TYR:O	6:D:624:ARG:HD3	2.21	0.41
4:B:24:GLU:HA	4:B:25:PRO:HA	1.75	0.41
5:C:479:THR:HG22	5:C:597:LEU:HD12	2.03	0.41
6:D:129:ILE:HG13	6:D:130:TYR:CD2	2.56	0.41
6:D:339:ASP:OD2	6:D:397:ARG:NH2	2.53	0.41
6:D:791:PHE:O	6:D:791:PHE:HD1	2.04	0.41
8:F:178:LEU:HG	8:F:239:ARG:NH2	2.36	0.41
8:F:411:GLY:O	8:F:415:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:3:DA:H2"	2:P:4:DT:C7	2.50	0.41
4:A:110:ILE:HG12	4:A:110:ILE:H	1.58	0.41
4:B:161:ARG:HD3	4:B:161:ARG:HA	1.65	0.41
4:B:56:ILE:HA	4:B:136:VAL:HA	2.03	0.41
5:C:954:LEU:O	5:C:955:TYR:C	2.59	0.41
6:D:1160:ARG:O	6:D:1164:ARG:HG3	2.20	0.41
5:C:723:GLU:O	6:D:536:PHE:HB2	2.21	0.41
7:E:84:LEU:CD1	7:E:84:LEU:H	2.29	0.41
8:F:199:GLN:HG2	9:J:82:TRP:CE2	2.56	0.41
4:A:104:VAL:HG13	4:A:127:THR:HG22	2.03	0.41
4:A:72:ASP:O	4:A:76:ILE:HG13	2.21	0.41
1:O:40:DT:OP2	5:C:458:ARG:HD3	2.21	0.41
6:D:1168:ILE:HD13	6:D:1176:PHE:HB3	2.03	0.41
6:D:745:LEU:O	6:D:749:GLU:HB3	2.21	0.41
6:D:990:ILE:HG22	6:D:990:ILE:O	2.21	0.41
6:D:1274:GLN:O	7:E:102:GLU:HG2	2.21	0.41
4:A:11:GLU:HB2	4:A:21:PHE:CE2	2.56	0.40
4:B:89:ASP:C	4:B:91:GLU:H	2.24	0.40
5:C:193:VAL:HG23	5:C:336:LEU:HG	2.03	0.40
5:C:335:TYR:OH	5:C:356:VAL:HA	2.21	0.40
5:C:403:ILE:HG13	5:C:404:THR:H	1.85	0.40
5:C:154:LYS:HD2	5:C:630:GLY:HA3	2.03	0.40
6:D:622:MET:HE2	6:D:629:VAL:HG22	2.02	0.40
5:C:1100:GLY:CA	6:D:458:LYS:HE3	2.51	0.40
5:C:1122:LEU:O	5:C:1123:CYS:HB2	2.21	0.40
5:C:638:THR:HG23	5:C:688:GLU:HA	2.03	0.40
5:C:935:TRP:HA	5:C:982:SER:HB2	2.03	0.40
8:F:293:ILE:O	8:F:297:MET:HG3	2.21	0.40
6:D:890:CYS:SG	6:D:892:THR:HG22	2.61	0.40
1:O:44:DG:H2"	1:O:45:DG:C8	2.56	0.40
4:A:14:VAL:CG1	4:A:18:ARG:HG3	2.51	0.40
4:B:147:VAL:O	4:B:147:VAL:HG22	2.21	0.40
5:C:348:VAL:CG1	5:C:349:PRO:HD2	2.50	0.40
6:D:596:THR:HG22	6:D:626:ALA:O	2.22	0.40
1:O:43:DC:H2"	1:O:44:DG:H8	1.85	0.40
2:P:32:DT:H2"	2:P:33:DT:OP2	2.18	0.40
4:B:105:VAL:C	4:B:125:ILE:HG23	2.42	0.40
5:C:35:LEU:HD12	5:C:35:LEU:N	2.37	0.40
5:C:632:VAL:HG22	5:C:694:ALA:O	2.21	0.40
5:C:958:PRO:O	5:C:961:SER:OG	2.31	0.40
6:D:517:VAL:HG12	6:D:518:GLU:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:31:GLY:C	7:E:33:THR:N	2.75	0.40
2:P:8:DT:H4'	6:D:1229:GLU:HG3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:782:ARG:NH1	6:D:171:GLU:OE2[2_356]	1.98	0.22

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	
4	A	218/350 (62%)	203 (93%)	13 (6%)	2 (1%)	20	64
4	B	231/350 (66%)	217 (94%)	13 (6%)	1 (0%)	38	77
5	C	1109/1169 (95%)	1031 (93%)	66 (6%)	12 (1%)	17	58
6	D	1224/1317 (93%)	1165 (95%)	53 (4%)	6 (0%)	32	74
7	E	72/107 (67%)	64 (89%)	5 (7%)	3 (4%)	3	23
8	F	310/466 (66%)	303 (98%)	5 (2%)	2 (1%)	28	72
9	J	84/114 (74%)	81 (96%)	3 (4%)	0	100	100
All	All	3248/3873 (84%)	3064 (94%)	158 (5%)	26 (1%)	22	65

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	C	57	GLY
5	C	274	PRO
5	C	939	VAL
6	D	104	ILE

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Mol	Chain	Res	Type
6	D	802	VAL
7	E	32	ILE
7	E	77	GLY
8	F	162	SER
4	A	49	ALA
5	C	248	ILE
5	C	544	ARG
6	D	969	SER
4	B	65	THR
7	E	76	VAL
5	C	202	TRP
5	C	810	ARG
5	C	967	VAL
5	C	987	ARG
6	D	1192	ARG
8	F	419	LEU
5	C	276	GLU
4	A	183	VAL
5	C	273	ARG
5	C	404	THR
6	D	1108	VAL
6	D	935	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	174/297 (59%)	154 (88%)	20 (12%)	6	28
4	B	170/297 (57%)	141 (83%)	29 (17%)	2	11
5	C	812/984 (82%)	718 (88%)	94 (12%)	6	27
6	D	953/1096 (87%)	866 (91%)	87 (9%)	11	39
7	E	62/86 (72%)	54 (87%)	8 (13%)	5	22
8	F	255/379 (67%)	233 (91%)	22 (9%)	12	43
9	J	65/98 (66%)	56 (86%)	9 (14%)	4	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2491/3237 (77%)	2222 (89%)	269 (11%)	7 31

All (269) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	2	LEU
4	A	6	ARG
4	A	9	LEU
4	A	11	GLU
4	A	14	VAL
4	A	60	LEU
4	A	62	GLU
4	A	72	ASP
4	A	83	LEU
4	A	109	ASP
4	A	110	ILE
4	A	111	VAL
4	A	117	THR
4	A	128	LEU
4	A	130	ASP
4	A	138	LEU
4	A	152	ASN
4	A	193	ILE
4	A	205	ARG
4	A	215	LEU
4	B	3	ILE
4	B	17	ASN
4	B	38	LEU
4	B	76	ILE
4	B	78	LEU
4	B	83	LEU
4	B	88	ASP
4	B	89	ASP
4	B	98	ARG
4	B	99	LYS
4	B	106	THR
4	B	110	ILE
4	B	116	VAL
4	B	123	MET
4	B	125	ILE
4	B	141	GLU
4	B	144	ARG

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Mol	Chain	Res	Type
4	B	147	VAL
4	B	161	ARG
4	B	176	TYR
4	B	189	PHE
4	B	192	LEU
4	B	200	ASN
4	B	202	ILE
4	B	205	ARG
4	B	218	LEU
4	B	221	LEU
4	B	223	ARG
4	B	228	ASP
5	C	30	VAL
5	C	34	LYS
5	C	46	ASP
5	C	56	VAL
5	C	61	TRP
5	C	81	LEU
5	C	96	LEU
5	C	106	VAL
5	C	110	VAL
5	C	119	THR
5	C	124	LEU
5	C	126	VAL
5	C	129	GLU
5	C	133	ASN
5	C	141	GLN
5	C	144	PHE
5	C	150	MET
5	C	154	LYS
5	C	179	ASP
5	C	191	HIS
5	C	235	THR
5	C	236	ASN
5	C	301	ARG
5	C	325	THR
5	C	336	LEU
5	C	338	ARG
5	C	340	HIS
5	C	357	GLU
5	C	358	VAL
5	C	364	PHE

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Mol	Chain	Res	Type
5	C	379	GLN
5	C	397	THR
5	C	428	SER
5	C	437	LEU
5	C	441	THR
5	C	449	LEU
5	C	458	ARG
5	C	463	VAL
5	C	466	VAL
5	C	481	GLU
5	C	505	THR
5	C	522	LEU
5	C	523	THR
5	C	525	ASP
5	C	531	VAL
5	C	545	PHE
5	C	552	VAL
5	C	561	PHE
5	C	568	ASP
5	C	575	ARG
5	C	578	VAL
5	C	597	LEU
5	C	616	LEU
5	C	623	LEU
5	C	636	ASP
5	C	658	ARG
5	C	660	SER
5	C	664	ARG
5	C	674	CYS
5	C	701	ASN
5	C	753	THR
5	C	767	VAL
5	C	777	GLU
5	C	778	ARG
5	C	787	VAL
5	C	804	GLU
5	C	809	GLU
5	C	815	ILE
5	C	830	VAL
5	C	848	ASP
5	C	849	ASP
5	C	851	GLU

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Mol	Chain	Res	Type
5	C	890	LEU
5	C	917	MET
5	C	927	LEU
5	C	946	TRP
5	C	952	GLU
5	C	965	THR
5	C	983	THR
5	C	985	PRO
5	C	988	ASP
5	C	991	VAL
5	C	1021	ILE
5	C	1029	ASP
5	C	1043	ILE
5	C	1045	GLN
5	C	1048	LEU
5	C	1092	LYS
5	C	1108	ILE
5	C	1128	VAL
5	C	1129	LEU
5	C	1138	MET
5	C	1139	ARG
5	C	1140	ASP
6	D	7	PHE
6	D	10	LEU
6	D	64	LYS
6	D	70	PHE
6	D	104	ILE
6	D	105	TRP
6	D	107	PHE
6	D	120	LEU
6	D	144	ARG
6	D	165	GLN
6	D	177	LEU
6	D	195	ARG
6	D	208	LEU
6	D	211	ARG
6	D	239	VAL
6	D	243	GLU
6	D	250	GLU
6	D	256	MET
6	D	267	ASN
6	D	270	ILE

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Mol	Chain	Res	Type
6	D	295	ARG
6	D	298	VAL
6	D	330	LEU
6	D	356	ARG
6	D	372	ARG
6	D	392	THR
6	D	397	ARG
6	D	417	LEU
6	D	449	LEU
6	D	456	VAL
6	D	458	LYS
6	D	479	GLN
6	D	490	VAL
6	D	491	ILE
6	D	499	ASN
6	D	504	LEU
6	D	505	HIS
6	D	520	LYS
6	D	580	ASP
6	D	581	MET
6	D	599	TYR
6	D	600	GLN
6	D	608	GLU
6	D	627	LEU
6	D	629	VAL
6	D	638	THR
6	D	664	GLU
6	D	666	THR
6	D	667	LEU
6	D	675	LEU
6	D	687	MET
6	D	713	ASP
6	D	724	THR
6	D	736	LEU
6	D	737	VAL
6	D	781	THR
6	D	791	PHE
6	D	796	ASN
6	D	822	LEU
6	D	830	PHE
6	D	850	ILE
6	D	864	LEU

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Mol	Chain	Res	Type
6	D	868	ASP
6	D	886	ARG
6	D	894	ARG
6	D	900	LEU
6	D	914	HIS
6	D	923	THR
6	D	938	GLU
6	D	941	HIS
6	D	956	ILE
6	D	961	VAL
6	D	962	ARG
6	D	964	VAL
6	D	984	THR
6	D	1009	LEU
6	D	1114	GLU
6	D	1122	VAL
6	D	1131	VAL
6	D	1165	ARG
6	D	1183	GLU
6	D	1207	VAL
6	D	1229	GLU
6	D	1234	LEU
6	D	1258	LEU
6	D	1263	THR
6	D	1278	GLU
7	E	34	ASN
7	E	50	LEU
7	E	53	TYR
7	E	57	ARG
7	E	62	ASN
7	E	85	GLN
7	E	99	ASP
7	E	103	HIS
8	F	166	VAL
8	F	172	GLN
8	F	204	LEU
8	F	211	LEU
8	F	213	VAL
8	F	239	ARG
8	F	246	LYS
8	F	255	PHE
8	F	291	GLN

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Mol	Chain	Res	Type
8	F	317	LEU
8	F	325	LEU
8	F	330	ARG
8	F	333	THR
8	F	344	THR
8	F	348	VAL
8	F	349	LEU
8	F	372	GLN
8	F	383	VAL
8	F	421	ASP
8	F	448	THR
8	F	454	HIS
8	F	465	LEU
9	J	39	GLU
9	J	47	ASP
9	J	49	GLU
9	J	55	LEU
9	J	76	LYS
9	J	79	ARG
9	J	86	LEU
9	J	88	ARG
9	J	105	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
5	C	141	GLN
5	C	236	ASN
5	C	534	GLN
5	C	576	GLN
6	D	165	GLN
6	D	1000	GLN
8	F	372	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	Q	3/4 (75%)	1 (33%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	Q	2	C

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	SO4	C	1201	-	4,4,4	0.15	0	6,6,6	0.06	0
10	SO4	D	2003	6	4,4,4	0.14	0	6,6,6	0.06	0
10	SO4	D	2004	-	4,4,4	0.14	0	6,6,6	0.06	0
10	SO4	D	2005	6	4,4,4	0.14	0	6,6,6	0.06	0
12	EDO	D	2006	-	3,3,3	0.44	0	2,2,2	0.31	0
10	SO4	F	501	8	4,4,4	0.16	0	6,6,6	0.07	0
10	SO4	F	502	-	4,4,4	0.14	0	6,6,6	0.06	0
12	EDO	F	503	-	3,3,3	0.45	0	2,2,2	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	SO4	C	1201	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	SO4	D	2003	6	-	0/0/0/0	0/0/0/0
10	SO4	D	2004	-	-	0/0/0/0	0/0/0/0
10	SO4	D	2005	6	-	0/0/0/0	0/0/0/0
12	EDO	D	2006	-	-	0/1/1/1	0/0/0/0
10	SO4	F	501	8	-	0/0/0/0	0/0/0/0
10	SO4	F	502	-	-	0/0/0/0	0/0/0/0
12	EDO	F	503	-	-	0/1/1/1	0/0/0/0

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.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	C	1201	SO4	2	0
10	D	2004	SO4	1	0
12	D	2006	EDO	3	0
10	F	501	SO4	1	0
10	F	502	SO4	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	O	49/50 (98%)	-0.33	1 (2%) 65 50	53, 109, 179, 196	0
2	P	44/50 (88%)	-0.29	1 (2%) 61 46	75, 107, 177, 193	0
3	Q	4/4 (100%)	0.08	0 100 100	119, 123, 126, 143	0
4	A	220/350 (62%)	0.03	6 (2%) 55 40	56, 91, 125, 159	0
4	B	233/350 (66%)	0.15	7 (3%) 51 35	78, 111, 137, 145	0
5	C	1113/1169 (95%)	0.04	32 (2%) 52 37	33, 84, 146, 168	0
6	D	1238/1317 (94%)	-0.09	8 (0%) 89 83	32, 76, 123, 152	0
7	E	76/107 (71%)	0.15	2 (2%) 56 41	55, 86, 121, 132	0
8	F	314/466 (67%)	0.01	4 (1%) 77 65	37, 80, 132, 154	0
9	J	86/114 (75%)	0.01	2 (2%) 61 46	58, 101, 138, 169	0
All	All	3377/3977 (84%)	-0.01	63 (1%) 67 52	32, 85, 138, 196	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	E	74	GLU	5.6
4	B	1	MET	5.0
4	A	187	THR	5.0
2	P	1	DG	4.6
6	D	609	GLN	4.3
8	F	337	LEU	4.2
5	C	261	THR	4.1
5	C	228	LEU	3.9
5	C	266	LEU	3.7
8	F	466	ASP	3.6
5	C	345	SER	3.5
5	C	226	THR	3.5
5	C	552	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
6	D	66	LYS	3.2
4	B	138	LEU	3.1
5	C	550	VAL	3.1
5	C	320	THR	3.1
5	C	260	GLY	3.0
4	A	26	LEU	3.0
4	A	37	SER	2.9
4	A	38	LEU	2.9
5	C	330	VAL	2.9
5	C	287	LEU	2.8
5	C	246	SER	2.7
4	B	10	SER	2.7
6	D	906	ASP	2.6
1	O	49	DC	2.6
5	C	262	ASP	2.6
5	C	231	ALA	2.5
5	C	560	GLU	2.5
5	C	264	ALA	2.4
4	A	16	GLU	2.4
6	D	905	PRO	2.4
5	C	131	ILE	2.3
5	C	459	ALA	2.3
5	C	561	PHE	2.3
8	F	452	LEU	2.2
5	C	951	PRO	2.2
6	D	738	PRO	2.2
5	C	551	MET	2.2
4	A	182	ARG	2.2
8	F	427	LEU	2.2
5	C	185	SER	2.2
6	D	832	PRO	2.2
4	B	65	THR	2.2
9	J	49	GLU	2.2
5	C	128	ALA	2.2
6	D	607	PRO	2.1
6	D	67	ARG	2.1
7	E	26	TYR	2.1
5	C	817	GLY	2.1
5	C	202	TRP	2.1
5	C	403	ILE	2.1
5	C	358	VAL	2.1
4	B	140	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
5	C	132	ASN	2.1
5	C	398	GLN	2.1
5	C	265	LEU	2.1
9	J	74	LYS	2.1
4	B	201	SER	2.1
5	C	321	SER	2.1
4	B	114	ALA	2.0
5	C	281	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(Å ²)	Q<0.9
11	ZN	D	2001	1/1	0.95	0.29	4.32	116,116,116,116	0
12	EDO	D	2006	4/4	0.90	0.20	-0.07	68,85,104,104	0
12	EDO	F	503	4/4	0.91	0.19	-0.19	76,91,105,111	0
11	ZN	D	2002	1/1	0.95	0.18	-0.41	100,100,100,100	0
10	SO4	D	2004	5/5	0.95	0.18	-0.46	83,90,99,120	0
10	SO4	F	501	5/5	0.86	0.17	-0.83	72,80,89,163	0
10	SO4	F	502	5/5	0.78	0.15	-1.20	73,78,115,167	0
10	SO4	D	2005	5/5	0.91	0.17	-1.23	85,92,116,121	0
10	SO4	D	2003	5/5	0.94	0.12	-	91,97,128,130	0
10	SO4	C	1201	5/5	0.60	0.51	-	120,128,134,230	0

6.5 Other polymers

There are no such residues in this entry.