Full wwPDB X-ray Structure Validation Report (i)

Dec 3, 2023 – 11:21 pm GMT

PDB ID	:	1HBX
Title	:	Ternary Complex of SAP-1 and SRF with specific SRE DNA
Authors	:	Hassler, M.; Richmond, T.J.
Deposited on	:	2001-04-20
Resolution	:	3.15 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

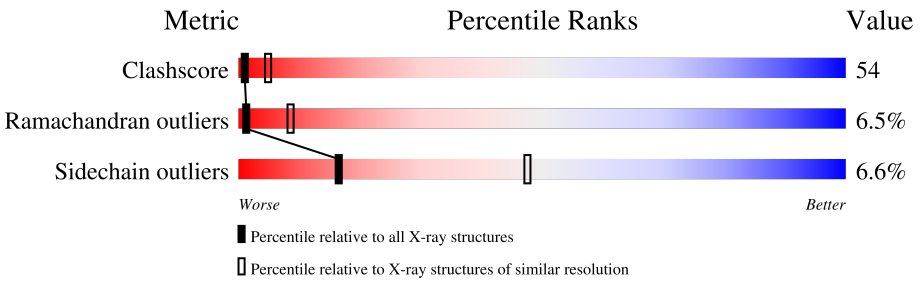
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.15 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))
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	92	49% 39% 5% • 5%
1	B	92	48% 38% 8% 7%
1	D	92	42% 47% • 7%
1	E	92	39% 50% 8% •
2	C	26	92% 8%
2	F	26	• 96%
3	G	157	17% 43% 11% 29%
3	H	157	17% 46% 6% • 31%

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Mol	Chain	Length	Quality of chain
4	W	26	85% 15%
4	X	26	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6682 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 SERUM RESPONSE FACTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	87	681	430	121	126	4	0	0	0
1	B	86	685	434	122	125	4	0	0	0
1	D	86	677	428	120	125	4	0	0	0
1	E	89	691	436	123	128	4	0	0	0

- Molecule 2 is a DNA chain called 5'-D(*GP*AP*TP*GP*GP*CP*CP*TP*AP*AP*TP*TP*AP* GP*GP*AP*CP*TP*TP*CP*CP*GP*GP*TP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	26	533	255	96	157	25	0	0	0
2	F	26	533	255	96	157	25	0	0	0

- Molecule 3 is a protein called ETS-DOMAIN PROTEIN ELK-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	112	925	598	163	160	4	0	0	0
3	H	109	903	587	156	156	4	0	0	0

- Molecule 4 is a DNA chain called 5'-D(*CP*AP*CP*AP*CP*CP*GP*GP*AP*AP*GP*TP*CP* CP*TP*AP*AP*TP*TP*AP*GP*GP*CP*CP*AP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	W	26	527	252	99	151	25	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	X	26	527	252	99	151	25	0	0	0

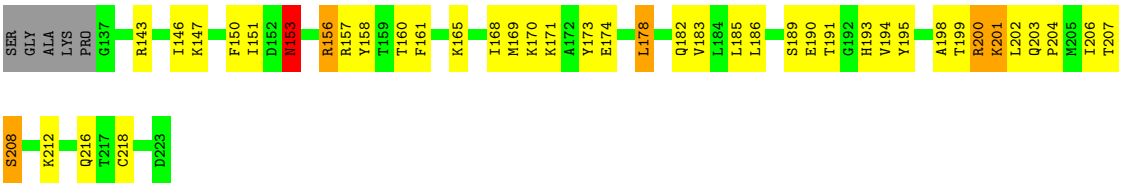
3 Residue-property plots (i)

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

Note EDS was not executed.

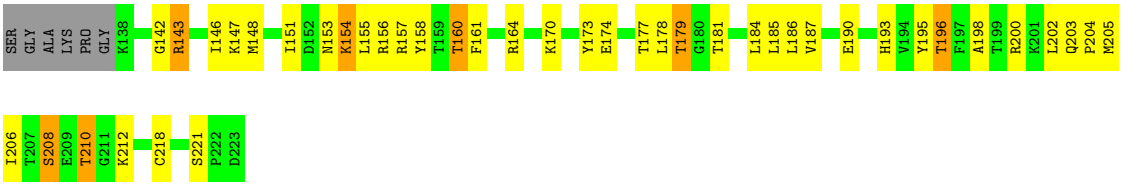
• Molecule 1: SERUM RESPONSE FACTOR

Chain A:



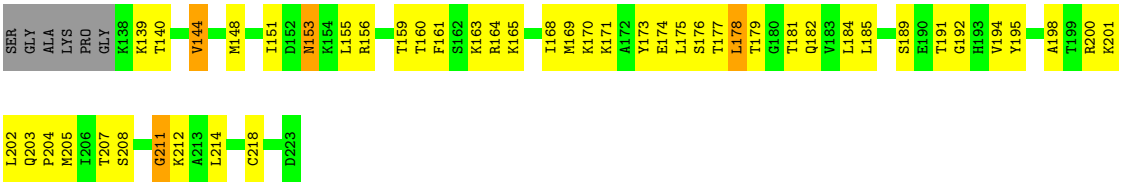
• Molecule 1: SERUM RESPONSE FACTOR

Chain B:



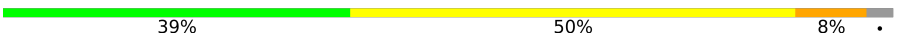
• Molecule 1: SERUM RESPONSE FACTOR

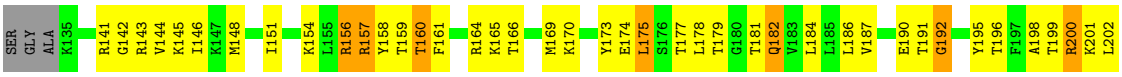
Chain D:

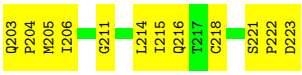


• Molecule 1: SERUM RESPONSE FACTOR

Chain E:

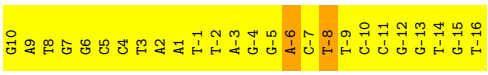






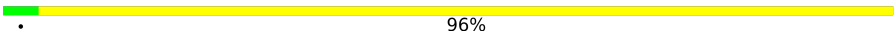
• Molecule 2: 5'-D(*GP*AP*TP*GP*GP*CP*CP*TP*AP*AP*TP*TP*AP* GP*GP*AP*CP* TP*TP*CP*CP*GP*GP*TP*G)-3'

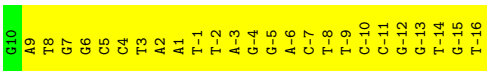
Chain C:



• Molecule 2: 5'-D(*GP*AP*TP*GP*GP*CP*CP*TP*AP*AP*TP*TP*AP* GP*GP*AP*CP* TP*TP*CP*CP*GP*GP*TP*G)-3'

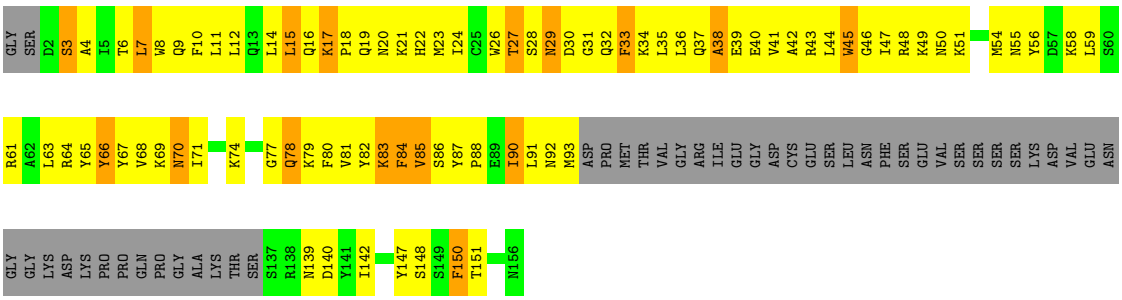
Chain F:





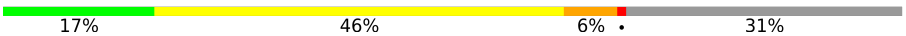
• Molecule 3: ETS-DOMAIN PROTEIN ELK-4

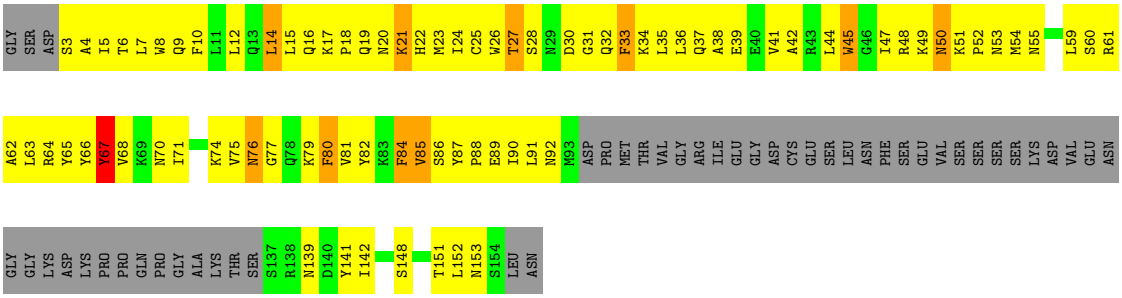
Chain G:



• Molecule 3: ETS-DOMAIN PROTEIN ELK-4

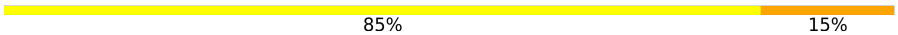
Chain H:

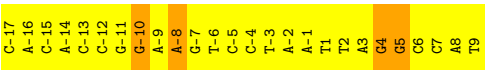




• Molecule 4: 5'-D(*CP*AP*CP*AP*CP*CP*GP*GP*AP*AP*GP*TP*CP* CP*TP*AP*AP* TP*TP*AP*GP*GP*CP*CP*AP*T)-3'

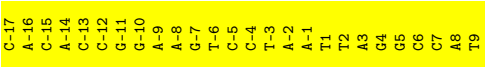
Chain W:





• Molecule 4: 5'-D(*CP*AP*CP*AP*CP*CP*GP*GP*AP*AP*GP*TP*CP* CP*TP*AP*AP* TP*TP*AP*GP*GP*CP*CP*AP*T)-3'

Chain X: 100%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	142.68Å 144.39Å 75.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.00 – 3.15	Depositor
% Data completeness (in resolution range)	98.8 (51.00-3.15)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.252 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6682	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	0.44	0/689	0.71	1/923 (0.1%)
1	B	0.48	0/693	0.66	0/926
1	D	0.44	0/685	0.67	0/918
1	E	0.43	0/700	0.65	0/938
2	C	0.71	0/597	0.88	1/921 (0.1%)
2	F	0.60	0/597	0.82	0/921
3	G	0.35	0/947	0.59	0/1274
3	H	0.32	0/925	0.52	0/1247
4	W	0.76	0/591	1.00	4/909 (0.4%)
4	X	0.59	0/591	0.85	0/909
All	All	0.51	0/7015	0.74	6/9886 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	W	5	DG	C5'-C4'-C3'	-6.96	101.57	114.10
1	A	178	LEU	CA-CB-CG	5.88	128.83	115.30
4	W	4	DG	C5'-C4'-C3'	-5.85	103.57	114.10
4	W	-8	DA	N9-C1'-C2'	5.36	122.78	112.60
2	C	-8	DT	C5'-C4'-C3'	-5.32	104.53	114.10
4	W	-10	DG	C5'-C4'-C3'	-5.07	104.98	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	-6	DA	Sidechain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	681	0	717	47	0
1	B	685	0	736	51	0
1	D	677	0	714	61	0
1	E	691	0	724	73	0
2	C	533	0	296	56	0
2	F	533	0	296	77	0
3	G	925	0	909	136	0
3	H	903	0	896	115	0
4	W	527	0	293	80	0
4	X	527	0	293	79	0
All	All	6682	0	5874	682	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 54.

All (682) 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)
4:X:-14:DA:C2'	4:X:-13:DC:H5"	1.66	1.25
2:F:4:DC:C2'	2:F:3:DT:H5"	1.69	1.23
2:F:-10:DC:C2'	2:F:-11:DC:H5"	1.71	1.20
2:F:4:DC:H2"	2:F:3:DT:C5'	1.76	1.15
2:C:-10:DC:C2'	2:C:-11:DC:H5"	1.76	1.14
2:C:1:DA:H2"	2:C:-1:DT:H5"	1.30	1.13
4:X:-14:DA:H2"	4:X:-13:DC:C5'	1.77	1.13
4:W:5:DG:H2"	4:W:6:DC:C5'	1.79	1.12
4:X:5:DG:H2"	4:X:6:DC:H5"	1.25	1.11
2:C:-10:DC:H2"	2:C:-11:DC:H5"	1.15	1.10
2:C:-10:DC:H2"	2:C:-11:DC:C5'	1.83	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:5:DG:H2"	4:X:6:DC:C5'	1.80	1.09
4:W:5:DG:C2'	4:W:6:DC:H5"	1.82	1.09
4:W:-14:DA:C2'	4:W:-13:DC:H5"	1.82	1.09
4:X:-13:DC:H2"	4:X:-12:DC:C5'	1.82	1.08
4:X:-13:DC:H2"	4:X:-12:DC:H5"	1.34	1.05
2:F:-10:DC:H2"	2:F:-11:DC:H5"	1.33	1.05
4:W:-14:DA:H2"	4:W:-13:DC:H5"	1.34	1.04
4:W:5:DG:H2"	4:W:6:DC:H5"	1.06	1.04
2:F:-7:DC:H2'	2:F:-8:DT:H71	1.39	1.03
2:C:-11:DC:H4'	2:C:-11:DC:OP1	1.59	1.02
4:W:-6:DT:H2"	4:W:-5:DC:H5'	1.42	1.01
4:X:2:DT:H2"	4:X:3:DA:H5"	1.41	1.01
4:W:-16:DA:H2"	4:W:-15:DC:H5"	1.42	0.98
2:F:-9:DT:H2"	2:F:-10:DC:O5'	1.63	0.97
4:W:-1:DA:H2"	4:W:1:DT:H5'	1.46	0.96
2:C:-11:DC:H2"	2:C:-12:DG:C8	2.00	0.96
4:W:2:DT:H2"	4:W:3:DA:H5'	1.46	0.96
2:C:-13:DG:H2"	2:C:-14:DT:H5"	1.46	0.96
4:W:-10:DG:H2"	4:W:-9:DA:H5"	1.48	0.95
4:W:-12:DC:C2'	4:W:-11:DG:H5"	1.96	0.95
2:F:1:DA:H2"	2:F:-1:DT:H5"	1.49	0.94
2:C:-7:DC:H2'	2:C:-8:DT:H71	1.49	0.94
2:F:-8:DT:H2"	2:F:-9:DT:H5'	1.49	0.94
2:F:-10:DC:H2"	2:F:-11:DC:C5'	1.98	0.93
2:C:1:DA:H2"	2:C:-1:DT:C5'	2.00	0.92
2:F:1:DA:H2"	2:F:-1:DT:C5'	1.99	0.91
3:H:34:LYS:HB2	3:H:81:VAL:HG12	1.55	0.89
4:W:-10:DG:H2"	4:W:-9:DA:C5'	2.02	0.89
4:X:7:DC:H2"	4:X:8:DA:H8	1.38	0.89
2:F:-11:DC:H2"	2:F:-12:DG:C8	2.08	0.89
2:C:2:DA:H2"	2:C:1:DA:OP2	1.71	0.88
4:W:-11:DG:H4'	4:W:-11:DG:OP1	1.72	0.88
2:F:5:DC:H2"	2:F:4:DC:O5'	1.75	0.87
2:C:1:DA:C2'	2:C:-1:DT:H5"	2.05	0.87
1:E:196:THR:HG23	3:H:148:SER:HB3	1.56	0.87
2:C:-8:DT:H2"	2:C:-9:DT:C5'	2.05	0.87
2:C:-11:DC:H2"	2:C:-12:DG:N7	1.90	0.87
4:W:-1:DA:H2"	4:W:1:DT:C5'	2.05	0.86
4:X:-10:DG:H2"	4:X:-9:DA:H5'	1.57	0.86
4:X:2:DT:C2'	4:X:3:DA:H5"	2.05	0.86
3:H:85:VAL:HG23	3:H:86:SER:H	1.41	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:-13:DG:H2"	2:F:-14:DT:H5"	1.59	0.85
2:C:7:DG:H2"	2:C:6:DG:H5'	1.57	0.85
4:W:-14:DA:H2"	4:W:-13:DC:C5'	2.08	0.84
2:F:-7:DC:C2'	2:F:-8:DT:H71	2.09	0.83
4:X:-15:DC:H2"	4:X:-14:DA:C8	2.14	0.83
4:X:5:DG:C2'	4:X:6:DC:H5"	2.07	0.83
4:W:-15:DC:H2"	4:W:-14:DA:C8	2.14	0.82
4:X:-13:DC:C2'	4:X:-12:DC:H5"	2.10	0.82
1:A:185:LEU:HD12	1:A:186:LEU:H	1.43	0.82
2:F:-11:DC:H4'	2:F:-11:DC:OP1	1.78	0.82
3:G:87:TYR:CD1	3:G:88:PRO:HA	2.14	0.82
1:D:161:PHE:HB2	1:E:179:THR:HG21	1.59	0.82
3:H:64:ARG:HA	3:H:67:TYR:CE1	2.16	0.81
3:H:5:ILE:HG13	3:H:6:THR:H	1.43	0.81
2:C:4:DC:H2"	2:C:3:DT:H5"	1.62	0.80
4:W:-13:DC:H4'	4:W:-13:DC:OP1	1.82	0.80
3:G:18:PRO:HA	3:G:21:LYS:HG3	1.64	0.80
4:X:-13:DC:H2"	4:X:-12:DC:H5'	1.65	0.79
4:X:-14:DA:H2"	4:X:-13:DC:H5"	0.84	0.79
1:A:178:LEU:HG	1:B:151:ILE:HD11	1.63	0.79
1:D:179:THR:OG1	1:D:181:THR:HG23	1.83	0.79
4:W:1:DT:H2'	4:W:2:DT:H72	1.66	0.78
3:G:33:PHE:CE2	3:G:82:TYR:HB2	2.17	0.78
4:X:7:DC:H2"	4:X:8:DA:C8	2.17	0.78
1:A:204:PRO:HG2	1:B:218:CYS:SG	2.25	0.77
3:G:40:GLU:O	3:G:44:LEU:HG	1.85	0.77
4:X:-1:DA:H2"	4:X:1:DT:C5'	2.14	0.77
4:W:1:DT:H2"	4:W:2:DT:OP2	1.84	0.76
2:C:-8:DT:H2"	2:C:-9:DT:H5'	1.67	0.76
2:F:-10:DC:H2'	2:F:-11:DC:H5"	1.68	0.76
3:G:17:LYS:HB3	3:G:19:GLN:HG2	1.66	0.76
2:C:-13:DG:H2"	2:C:-14:DT:C5'	2.15	0.75
2:F:-10:DC:C2'	2:F:-11:DC:C5'	2.58	0.75
3:H:139:ASN:HB3	3:H:142:ILE:HD12	1.69	0.75
4:W:-4:DC:H1'	4:W:-3:DT:H5"	1.67	0.75
3:G:83:LYS:HB2	3:G:83:LYS:NZ	2.00	0.75
4:W:2:DT:C2'	4:W:3:DA:H5'	2.17	0.75
4:W:-12:DC:H2"	4:W:-11:DG:H5"	1.66	0.75
1:D:178:LEU:HD13	1:E:148:MET:HE3	1.67	0.74
1:E:203:GLN:N	1:E:204:PRO:HD2	2.01	0.74
2:F:-8:DT:H2'	2:F:-9:DT:H71	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:X:-11:DG:H4'	4:X:-11:DG:OP1	1.88	0.74
3:G:37:GLN:O	3:G:41:VAL:HG23	1.86	0.74
2:C:-8:DT:H2"	2:C:-9:DT:H5"	1.68	0.74
1:D:178:LEU:HD13	1:E:148:MET:CE	2.18	0.74
3:H:41:VAL:HA	3:H:44:LEU:HD12	1.68	0.73
2:F:-10:DC:H4'	2:F:-10:DC:OP1	1.88	0.73
3:G:87:TYR:CG	3:G:88:PRO:HA	2.23	0.73
3:G:29:ASN:HD22	3:G:29:ASN:H	1.37	0.73
3:H:33:PHE:CE2	3:H:82:TYR:HB2	2.23	0.73
4:X:3:DA:H2"	4:X:4:DG:C8	2.23	0.73
1:D:151:ILE:HD11	1:E:178:LEU:HD22	1.71	0.73
3:G:8:TRP:CE2	3:G:9:GLN:HG3	2.24	0.72
4:X:-1:DA:H2"	4:X:1:DT:H5"	1.71	0.72
1:A:174:GLU:O	1:A:178:LEU:HB2	1.90	0.72
1:D:177:THR:HB	1:E:148:MET:HE2	1.71	0.72
4:X:1:DT:H2'	4:X:2:DT:H72	1.70	0.72
1:B:154:LYS:HG2	1:B:158:TYR:CE2	2.24	0.72
2:C:-1:DT:H2'	2:C:-2:DT:H72	1.72	0.72
4:W:1:DT:C2'	4:W:2:DT:H72	2.19	0.72
4:X:5:DG:H2"	4:X:6:DC:H5'	1.72	0.72
1:D:140:THR:HG21	2:F:-5:DG:H21	1.55	0.72
4:W:-2:DA:H2"	4:W:-1:DA:OP2	1.88	0.72
3:G:49:LYS:CB	3:G:49:LYS:HZ3	2.02	0.71
3:G:49:LYS:HZ3	3:G:49:LYS:HB3	1.55	0.71
1:B:179:THR:O	1:B:181:THR:HG23	1.89	0.71
2:F:1:DA:C2'	2:F:-1:DT:H5"	2.20	0.71
1:A:185:LEU:HD12	1:A:186:LEU:N	2.05	0.71
1:E:165:LYS:HD2	1:E:195:TYR:CD2	2.25	0.71
2:F:-11:DC:H2"	2:F:-12:DG:N7	2.04	0.71
3:G:33:PHE:HE2	3:G:82:TYR:HB2	1.54	0.71
4:W:-16:DA:C2'	4:W:-15:DC:H5"	2.17	0.71
2:C:-3:DA:H2"	2:C:-4:DG:C8	2.25	0.71
1:B:146:ILE:HD13	4:W:4:DG:H5'	1.73	0.70
2:F:4:DC:H2"	2:F:3:DT:H5"	0.81	0.70
1:D:144:VAL:HG22	2:F:-4:DG:H4'	1.72	0.69
4:X:-13:DC:H4'	4:X:-13:DC:OP1	1.91	0.69
1:D:204:PRO:HG2	1:E:218:CYS:SG	2.33	0.69
3:G:23:MET:HB3	3:G:37:GLN:HB2	1.75	0.69
2:F:-12:DG:H2"	2:F:-13:DG:H8	1.58	0.69
3:G:61:ARG:NE	4:W:-11:DG:N7	2.41	0.69
3:G:23:MET:SD	3:G:44:LEU:HD11	2.33	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:139:ASN:HB3	3:G:142:ILE:HD12	1.75	0.69
3:H:12:LEU:HD21	3:H:91:LEU:HD23	1.75	0.69
4:X:-3:DT:H2"	4:X:-2:DA:C8	2.27	0.69
3:G:88:PRO:HB2	3:G:91:LEU:CD1	2.24	0.68
3:G:88:PRO:HB2	3:G:91:LEU:HD12	1.74	0.68
4:W:-4:DC:H1'	4:W:-3:DT:C5'	2.21	0.68
1:D:203:GLN:N	1:D:204:PRO:HD2	2.08	0.68
3:H:10:PHE:O	3:H:14:LEU:HD23	1.93	0.68
3:H:88:PRO:HB3	3:H:91:LEU:HD12	1.75	0.68
2:F:-12:DG:H2"	2:F:-13:DG:H5"	1.76	0.68
1:E:186:LEU:HD23	1:E:187:VAL:N	2.09	0.68
2:C:-10:DC:C2'	2:C:-11:DC:C5'	2.58	0.68
2:F:1:DA:H2"	2:F:-1:DT:H5'	1.74	0.68
1:A:158:TYR:OH	4:W:-9:DA:H5'	1.93	0.68
4:X:-8:DA:H2"	4:X:-7:DG:H8	1.57	0.68
2:C:-8:DT:H4'	3:G:51:LYS:HE3	1.75	0.68
3:H:75:VAL:HB	3:H:81:VAL:HG23	1.75	0.67
3:H:39:GLU:O	3:H:42:ALA:HB3	1.93	0.67
2:C:-7:DC:C2'	2:C:-8:DT:H71	2.24	0.67
4:W:-7:DG:H2"	4:W:-6:DT:H71	1.76	0.67
3:H:36:LEU:HD12	3:H:36:LEU:H	1.58	0.67
4:X:3:DA:H2"	4:X:4:DG:N7	2.10	0.67
2:F:-3:DA:H2"	2:F:-4:DG:C8	2.30	0.66
3:G:20:ASN:HB3	3:G:23:MET:SD	2.36	0.66
3:G:77:GLY:O	3:G:79:LYS:N	2.28	0.66
1:D:214:LEU:HG	1:E:205:MET:SD	2.35	0.66
4:X:8:DA:C2'	4:X:9:DT:H71	2.24	0.66
2:F:-10:DC:H2"	2:F:-11:DC:C4'	2.25	0.66
3:G:74:LYS:HD3	3:G:82:TYR:CE2	2.31	0.66
3:G:16:GLN:HE21	3:G:16:GLN:HA	1.61	0.66
3:H:42:ALA:HB1	3:H:55:ASN:HA	1.77	0.66
1:D:161:PHE:CD1	1:E:181:THR:HG21	2.30	0.66
3:G:61:ARG:HD2	3:G:64:ARG:HD2	1.77	0.65
3:H:7:LEU:HB3	3:H:66:TYR:OH	1.95	0.65
3:G:87:TYR:HD1	3:G:90:ILE:HD11	1.62	0.65
1:B:158:TYR:HE1	1:B:190:GLU:HB3	1.59	0.65
2:C:-10:DC:H2"	2:C:-11:DC:C4'	2.26	0.65
4:X:7:DC:H4'	4:X:7:DC:OP1	1.97	0.65
4:W:-6:DT:C2'	4:W:-5:DC:H5'	2.22	0.65
1:D:161:PHE:CE1	1:E:181:THR:HG21	2.32	0.64
2:F:2:DA:H2"	2:F:1:DA:OP2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:182:GLN:OE1	1:D:201:LYS:HB2	1.97	0.64
4:X:2:DT:C3'	4:X:3:DA:H5"	2.27	0.64
1:D:178:LEU:HG	1:E:151:ILE:HD11	1.78	0.64
4:W:5:DG:C3'	4:W:6:DC:H5"	2.28	0.64
2:F:9:DA:H1'	2:F:8:DT:H5"	1.80	0.64
3:H:8:TRP:CE2	3:H:9:GLN:HG3	2.33	0.63
4:X:-8:DA:H2"	4:X:-7:DG:C8	2.33	0.63
1:D:153:ASN:OD1	1:D:156:ARG:HG3	1.98	0.63
3:G:35:LEU:HD22	3:G:41:VAL:HG21	1.79	0.63
3:H:35:LEU:HB3	3:H:38:ALA:HB2	1.78	0.63
4:X:7:DC:C2'	4:X:8:DA:H8	2.11	0.63
3:H:63:LEU:HA	3:H:66:TYR:CD2	2.33	0.63
3:G:12:LEU:HD21	3:G:84:PHE:CE1	2.34	0.63
4:W:-14:DA:C2'	4:W:-13:DC:C5'	2.69	0.62
4:W:-10:DG:C2'	4:W:-9:DA:H5"	2.27	0.62
4:X:7:DC:C2'	4:X:8:DA:C8	2.81	0.62
4:W:-14:DA:H2'	4:W:-13:DC:H5"	1.80	0.62
4:W:-3:DT:H2"	4:W:-2:DA:C8	2.34	0.62
4:X:-1:DA:H2"	4:X:1:DT:H5'	1.81	0.62
3:G:63:LEU:HA	3:G:66:TYR:HD2	1.64	0.62
4:W:-7:DG:C2'	4:W:-6:DT:H71	2.30	0.62
4:X:-10:DG:C2'	4:X:-9:DA:H5'	2.28	0.62
3:H:88:PRO:HB3	3:H:91:LEU:CD1	2.28	0.62
1:A:201:LYS:HE3	1:B:221:SER:O	2.00	0.62
2:C:-9:DT:H2'	3:G:58:LYS:HE3	1.82	0.62
2:F:-14:DT:H2"	2:F:-15:DG:O5'	2.00	0.62
3:G:16:GLN:HA	3:G:16:GLN:NE2	2.14	0.62
4:W:-12:DC:H2"	4:W:-11:DG:O4'	2.00	0.62
1:E:170:LYS:NZ	4:X:2:DT:OP1	2.22	0.61
1:D:174:GLU:O	1:D:178:LEU:HB2	2.00	0.61
2:F:8:DT:H2"	2:F:7:DG:C8	2.35	0.61
3:G:30:ASP:O	3:G:87:TYR:HB3	1.99	0.61
1:E:154:LYS:HE3	1:E:158:TYR:CE2	2.36	0.61
2:F:-8:DT:H4'	3:H:51:LYS:HE3	1.83	0.61
3:G:35:LEU:O	3:G:80:PHE:HB3	2.00	0.61
4:W:-10:DG:H2"	4:W:-9:DA:H5'	1.81	0.61
1:E:182:GLN:OE1	1:E:201:LYS:HB2	2.00	0.61
3:G:49:LYS:O	3:G:51:LYS:HG2	2.00	0.60
3:H:45:TRP:CE3	3:H:45:TRP:HA	2.36	0.60
2:C:-6:DA:H1'	2:C:-7:DC:H5"	1.84	0.60
3:G:42:ALA:HB1	3:G:54:MET:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:79:LYS:O	3:G:80:PHE:HB2	2.01	0.60
3:H:7:LEU:HD13	3:H:45:TRP:CE2	2.37	0.60
3:H:18:PRO:O	3:H:21:LYS:HG2	2.01	0.60
2:F:-8:DT:C2'	2:F:-9:DT:H5'	2.29	0.60
1:D:198:ALA:HB3	1:D:203:GLN:NE2	2.17	0.59
3:H:23:MET:HA	3:H:36:LEU:HB2	1.83	0.59
3:H:45:TRP:HA	3:H:45:TRP:HE3	1.67	0.59
3:H:79:LYS:O	3:H:81:VAL:HG22	2.02	0.59
1:E:154:LYS:HE3	1:E:158:TYR:HE2	1.65	0.59
1:B:196:THR:OG1	1:B:206:ILE:HD13	2.03	0.59
1:E:182:GLN:HA	1:E:182:GLN:NE2	2.16	0.59
3:G:20:ASN:HA	3:G:22:HIS:CE1	2.38	0.59
2:C:-13:DG:C2'	2:C:-14:DT:H5"	2.29	0.59
1:D:202:LEU:C	1:D:204:PRO:HD2	2.23	0.59
1:E:173:TYR:O	1:E:177:THR:HG23	2.02	0.59
2:F:-10:DC:C3'	2:F:-11:DC:H5"	2.33	0.59
4:W:-12:DC:H2"	4:W:-11:DG:C5'	2.32	0.59
3:G:18:PRO:HD2	3:G:19:GLN:HE21	1.67	0.59
3:H:5:ILE:HG13	3:H:6:THR:N	2.13	0.59
1:D:174:GLU:HA	1:E:148:MET:HE2	1.85	0.59
1:A:174:GLU:HB3	1:B:148:MET:HE1	1.84	0.59
2:F:-6:DA:H1'	2:F:-7:DC:O4'	2.03	0.59
1:E:166:THR:O	1:E:169:MET:HB2	2.04	0.58
1:D:184:LEU:HD22	1:D:205:MET:HG2	1.84	0.58
1:B:179:THR:OG1	1:B:181:THR:HG23	2.03	0.58
4:X:-2:DA:H2"	4:X:-1:DA:OP2	2.04	0.58
2:F:-6:DA:H2"	2:F:-7:DC:H5"	1.86	0.58
1:A:178:LEU:CG	1:B:151:ILE:HD11	2.31	0.58
3:H:27:THR:O	3:H:27:THR:HG22	2.04	0.58
4:X:-9:DA:H2"	4:X:-8:DA:OP2	2.04	0.58
1:A:203:GLN:N	1:A:204:PRO:HD2	2.19	0.58
3:G:64:ARG:HA	3:G:67:TYR:CE1	2.39	0.58
3:H:14:LEU:HD13	3:H:17:LYS:HE2	1.86	0.58
3:G:20:ASN:HB3	3:G:23:MET:CG	2.34	0.57
4:X:-12:DC:H2"	4:X:-11:DG:O4'	2.04	0.57
3:H:14:LEU:HD13	3:H:17:LYS:CE	2.34	0.57
4:X:4:DG:H2"	4:X:5:DG:OP2	2.03	0.57
1:A:168:ILE:HG23	1:A:169:MET:N	2.19	0.57
2:C:4:DC:C2'	2:C:3:DT:H5"	2.35	0.57
3:G:29:ASN:H	3:G:29:ASN:ND2	2.03	0.57
3:H:26:TRP:HA	3:H:33:PHE:HA	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:87:TYR:CD1	3:H:88:PRO:HA	2.40	0.57
4:X:8:DA:H2"	4:X:9:DT:H71	1.87	0.57
3:G:18:PRO:HG2	3:G:19:GLN:NE2	2.20	0.57
4:W:-12:DC:H2'	4:W:-11:DG:H5"	1.84	0.57
4:X:1:DT:H2'	4:X:2:DT:C7	2.34	0.57
1:E:141:ARG:HG2	1:E:141:ARG:HH11	1.70	0.57
1:E:160:THR:HG22	1:E:161:PHE:N	2.19	0.57
2:F:7:DG:H2"	2:F:6:DG:H5'	1.87	0.57
2:F:-7:DC:OP1	3:H:6:THR:HB	2.05	0.57
3:G:3:SER:O	3:G:4:ALA:HB3	2.05	0.57
3:G:45:TRP:CD1	3:G:59:LEU:HD12	2.40	0.57
4:X:-14:DA:C2'	4:X:-13:DC:C5'	2.58	0.57
3:G:78:GLN:HB3	3:G:81:VAL:CB	2.35	0.56
3:H:63:LEU:HA	3:H:66:TYR:HD2	1.70	0.56
1:B:185:LEU:HD12	1:B:186:LEU:N	2.21	0.56
1:D:179:THR:HG21	1:E:161:PHE:HB2	1.87	0.56
1:E:182:GLN:HE21	1:E:182:GLN:CA	2.16	0.56
1:B:184:LEU:HD12	1:B:185:LEU:N	2.20	0.56
3:H:65:TYR:O	3:H:68:VAL:HG12	2.05	0.56
2:C:-3:DA:H2"	2:C:-4:DG:N7	2.20	0.56
3:H:85:VAL:HG23	3:H:86:SER:N	2.15	0.56
3:H:87:TYR:CD2	3:H:88:PRO:HG3	2.40	0.56
2:C:10:DG:H2"	2:C:9:DA:O5'	2.04	0.56
3:G:70:ASN:ND2	3:G:85:VAL:HG21	2.20	0.56
3:G:23:MET:CB	3:G:37:GLN:HB2	2.35	0.56
3:G:11:LEU:N	3:G:11:LEU:HD23	2.21	0.56
3:G:20:ASN:HD22	3:G:23:MET:CE	2.19	0.55
1:A:178:LEU:O	1:B:151:ILE:HG12	2.07	0.55
1:E:182:GLN:NE2	1:E:182:GLN:CA	2.65	0.55
3:G:7:LEU:O	3:G:10:PHE:N	2.39	0.55
1:B:185:LEU:HD11	1:B:187:VAL:HG23	1.88	0.55
1:E:186:LEU:HD23	1:E:186:LEU:C	2.27	0.55
3:G:83:LYS:HB2	3:G:83:LYS:HZ2	1.72	0.55
1:E:175:LEU:HD22	1:E:175:LEU:O	2.07	0.55
3:G:64:ARG:NH1	4:W:-11:DG:O6	2.38	0.55
1:D:139:LYS:CB	4:X:-4:DC:H4'	2.37	0.55
3:H:151:THR:HG22	3:H:153:ASN:H	1.72	0.55
1:B:204:PRO:O	1:B:208:SER:HB3	2.06	0.54
4:W:-1:DA:H2"	4:W:1:DT:H5"	1.89	0.54
3:G:64:ARG:CZ	4:W:-12:DC:C5	2.91	0.54
3:G:84:PHE:HD2	3:G:84:PHE:N	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:84:PHE:N	3:G:84:PHE:CD2	2.74	0.54
4:W:4:DG:OP2	4:W:4:DG:H8	1.89	0.54
3:G:45:TRP:CH2	3:G:49:LYS:HD3	2.43	0.54
3:H:30:ASP:O	3:H:87:TYR:HB3	2.08	0.54
2:F:-8:DT:P	3:H:49:LYS:HZ1	2.30	0.54
1:A:218:CYS:SG	1:B:204:PRO:HB2	2.47	0.54
4:W:-1:DA:C2'	4:W:1:DT:C5'	2.82	0.54
1:D:218:CYS:SG	1:E:204:PRO:HG2	2.48	0.54
3:H:15:LEU:HD22	3:H:25:CYS:O	2.08	0.54
2:C:-8:DT:C2'	2:C:-9:DT:H5"	2.37	0.53
2:F:-6:DA:H2"	2:F:-7:DC:OP2	2.08	0.53
3:H:23:MET:O	3:H:36:LEU:N	2.42	0.53
1:D:194:VAL:HG23	1:D:194:VAL:O	2.07	0.53
2:F:-9:DT:P	3:H:51:LYS:HD2	2.48	0.53
1:B:147:LYS:HD3	1:E:223:ASP:O	2.07	0.53
3:G:87:TYR:OH	3:G:91:LEU:HD21	2.08	0.53
4:W:-15:DC:H2"	4:W:-14:DA:H8	1.72	0.53
3:G:64:ARG:CZ	4:W:-12:DC:H5	2.21	0.53
3:H:64:ARG:HA	3:H:67:TYR:CD1	2.42	0.53
1:B:154:LYS:CG	1:B:158:TYR:CE2	2.91	0.53
2:C:8:DT:C2	2:C:7:DG:N7	2.76	0.53
3:H:89:GLU:H	3:H:89:GLU:CD	2.12	0.53
3:H:87:TYR:CE2	3:H:88:PRO:HG3	2.44	0.53
4:X:-7:DG:H2"	4:X:-6:DT:OP2	2.09	0.53
1:A:202:LEU:O	1:A:203:GLN:C	2.46	0.53
3:G:38:ALA:HB1	3:G:56:TYR:CD1	2.43	0.53
3:H:25:CYS:SG	3:H:36:LEU:HD11	2.48	0.53
2:C:-3:DA:H4'	2:C:-3:DA:OP1	2.08	0.53
1:E:142:GLY:C	4:X:4:DG:H21	2.12	0.53
1:E:192:GLY:O	3:H:152:LEU:HB2	2.09	0.53
1:B:153:ASN:OD1	1:B:156:ARG:HG3	2.08	0.53
3:H:59:LEU:HD23	3:H:59:LEU:O	2.09	0.53
3:G:23:MET:O	3:G:36:LEU:N	2.42	0.52
3:G:86:SER:O	3:G:90:ILE:HG13	2.10	0.52
3:G:48:ARG:O	3:G:49:LYS:HB2	2.10	0.52
3:H:59:LEU:O	3:H:62:ALA:HB3	2.10	0.52
1:B:160:THR:HG22	1:B:161:PHE:N	2.25	0.52
2:F:-8:DT:H2"	2:F:-9:DT:C5'	2.30	0.52
2:F:-10:DC:H2"	2:F:-11:DC:O4'	2.09	0.52
3:G:26:TRP:HZ3	3:G:31:GLY:HA2	1.75	0.52
1:E:142:GLY:C	4:X:4:DG:N2	2.62	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:ARG:O	1:E:157:ARG:C	2.48	0.52
2:F:7:DG:H2"	2:F:6:DG:C5'	2.40	0.52
3:G:92:ASN:N	3:G:92:ASN:HD22	2.07	0.52
2:C:8:DT:H2"	2:C:7:DG:H8	1.74	0.52
1:A:168:ILE:CG2	1:A:169:MET:N	2.72	0.51
1:D:170:LYS:HZ3	2:F:-2:DT:P	2.31	0.51
1:A:158:TYR:HH	4:W:-9:DA:H5'	1.75	0.51
1:D:211:GLY:O	1:D:212:LYS:C	2.48	0.51
3:H:12:LEU:HD11	3:H:91:LEU:HD21	1.93	0.51
3:H:79:LYS:O	3:H:81:VAL:N	2.44	0.51
1:B:148:MET:O	1:B:148:MET:HG3	2.09	0.51
1:E:184:LEU:HB2	1:E:202:LEU:HD13	1.92	0.51
3:G:45:TRP:HA	3:G:45:TRP:CE3	2.46	0.51
4:X:6:DC:H2"	4:X:7:DC:O5'	2.10	0.51
1:E:192:GLY:O	3:H:152:LEU:N	2.42	0.51
3:G:45:TRP:HA	3:G:45:TRP:HE3	1.76	0.51
3:H:23:MET:HA	3:H:37:GLN:H	1.75	0.51
3:H:30:ASP:OD2	3:H:31:GLY:N	2.44	0.51
4:X:-6:DT:C2	4:X:-5:DC:C5	2.99	0.51
1:B:208:SER:HG	1:B:210:THR:HB	1.76	0.51
1:D:155:LEU:O	1:D:159:THR:HG23	2.10	0.51
4:W:-17:DC:H2"	4:W:-16:DA:H8	1.76	0.51
4:X:-1:DA:C2'	4:X:1:DT:H5"	2.40	0.51
2:C:-8:DT:OP1	3:G:49:LYS:NZ	2.36	0.51
1:A:146:ILE:HD11	1:A:156:ARG:HH22	1.77	0.50
3:H:12:LEU:HD13	3:H:84:PHE:CE1	2.45	0.50
4:W:-1:DA:C2'	4:W:1:DT:H5"	2.41	0.50
1:D:160:THR:CG2	1:D:164:ARG:HG3	2.41	0.50
1:D:164:ARG:CB	1:E:175:LEU:HD23	2.41	0.50
3:G:24:ILE:HD11	3:G:33:PHE:CD1	2.46	0.50
3:H:66:TYR:CD1	3:H:71:ILE:HB	2.46	0.50
1:E:184:LEU:CD1	1:E:198:ALA:HB2	2.42	0.50
2:F:8:DT:H2"	2:F:7:DG:H8	1.77	0.50
4:X:-9:DA:C6	4:X:-8:DA:C6	3.00	0.50
1:A:208:SER:O	1:A:212:LYS:HG3	2.12	0.50
3:G:12:LEU:HD11	3:G:84:PHE:HE1	1.76	0.50
3:G:24:ILE:HD11	3:G:33:PHE:HD1	1.77	0.50
1:A:178:LEU:CD1	1:B:151:ILE:HD11	2.42	0.50
1:D:204:PRO:HA	1:D:207:THR:OG1	2.12	0.50
4:W:-13:DC:H2"	4:W:-12:DC:H5"	1.93	0.50
1:E:142:GLY:HA2	4:X:4:DG:N2	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:LYS:O	1:A:173:TYR:HB3	2.12	0.49
4:W:1:DT:C2'	4:W:2:DT:C7	2.89	0.49
1:A:182:GLN:NE2	1:A:201:LYS:HD3	2.26	0.49
3:G:34:LYS:HE2	3:G:36:LEU:HD23	1.94	0.49
4:X:-12:DC:H5'	4:X:-12:DC:H6	1.77	0.49
1:B:157:ARG:NH1	1:B:190:GLU:OE1	2.45	0.49
1:B:208:SER:O	1:B:212:LYS:HB2	2.12	0.49
1:D:184:LEU:CD2	1:D:205:MET:HG2	2.42	0.49
1:B:142:GLY:O	1:B:143:ARG:C	2.51	0.49
1:B:185:LEU:HD12	1:B:186:LEU:H	1.76	0.49
1:B:203:GLN:HB3	1:B:204:PRO:HD3	1.95	0.49
1:D:208:SER:O	1:D:212:LYS:HG3	2.12	0.49
3:G:18:PRO:HB3	3:G:21:LYS:HZ3	1.77	0.49
3:G:15:LEU:HD11	3:G:33:PHE:CD1	2.46	0.49
2:F:3:DT:H2"	2:F:2:DA:C8	2.47	0.49
3:G:7:LEU:HD13	3:G:45:TRP:CE2	2.48	0.49
3:H:20:ASN:HB3	3:H:23:MET:CG	2.43	0.49
2:C:7:DG:H2"	2:C:6:DG:C5'	2.35	0.49
3:G:29:ASN:HD22	3:G:29:ASN:N	2.01	0.49
3:G:54:MET:HG3	3:G:55:ASN:N	2.28	0.49
4:W:-12:DC:C2'	4:W:-11:DG:C5'	2.80	0.49
1:B:174:GLU:O	1:B:178:LEU:HB2	2.13	0.49
2:C:-1:DT:H2"	2:C:-2:DT:OP2	2.12	0.49
2:F:-1:DT:H2"	2:F:-2:DT:C6	2.48	0.49
3:H:61:ARG:HD3	4:X:-11:DG:O6	2.13	0.49
3:H:74:LYS:HG2	4:X:-12:DC:OP1	2.12	0.49
2:C:-2:DT:C2'	2:C:-3:DA:C8	2.96	0.48
2:F:-8:DT:C2'	2:F:-9:DT:H71	2.42	0.48
3:G:38:ALA:O	3:G:41:VAL:N	2.47	0.48
3:G:70:ASN:C	3:G:85:VAL:HG21	2.33	0.48
3:H:16:GLN:O	3:H:18:PRO:HD3	2.13	0.48
1:A:218:CYS:HB3	1:B:202:LEU:HD23	1.95	0.48
3:G:18:PRO:HA	3:G:21:LYS:HZ2	1.79	0.48
3:G:83:LYS:HB2	3:G:83:LYS:HZ3	1.73	0.48
1:E:211:GLY:O	1:E:215:ILE:HG13	2.13	0.48
3:G:27:THR:O	3:G:32:GLN:HB3	2.13	0.48
3:H:23:MET:CA	3:H:36:LEU:HB2	2.43	0.48
3:H:42:ALA:O	3:H:45:TRP:N	2.45	0.48
4:X:-16:DA:H2"	4:X:-15:DC:C6	2.48	0.48
1:B:202:LEU:O	1:B:205:MET:HB2	2.13	0.48
3:G:64:ARG:O	3:G:67:TYR:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:3:SER:O	3:H:5:ILE:N	2.47	0.48
3:H:84:PHE:N	3:H:84:PHE:CD2	2.81	0.48
1:D:211:GLY:O	1:D:214:LEU:N	2.47	0.48
3:G:16:GLN:O	3:G:17:LYS:HD2	2.13	0.48
3:H:67:TYR:HD1	3:H:67:TYR:H	1.61	0.48
1:D:218:CYS:CB	1:E:202:LEU:HD23	2.44	0.48
3:G:46:GLY:O	3:G:47:ILE:C	2.52	0.48
3:H:70:ASN:O	3:H:85:VAL:HG21	2.14	0.48
3:H:84:PHE:N	3:H:84:PHE:HD2	2.12	0.48
1:D:191:THR:HG21	4:X:-9:DA:OP2	2.14	0.48
3:H:61:ARG:HD2	3:H:64:ARG:HD2	1.96	0.47
1:A:170:LYS:NZ	2:C:-2:DT:OP1	2.41	0.47
1:B:195:TYR:HD1	3:G:147:TYR:OH	1.98	0.47
2:C:-10:DC:H2"	2:C:-11:DC:O4'	2.13	0.47
3:G:29:ASN:ND2	3:G:29:ASN:N	2.61	0.47
3:G:40:GLU:HA	3:G:43:ARG:HB2	1.96	0.47
1:A:161:PHE:CE2	1:A:165:LYS:HD3	2.49	0.47
3:H:27:THR:O	3:H:28:SER:HB2	2.13	0.47
4:W:-4:DC:C1'	4:W:-3:DT:H5"	2.39	0.47
3:G:45:TRP:O	3:G:48:ARG:O	2.33	0.47
1:A:157:ARG:NH1	1:A:190:GLU:OE2	2.47	0.47
1:B:154:LYS:CG	1:B:158:TYR:HE2	2.27	0.47
1:B:184:LEU:HD13	1:B:198:ALA:HB2	1.96	0.47
3:G:65:TYR:O	3:G:67:TYR:N	2.48	0.47
3:G:68:VAL:C	3:G:70:ASN:H	2.16	0.47
4:W:-4:DC:H2"	4:W:-3:DT:H5"	1.96	0.47
1:B:143:ARG:HB2	4:W:3:DA:C2	2.50	0.47
3:G:34:LYS:HA	3:G:80:PHE:O	2.15	0.47
4:W:-13:DC:H2"	4:W:-12:DC:C5'	2.45	0.47
1:B:154:LYS:HG2	1:B:158:TYR:HE2	1.75	0.47
1:B:208:SER:OG	1:B:210:THR:HB	2.14	0.47
1:D:164:ARG:HB3	1:E:175:LEU:HD23	1.96	0.47
1:D:202:LEU:O	1:D:203:GLN:C	2.52	0.47
3:G:74:LYS:HD3	3:G:82:TYR:CD2	2.49	0.47
4:W:-12:DC:C3'	4:W:-11:DG:H5"	2.44	0.47
1:B:154:LYS:HG2	1:B:158:TYR:CD2	2.50	0.47
3:H:33:PHE:HE2	3:H:82:TYR:HB2	1.74	0.47
1:B:203:GLN:N	1:B:204:PRO:CD	2.78	0.47
2:F:1:DA:C2'	2:F:-1:DT:C5'	2.84	0.47
3:G:18:PRO:HA	3:G:21:LYS:NZ	2.30	0.47
1:A:153:ASN:HD22	1:A:153:ASN:C	2.17	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:-4:DG:C5	2:F:-5:DG:C6	3.03	0.46
3:G:38:ALA:O	3:G:40:GLU:N	2.48	0.46
3:H:8:TRP:CZ3	3:H:90:ILE:HD12	2.51	0.46
2:C:9:DA:H2"	2:C:8:DT:H5"	1.96	0.46
3:G:49:LYS:O	3:G:51:LYS:N	2.48	0.46
3:H:47:ILE:HG13	3:H:48:ARG:N	2.29	0.46
2:C:-4:DG:H1'	2:C:-5:DG:H5'	1.97	0.46
2:F:-8:DT:C2	2:F:-9:DT:C5	3.03	0.46
2:F:-9:DT:C2'	2:F:-10:DC:O5'	2.45	0.46
4:X:1:DT:H2"	4:X:2:DT:OP2	2.14	0.46
1:A:150:PHE:CE2	1:A:151:ILE:O	2.68	0.46
2:C:-2:DT:H2'	2:C:-3:DA:C8	2.50	0.46
2:C:-15:DG:H1'	2:C:-16:DT:O5'	2.15	0.46
3:G:7:LEU:O	3:G:8:TRP:C	2.53	0.46
3:G:54:MET:CG	3:G:55:ASN:N	2.79	0.46
3:H:20:ASN:HB3	3:H:23:MET:HG3	1.98	0.46
4:W:1:DT:H2"	4:W:2:DT:C7	2.46	0.46
1:D:165:LYS:HD2	1:D:195:TYR:CG	2.50	0.46
1:E:144:VAL:O	4:X:4:DG:H4'	2.15	0.46
3:G:40:GLU:O	3:G:43:ARG:HB3	2.15	0.46
4:W:1:DT:C2'	4:W:2:DT:OP2	2.57	0.46
3:G:15:LEU:HD22	3:G:26:TRP:NE1	2.30	0.46
3:G:18:PRO:HA	3:G:21:LYS:CG	2.42	0.46
3:G:66:TYR:HA	3:G:69:LYS:HB2	1.97	0.46
1:D:161:PHE:CB	1:E:179:THR:HG21	2.39	0.46
1:E:203:GLN:N	1:E:204:PRO:CD	2.74	0.46
3:G:18:PRO:CD	3:G:19:GLN:HE21	2.29	0.46
1:A:195:TYR:N	1:A:195:TYR:CD2	2.83	0.46
2:F:4:DC:H4'	2:F:4:DC:OP1	2.16	0.46
1:D:163:LYS:HE3	2:F:-5:DG:O6	2.16	0.45
1:E:143:ARG:HB2	4:X:3:DA:N3	2.31	0.45
4:W:5:DG:H2"	4:W:6:DC:H5'	1.86	0.45
1:A:143:ARG:HB3	4:W:-2:DA:N3	2.32	0.45
2:C:-7:DC:OP1	3:G:6:THR:HB	2.15	0.45
1:D:173:TYR:O	1:D:176:SER:OG	2.34	0.45
1:D:181:THR:HG21	1:E:161:PHE:CD1	2.51	0.45
1:E:160:THR:CG2	1:E:161:PHE:N	2.78	0.45
4:X:-7:DG:C2'	4:X:-6:DT:H71	2.47	0.45
3:H:90:ILE:HG13	3:H:91:LEU:N	2.31	0.45
1:A:182:GLN:CD	1:A:201:LYS:HB2	2.36	0.45
2:C:-9:DT:C4	2:C:-10:DC:N4	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:61:ARG:NE	4:W:-11:DG:C5	2.84	0.45
3:G:65:TYR:O	3:G:66:TYR:C	2.54	0.45
3:H:6:THR:OG1	3:H:9:GLN:HB2	2.16	0.45
3:H:15:LEU:HD11	3:H:33:PHE:CD1	2.52	0.45
1:A:201:LYS:O	1:B:218:CYS:HB3	2.16	0.45
1:B:160:THR:HG23	1:B:164:ARG:HD2	1.97	0.45
1:B:170:LYS:NZ	1:B:174:GLU:OE2	2.49	0.45
3:G:63:LEU:O	3:G:66:TYR:HB2	2.17	0.45
3:G:69:LYS:HE2	3:G:69:LYS:HB3	1.84	0.45
1:D:195:TYR:HE1	4:X:-8:DA:OP1	2.00	0.45
4:X:-7:DG:H2"	4:X:-6:DT:H71	1.99	0.45
1:A:182:GLN:OE1	1:A:201:LYS:HB2	2.16	0.45
2:C:-8:DT:N3	2:C:-9:DT:C4	2.84	0.45
2:F:4:DC:C2'	2:F:3:DT:C5'	2.61	0.45
1:A:206:ILE:C	1:A:206:ILE:HD12	2.36	0.45
2:F:-15:DG:H1'	2:F:-16:DT:O5'	2.17	0.45
2:C:-10:DC:H2'	2:C:-11:DC:H5"	1.82	0.45
1:D:171:LYS:NZ	4:X:3:DA:OP1	2.35	0.45
2:F:5:DC:H2'	2:F:5:DC:O5'	2.17	0.45
1:A:156:ARG:HH11	1:A:156:ARG:HG2	1.82	0.45
3:G:64:ARG:HA	3:G:67:TYR:CD1	2.52	0.45
4:W:-6:DT:C4	4:W:-5:DC:N4	2.84	0.45
4:W:8:DA:H2"	4:W:9:DT:H6	1.81	0.45
1:B:143:ARG:HB2	4:W:3:DA:H2	1.83	0.44
1:E:157:ARG:NH1	1:E:190:GLU:OE1	2.49	0.44
3:G:150:PHE:CD1	3:G:151:THR:N	2.85	0.44
1:D:148:MET:CE	1:E:177:THR:OG1	2.65	0.44
3:G:77:GLY:O	3:G:78:GLN:C	2.55	0.44
3:H:61:ARG:O	3:H:62:ALA:C	2.56	0.44
3:H:87:TYR:CE1	3:H:91:LEU:HD11	2.52	0.44
2:C:-9:DT:P	3:G:51:LYS:HD2	2.57	0.44
2:F:-12:DG:H2"	2:F:-13:DG:C8	2.46	0.44
2:F:-8:DT:H5'	3:H:54:MET:CE	2.48	0.44
3:H:67:TYR:OH	4:X:-12:DC:OP2	2.21	0.44
1:E:142:GLY:CA	4:X:4:DG:N2	2.80	0.44
2:F:-11:DC:C2'	2:F:-12:DG:N7	2.80	0.44
3:G:26:TRP:CZ3	3:G:31:GLY:HA2	2.52	0.44
3:H:8:TRP:HZ3	3:H:90:ILE:HD12	1.81	0.44
4:W:-4:DC:C2'	4:W:-3:DT:H5"	2.48	0.44
1:A:189:SER:C	1:A:191:THR:H	2.21	0.44
1:B:193:HIS:HB3	1:B:195:TYR:CE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:177:THR:HB	1:E:148:MET:CE	2.45	0.44
3:H:15:LEU:HB3	3:H:26:TRP:NE1	2.33	0.44
4:W:-9:DA:C6	4:W:-8:DA:C6	3.06	0.44
4:W:6:DC:H2"	4:W:7:DC:H5'	2.00	0.44
4:X:-6:DT:C4	4:X:-5:DC:N4	2.86	0.44
1:A:171:LYS:NZ	4:W:3:DA:OP1	2.29	0.43
1:A:198:ALA:HB3	1:A:203:GLN:NE2	2.33	0.43
3:H:66:TYR:O	3:H:68:VAL:N	2.51	0.43
4:X:8:DA:H2"	4:X:9:DT:OP2	2.18	0.43
2:C:-9:DT:OP1	3:G:51:LYS:HD2	2.18	0.43
1:E:199:THR:O	1:E:200:ARG:C	2.55	0.43
3:H:5:ILE:CG1	3:H:6:THR:H	2.23	0.43
3:H:64:ARG:NH1	4:X:-12:DC:C5	2.86	0.43
4:X:1:DT:C2'	4:X:2:DT:C7	2.96	0.43
1:A:199:THR:O	1:A:200:ARG:C	2.56	0.43
3:G:27:THR:O	3:G:28:SER:HB2	2.18	0.43
1:D:161:PHE:C	1:D:161:PHE:CD2	2.91	0.43
1:D:189:SER:O	1:D:192:GLY:N	2.52	0.43
1:E:154:LYS:HG3	1:E:158:TYR:CE2	2.53	0.43
3:H:66:TYR:O	3:H:67:TYR:C	2.56	0.43
2:F:-9:DT:C2	2:F:-10:DC:C5	3.07	0.43
3:G:64:ARG:NH1	4:W:-12:DC:C5	2.87	0.43
3:G:87:TYR:HD1	3:G:90:ILE:CD1	2.31	0.43
3:H:88:PRO:CB	3:H:91:LEU:HD12	2.45	0.43
2:F:-3:DA:H2"	2:F:-4:DG:N7	2.33	0.43
3:H:68:VAL:HG22	3:H:68:VAL:O	2.19	0.43
4:W:-11:DG:H2"	4:W:-10:DG:C8	2.54	0.43
3:G:45:TRP:O	3:G:48:ARG:N	2.51	0.43
3:G:22:HIS:CE1	3:G:23:MET:HE3	2.54	0.42
4:X:-13:DC:C1'	4:X:-12:DC:H5"	2.49	0.42
1:E:173:TYR:CE1	1:E:177:THR:HG21	2.54	0.42
3:G:27:THR:HG21	3:G:32:GLN:HE21	1.84	0.42
3:H:61:ARG:NE	4:X:-11:DG:N7	2.68	0.42
4:W:8:DA:H2'	4:W:9:DT:C7	2.49	0.42
4:X:-5:DC:C2	4:X:-4:DC:C4	3.07	0.42
4:X:-3:DT:H6	4:X:-3:DT:H5"	1.84	0.42
3:H:24:ILE:HG13	3:H:24:ILE:O	2.20	0.42
3:H:80:PHE:N	4:X:-13:DC:OP2	2.52	0.42
1:A:165:LYS:HD2	1:A:195:TYR:CG	2.55	0.42
1:B:161:PHE:CZ	1:B:187:VAL:CG1	3.02	0.42
1:D:204:PRO:CG	1:E:218:CYS:SG	3.05	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:18:PRO:O	3:G:19:GLN:C	2.57	0.42
3:H:139:ASN:HB3	3:H:142:ILE:CD1	2.45	0.42
3:G:87:TYR:CE2	3:G:88:PRO:HB3	2.55	0.42
3:H:14:LEU:HB3	3:H:24:ILE:HD11	2.02	0.42
3:H:152:LEU:O	3:H:152:LEU:HD23	2.20	0.42
1:B:158:TYR:CZ	1:B:190:GLU:OE1	2.73	0.42
2:C:-8:DT:H5'	3:G:54:MET:HE2	2.02	0.42
2:C:-15:DG:H1'	2:C:-16:DT:C5'	2.49	0.42
2:F:-1:DT:H2'	2:F:-2:DT:H72	2.01	0.42
3:G:49:LYS:HB3	3:G:49:LYS:NZ	2.31	0.42
2:C:-2:DT:H2"	2:C:-3:DA:C8	2.55	0.42
2:F:-10:DC:C3'	2:F:-11:DC:C5'	2.96	0.42
3:H:51:LYS:O	3:H:53:ASN:N	2.53	0.42
3:H:90:ILE:O	3:H:92:ASN:ND2	2.53	0.42
4:W:-13:DC:OP1	4:W:-13:DC:C4'	2.62	0.42
1:B:153:ASN:O	1:B:155:LEU:N	2.53	0.42
2:C:6:DG:H2"	2:C:5:DC:OP2	2.20	0.42
3:H:18:PRO:C	3:H:20:ASN:H	2.22	0.42
4:X:5:DG:C6	4:X:6:DC:N3	2.88	0.42
1:A:183:VAL:H	1:A:199:THR:CG2	2.32	0.42
3:G:35:LEU:N	3:G:80:PHE:O	2.40	0.42
1:A:216:GLN:HA	1:A:216:GLN:OE1	2.20	0.41
1:D:175:LEU:HD13	1:E:164:ARG:HB2	2.02	0.41
1:D:181:THR:HG21	1:E:161:PHE:CE1	2.55	0.41
3:H:23:MET:O	3:H:35:LEU:HA	2.19	0.41
3:H:60:SER:O	3:H:63:LEU:HB2	2.19	0.41
3:H:84:PHE:HD2	3:H:84:PHE:H	1.67	0.41
1:A:146:ILE:HG13	1:A:147:LYS:N	2.35	0.41
2:F:-9:DT:N3	2:F:-10:DC:C4	2.88	0.41
3:G:14:LEU:O	3:G:24:ILE:HG21	2.20	0.41
3:G:23:MET:HA	3:G:37:GLN:H	1.84	0.41
3:G:12:LEU:CG	3:G:84:PHE:HE1	2.33	0.41
3:G:65:TYR:O	3:G:68:VAL:HG12	2.20	0.41
3:H:38:ALA:O	3:H:41:VAL:N	2.52	0.41
4:X:6:DC:C6	4:X:7:DC:C5	3.09	0.41
1:A:218:CYS:CB	1:B:202:LEU:HD23	2.50	0.41
1:E:196:THR:OG1	1:E:206:ILE:HD13	2.21	0.41
1:E:196:THR:CG2	3:H:148:SER:HB3	2.38	0.41
2:F:9:DA:H2"	2:F:8:DT:H5"	2.01	0.41
3:H:20:ASN:C	3:H:22:HIS:H	2.23	0.41
4:X:-15:DC:H2"	4:X:-14:DA:H8	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:168:ILE:HG23	1:D:185:LEU:HD21	2.02	0.41
1:E:141:ARG:HG2	1:E:141:ARG:NH1	2.34	0.41
1:E:145:LYS:NZ	2:F:-1:DT:OP2	2.39	0.41
3:H:76:ASN:OD1	3:H:77:GLY:N	2.53	0.41
1:D:144:VAL:HG22	2:F:-4:DG:O3'	2.20	0.41
3:G:22:HIS:O	3:G:36:LEU:HB2	2.20	0.41
3:G:24:ILE:HG23	3:G:24:ILE:O	2.21	0.41
3:G:71:ILE:C	3:G:85:VAL:HG23	2.41	0.41
3:G:147:TYR:CG	3:G:148:SER:N	2.89	0.41
3:H:23:MET:C	3:H:36:LEU:HD13	2.41	0.41
3:H:38:ALA:O	3:H:39:GLU:C	2.59	0.41
1:A:153:ASN:C	1:A:153:ASN:ND2	2.74	0.41
1:E:186:LEU:C	1:E:186:LEU:CD2	2.89	0.41
2:F:-8:DT:O3'	3:H:51:LYS:HD2	2.21	0.41
3:G:16:GLN:OE1	3:G:26:TRP:HZ2	2.04	0.41
3:H:14:LEU:C	3:H:16:GLN:H	2.24	0.41
3:H:141:TYR:CE1	3:H:142:ILE:HG13	2.55	0.41
4:W:5:DG:C2'	4:W:6:DC:C5'	2.64	0.41
1:A:161:PHE:CD2	1:A:161:PHE:O	2.74	0.41
2:C:6:DG:C5	2:C:5:DC:N4	2.88	0.41
1:D:140:THR:HG21	2:F:-5:DG:N2	2.31	0.41
1:D:179:THR:OG1	1:D:181:THR:CG2	2.60	0.41
2:F:-12:DG:C4	2:F:-13:DG:N7	2.89	0.41
3:G:41:VAL:HA	3:G:44:LEU:CD1	2.51	0.41
3:G:150:PHE:HD1	3:G:151:THR:N	2.17	0.41
3:H:65:TYR:O	3:H:66:TYR:C	2.57	0.41
1:E:158:TYR:CZ	1:E:190:GLU:OE1	2.74	0.41
1:E:182:GLN:HE21	1:E:182:GLN:N	2.18	0.41
2:F:-4:DG:C6	2:F:-5:DG:C6	3.09	0.41
2:F:-10:DC:OP1	2:F:-10:DC:C4'	2.62	0.41
3:H:70:ASN:C	3:H:85:VAL:HG11	2.40	0.41
4:W:6:DC:C4	4:W:7:DC:N4	2.89	0.41
1:A:204:PRO:HA	1:A:207:THR:HB	2.02	0.40
2:C:-8:DT:C2	2:C:-9:DT:C5	3.09	0.40
1:D:160:THR:O	1:D:161:PHE:C	2.59	0.40
1:D:170:LYS:O	1:D:174:GLU:HG3	2.21	0.40
1:E:142:GLY:CA	4:X:4:DG:H21	2.35	0.40
3:G:61:ARG:HD3	3:G:64:ARG:NH1	2.37	0.40
4:W:-8:DA:C4	4:W:-7:DG:N7	2.89	0.40
4:X:-17:DC:C2	4:X:-16:DA:N7	2.90	0.40
1:A:194:VAL:O	1:A:194:VAL:HG12	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:MET:HE1	1:E:177:THR:OG1	2.20	0.40
1:D:151:ILE:N	1:D:151:ILE:HD12	2.36	0.40
3:H:49:LYS:O	3:H:50:ASN:C	2.59	0.40
1:D:168:ILE:HG23	1:D:169:MET:N	2.37	0.40
1:E:170:LYS:O	1:E:174:GLU:HG3	2.21	0.40
1:E:221:SER:HA	1:E:222:PRO:HD3	1.95	0.40
4:W:2:DT:H2"	4:W:3:DA:C8	2.56	0.40
1:B:173:TYR:O	1:B:177:THR:HG23	2.21	0.40
1:E:184:LEU:HD13	1:E:198:ALA:HB2	2.02	0.40
2:F:1:DA:C2	2:F:-1:DT:C2	3.10	0.40
3:H:18:PRO:O	3:H:20:ASN:N	2.54	0.40
4:W:-12:DC:H2"	4:W:-11:DG:C4'	2.51	0.40
1:B:153:ASN:O	1:B:154:LYS:C	2.58	0.40
1:E:156:ARG:O	1:E:159:THR:N	2.54	0.40
1:E:158:TYR:OH	1:E:190:GLU:OE1	2.31	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	85/92 (92%)	64 (75%)	17 (20%)	4 (5%)	2 15
1	B	84/92 (91%)	73 (87%)	8 (10%)	3 (4%)	3 20
1	D	84/92 (91%)	73 (87%)	9 (11%)	2 (2%)	6 30
1	E	87/92 (95%)	76 (87%)	6 (7%)	5 (6%)	1 12
3	G	108/157 (69%)	67 (62%)	30 (28%)	11 (10%)	0 2
3	H	105/157 (67%)	67 (64%)	27 (26%)	11 (10%)	0 2
All	All	553/682 (81%)	420 (76%)	97 (18%)	36 (6%)	1 8

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	3	SER
3	G	50	ASN
3	G	78	GLN
3	H	50	ASN
3	H	80	PHE
3	H	85	VAL
1	A	208	SER
1	B	154	LYS
1	E	191	THR
3	G	39	GLU
3	G	90	ILE
3	H	4	ALA
1	E	157	ARG
1	E	200	ARG
3	G	85	VAL
3	H	21	LYS
3	H	27	THR
3	H	32	GLN
3	H	76	ASN
1	A	200	ARG
1	A	201	LYS
1	D	200	ARG
1	E	192	GLY
3	G	38	ALA
3	G	66	TYR
3	G	150	PHE
1	B	143	ARG
3	G	7	LEU
3	H	19	GLN
3	H	67	TYR
1	A	153	ASN
1	B	210	THR
1	E	156	ARG
3	G	27	THR
3	H	52	PRO
1	D	211	GLY

5.3.2 Protein sidechains (i)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	75/80 (94%)	71 (95%)	4 (5%)	22	55
1	B	77/80 (96%)	72 (94%)	5 (6%)	17	48
1	D	75/80 (94%)	72 (96%)	3 (4%)	31	64
1	E	76/80 (95%)	70 (92%)	6 (8%)	12	40
3	G	97/142 (68%)	87 (90%)	10 (10%)	7	26
3	H	97/142 (68%)	92 (95%)	5 (5%)	23	55
All	All	497/604 (82%)	464 (93%)	33 (7%)	16	47

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ASN
1	A	156	ARG
1	A	160	THR
1	A	193	HIS
1	B	160	THR
1	B	179	THR
1	B	196	THR
1	B	200	ARG
1	B	208	SER
1	D	144	VAL
1	D	153	ASN
1	D	178	LEU
1	E	146	ILE
1	E	160	THR
1	E	175	LEU
1	E	182	GLN
1	E	214	LEU
1	E	216	GLN
3	G	15	LEU
3	G	17	LYS
3	G	29	ASN
3	G	33	PHE
3	G	45	TRP
3	G	70	ASN
3	G	83	LYS
3	G	84	PHE
3	G	93	MET
3	G	140	ASP

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Mol	Chain	Res	Type
3	H	14	LEU
3	H	33	PHE
3	H	45	TRP
3	H	67	TYR
3	H	84	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	ASN
1	A	203	GLN
1	B	220	ASN
1	D	153	ASN
1	D	203	GLN
1	E	182	GLN
1	E	203	GLN
3	G	9	GLN
3	G	16	GLN
3	G	19	GLN
3	G	20	ASN
3	G	29	ASN
3	G	32	GLN
3	G	37	GLN
3	G	70	ASN
3	G	92	ASN
3	H	13	GLN
3	H	32	GLN
3	H	92	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.