



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:30 AM UTC

PDB ID : 4J01 / pdb_00004j01
Title : Crystal Structure of Fischerella Transcription Factor HetR complexed with 29mer DNA target
Authors : Kim, Y.; Joachimiak, G.; Gornicki, P.; Joachimiak, A.; MCSG; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2013-01-30
Resolution : 3.25 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

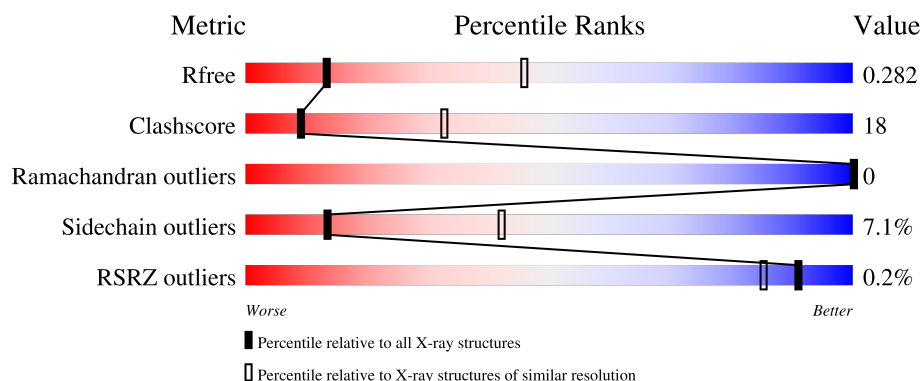
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

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



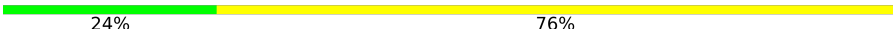
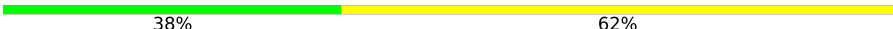
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	302	58% 35% • •
1	B	302	54% 40% • •
1	E	302	49% 45% • •
1	F	302	60% 33% • •
2	C	29	66% 34%

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Mol	Chain	Length	Quality of chain
2	D	29	 55% 45%
2	G	29	 24% 76%
2	H	29	 38% 62%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12033 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 Transcription Factor HetR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2414	1540	424	434	16			
1	B	294	Total	C	N	O	S	0	0	0
			2414	1540	424	434	16			
1	E	294	Total	C	N	O	S	0	0	0
			2414	1540	424	434	16			
1	F	294	Total	C	N	O	S	0	0	0
			2414	1540	424	434	16			

- Molecule 2 is a DNA chain called DNA (29-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	29	Total	C	N	O	P	0	0	0
			591	279	111	173	28			
2	D	29	Total	C	N	O	P	0	0	0
			591	279	111	173	28			
2	G	29	Total	C	N	O	P	0	0	0
			591	279	111	173	28			
2	H	29	Total	C	N	O	P	0	0	0
			591	279	111	173	28			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	O	S	0	0
			5	4	1		

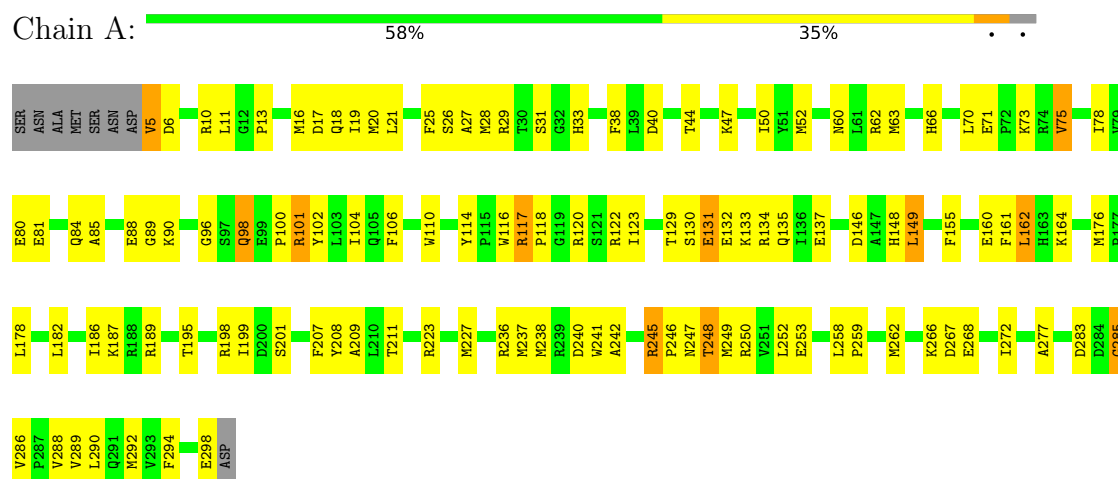
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			1	1		
4	B	1	Total	O	0	0
			1	1		
4	C	3	Total	O	0	0
			3	3		
4	D	1	Total	O	0	0
			1	1		
4	F	1	Total	O	0	0
			1	1		
4	H	1	Total	O	0	0
			1	1		

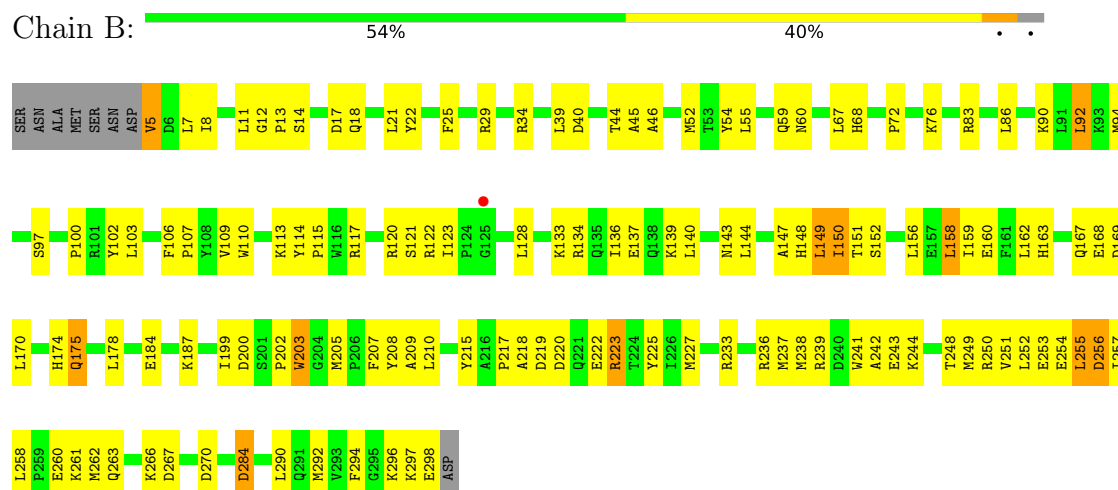
3 Residue-property plots

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

• Molecule 1: Transcription Factor HetR



• Molecule 1: Transcription Factor HetR



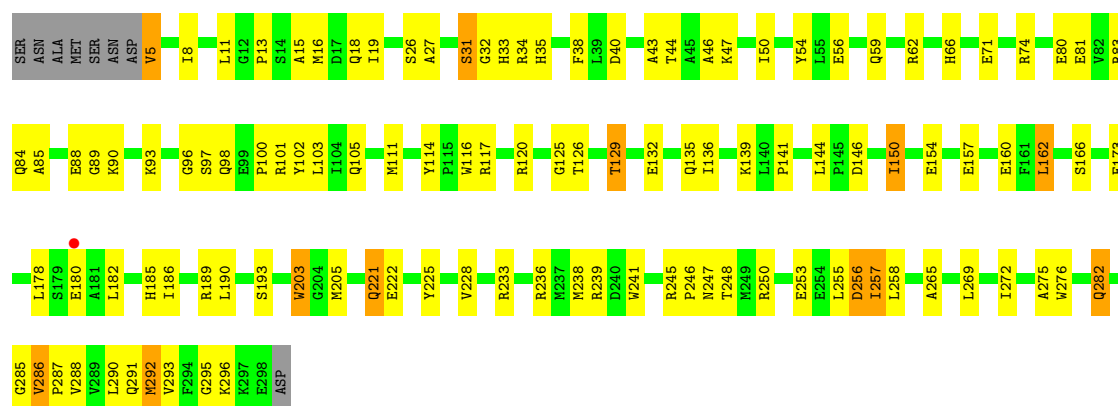
• Molecule 1: Transcription Factor HetR





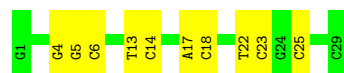
• Molecule 1: Transcription Factor HetR

Chain F: 60% 33%



• Molecule 2: DNA (29-MER)

Chain C: 66% 34%



• Molecule 2: DNA (29-MER)

Chain D: 55% 45%

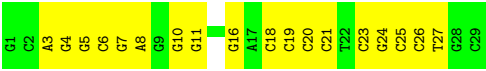


• Molecule 2: DNA (29-MER)

Chain G: 24% 76%



● Molecule 2: DNA (29-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.16Å 182.18Å 78.37Å 90.00° 91.38° 90.00°	Depositor
Resolution (Å)	35.90 – 3.25 35.90 – 3.25	Depositor EDS
% Data completeness (in resolution range)	97.6 (35.90-3.25) 97.3 (35.90-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 3.25Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1161), REFMAC	Depositor
R, R_{free}	0.241 , 0.276 0.231 , 0.282	Depositor DCC
R_{free} test set	1742 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	86.2	Xtriage
Anisotropy	0.652	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 73.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.042 for l,k,-h 0.054 for h,-k,-l 0.398 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12033	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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: SO4

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	0.35	0/2473	0.84	6/3338 (0.2%)
1	B	0.34	0/2473	0.78	0/3338
1	E	0.35	0/2473	0.82	4/3338 (0.1%)
1	F	0.35	0/2473	0.78	1/3338 (0.0%)
2	C	0.17	0/662	0.64	0/1020
2	D	0.15	0/662	0.63	0/1020
2	G	0.17	0/662	0.65	0/1020
2	H	0.16	0/662	0.72	0/1020
All	All	0.32	0/12540	0.77	11/17432 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	258	LEU	CA-C-N	6.66	126.91	119.32
1	E	258	LEU	C-N-CA	6.66	126.91	119.32
1	A	245	ARG	CA-C-N	6.55	128.03	119.84
1	A	245	ARG	C-N-CA	6.55	128.03	119.84
1	A	285	GLY	N-CA-C	6.24	120.42	111.12
1	A	289	VAL	N-CA-C	5.97	116.52	108.17
1	A	258	LEU	CA-C-N	5.51	124.70	118.97
1	A	258	LEU	C-N-CA	5.51	124.70	118.97
1	E	205	MET	CA-C-N	5.24	125.69	120.14
1	E	205	MET	C-N-CA	5.24	125.69	120.14
1	F	257	ILE	N-CA-C	5.01	115.93	108.46

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	A	2414	0	2416	112	0
1	B	2414	0	2416	115	0
1	E	2414	0	2416	135	0
1	F	2414	0	2416	106	0
2	C	591	0	325	9	0
2	D	591	0	325	10	0
2	G	591	0	325	19	0
2	H	591	0	325	22	0
3	G	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	3	0	0	0	0
4	D	1	0	0	1	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
All	All	12033	0	10964	416	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 18.

All (416) 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)
1:E:69:HIS:CE1	1:F:182:LEU:HD13	2.03	0.94
1:A:277:ALA:HB1	1:B:253:GLU:HG3	1.53	0.90
1:A:227:MET:HG3	1:B:238:MET:HB3	1.61	0.82
1:A:253:GLU:H	1:B:290:LEU:HB3	1.45	0.80
1:E:227:MET:HG3	1:F:238:MET:HB3	1.65	0.79
1:E:69:HIS:ND1	1:F:182:LEU:HD13	2.00	0.76
1:A:13:PRO:HG2	1:A:18:GLN:HG2	1.69	0.75
1:A:84:GLN:O	1:A:89:GLY:N	2.21	0.73
1:E:290:LEU:HD11	1:F:292:MET:HE1	1.71	0.73
1:F:96:GLY:O	1:F:101:ARG:NH2	2.22	0.72
1:B:123:ILE:H	1:B:133:LYS:HZ1	1.36	0.71
1:A:283:ASP:HB3	1:E:139:LYS:HD3	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:SER:OG	1:B:133:LYS:NZ	2.23	0.70
1:B:219:ASP:HB3	1:B:222:GLU:HG2	1.71	0.70
1:E:110:TRP:HB3	1:E:210:LEU:HD22	1.72	0.69
1:B:170:LEU:HB3	1:B:174:HIS:HB3	1.74	0.69
1:E:268:GLU:HG2	1:F:276:TRP:HE1	1.58	0.69
1:A:249:MET:HE1	1:B:270:ASP:HB2	1.73	0.69
1:E:297:LYS:HG2	1:F:287:PRO:HB2	1.74	0.69
1:B:100:PRO:HB3	1:B:102:TYR:CZ	2.28	0.69
1:F:74:ARG:HH21	2:H:16:DG:H3'	1.59	0.68
2:G:10:DG:H2'	2:G:11:DG:H8	1.58	0.68
1:F:83:ARG:HH11	1:F:84:GLN:HG2	1.58	0.67
1:A:245:ARG:HG2	1:B:296:LYS:HD2	1.77	0.67
1:F:40:ASP:HB3	1:F:93:LYS:HB3	1.77	0.67
1:B:115:PRO:HA	1:B:147:ALA:HA	1.76	0.67
1:F:111:MET:HE3	1:F:146:ASP:H	1.60	0.67
1:E:185:HIS:ND1	1:F:66:HIS:O	2.26	0.66
1:E:131:GLU:HA	1:E:134:ARG:HD2	1.77	0.66
1:A:246:PRO:O	1:B:266:LYS:NZ	2.29	0.66
1:A:238:MET:HB3	1:B:227:MET:HG3	1.78	0.66
1:E:239:ARG:NH1	1:E:243:GLU:OE1	2.29	0.66
1:A:117:ARG:HG3	1:A:118:PRO:HD2	1.78	0.65
1:E:62:ARG:O	1:E:66:HIS:ND1	2.29	0.65
1:B:139:LYS:NZ	1:B:200:ASP:O	2.24	0.65
1:B:110:TRP:HZ2	1:B:149:LEU:HA	1.61	0.64
1:E:123:ILE:HD12	1:E:133:LYS:HZ2	1.62	0.64
1:A:268:GLU:HG2	1:A:272:ILE:HD13	1.79	0.64
1:E:251:VAL:O	1:F:291:GLN:NE2	2.31	0.64
2:D:3:DA:H2''	2:D:4:DG:C8	2.33	0.64
2:G:10:DG:H1	2:H:20:DC:H42	1.46	0.64
1:E:281:HIS:HB2	1:F:255:LEU:HD12	1.80	0.63
1:E:86:LEU:HD23	1:F:11:LEU:HD21	1.81	0.62
2:G:9:DG:H1	2:H:21:DC:H42	1.47	0.62
1:A:117:ARG:HD3	1:E:101:ARG:HH12	1.63	0.62
1:E:289:VAL:N	1:F:295:GLY:O	2.30	0.62
1:A:247:ASN:H	1:B:296:LYS:HE2	1.64	0.62
1:B:100:PRO:HB3	1:B:102:TYR:CE2	2.35	0.62
1:E:280:TYR:HB3	1:F:257:ILE:HG23	1.80	0.62
1:B:83:ARG:HA	1:B:86:LEU:HD12	1.83	0.61
1:B:115:PRO:O	1:B:120:ARG:NH2	2.33	0.61
1:B:7:LEU:O	1:B:11:LEU:N	2.34	0.61
1:A:242:ALA:HA	1:B:223:ARG:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ARG:O	1:A:66:HIS:ND1	2.27	0.61
1:F:136:ILE:HA	1:F:139:LYS:HE3	1.82	0.61
1:F:103:LEU:HD21	1:F:186:ILE:HG23	1.83	0.60
1:B:167:GLN:HG2	1:B:175:GLN:HB2	1.82	0.60
1:B:14:SER:OG	1:B:17:ASP:OD2	2.20	0.60
1:A:148:HIS:ND1	1:A:149:LEU:O	2.34	0.60
1:A:62:ARG:HH11	2:D:6:DC:H5	1.49	0.60
1:F:34:ARG:NE	1:F:102:TYR:OH	2.20	0.60
1:F:125:GLY:O	1:F:126:THR:HB	2.02	0.60
1:A:27:ALA:HA	1:A:31:SER:HB2	1.82	0.60
1:B:44:THR:HG21	1:B:94:MET:HG3	1.84	0.60
1:A:237:MET:O	1:A:241:TRP:N	2.36	0.59
1:E:83:ARG:HA	1:E:86:LEU:HD12	1.84	0.59
1:E:229:GLU:HG3	1:E:233:ARG:HH12	1.67	0.59
1:A:266:LYS:HG3	1:A:294:PHE:CE1	2.38	0.59
1:E:26:SER:HA	1:E:30:THR:HB	1.85	0.59
1:B:260:GLU:OE2	1:B:260:GLU:N	2.34	0.59
1:E:265:ALA:O	1:E:269:LEU:N	2.30	0.59
2:G:13:DT:H2''	2:G:14:DC:H5'	1.85	0.59
1:A:33:HIS:NE2	1:A:98:GLN:O	2.33	0.58
1:A:40:ASP:O	1:A:44:THR:N	2.31	0.58
1:E:268:GLU:HA	1:E:271:GLU:HB3	1.84	0.58
1:B:263:GLN:NE2	1:B:267:ASP:OD2	2.33	0.58
1:E:38:PHE:CD2	1:F:46:ALA:HB2	2.39	0.58
2:C:22:DT:H2''	2:C:23:DC:H5'	1.84	0.58
1:E:134:ARG:HA	1:E:137:GLU:HB2	1.84	0.58
1:B:134:ARG:HA	1:B:137:GLU:HB2	1.86	0.58
1:A:249:MET:N	1:B:294:PHE:O	2.27	0.58
1:E:85:ALA:HA	1:E:90:LYS:HB3	1.85	0.58
1:E:148:HIS:ND1	1:E:149:LEU:O	2.37	0.58
1:A:129:THR:HB	1:A:132:GLU:H	1.68	0.57
1:A:247:ASN:ND2	1:B:262:MET:SD	2.77	0.57
1:B:136:ILE:O	1:B:139:LYS:HG2	2.04	0.57
1:E:129:THR:HB	1:E:132:GLU:HB2	1.84	0.57
1:B:54:TYR:CZ	1:B:59:GLN:HA	2.39	0.57
2:G:10:DG:H2'	2:G:11:DG:C8	2.39	0.57
1:B:258:LEU:HD12	1:B:261:LYS:HD3	1.85	0.57
1:B:284:ASP:OD1	1:B:284:ASP:N	2.38	0.57
1:E:69:HIS:ND1	1:F:182:LEU:CD1	2.68	0.57
1:B:123:ILE:H	1:B:133:LYS:NZ	2.03	0.56
1:A:195:THR:O	1:A:211:THR:OG1	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:TRP:HE3	1:A:146:ASP:HA	1.69	0.56
1:B:158:LEU:O	1:B:162:LEU:N	2.30	0.56
1:A:146:ASP:OD1	1:E:105:GLN:NE2	2.38	0.56
2:D:11:DG:N7	4:D:101:HOH:O	2.33	0.56
1:F:27:ALA:O	1:F:32:GLY:N	2.35	0.56
2:G:5:DG:H1	2:H:25:DC:H42	1.52	0.56
1:E:62:ARG:NH1	2:H:7:DG:O6	2.39	0.56
1:B:163:HIS:CD2	1:B:178:LEU:HB2	2.40	0.55
2:H:10:DG:H2'	2:H:11:DG:H8	1.71	0.55
1:E:25:PHE:O	1:E:30:THR:N	2.39	0.55
1:A:199:ILE:O	1:A:207:PHE:N	2.32	0.55
1:A:245:ARG:HB3	1:A:248:THR:OG1	2.06	0.55
1:F:265:ALA:HA	1:F:269:LEU:HB3	1.87	0.55
1:F:291:GLN:HE21	1:F:292:MET:H	1.54	0.55
1:B:8:ILE:H	1:B:8:ILE:HD12	1.72	0.55
1:F:221:GLN:H	1:F:221:GLN:NE2	2.05	0.55
1:B:266:LYS:HG2	1:B:294:PHE:HE2	1.72	0.55
1:E:95:LEU:HD13	1:F:16:MET:HE3	1.89	0.55
1:F:40:ASP:O	1:F:44:THR:OG1	2.24	0.55
1:F:54:TYR:CZ	1:F:59:GLN:HB3	2.42	0.55
1:F:84:GLN:O	1:F:89:GLY:N	2.40	0.55
1:A:123:ILE:HB	1:A:133:LYS:HD3	1.89	0.55
1:A:236:ARG:HH22	1:B:297:LYS:HA	1.72	0.55
1:F:245:ARG:HG3	1:F:246:PRO:HD2	1.89	0.54
2:G:6:DC:H2'	2:G:7:DG:C8	2.43	0.54
1:E:110:TRP:CD2	1:E:210:LEU:HB2	2.43	0.54
1:E:287:PRO:HG2	1:F:296:LYS:NZ	2.23	0.54
1:B:241:TRP:CZ2	1:B:250:ARG:HD2	2.43	0.53
1:E:47:LYS:HB3	1:E:78:ILE:HG23	1.90	0.53
1:B:241:TRP:HE1	1:B:250:ARG:HB2	1.73	0.53
2:G:14:DC:H2''	2:G:15:DT:H72	1.90	0.53
1:A:223:ARG:NE	1:B:244:LYS:HG2	2.24	0.53
1:E:296:LYS:HA	1:F:288:VAL:HG12	1.89	0.53
1:E:62:ARG:HB2	2:H:6:DC:H5''	1.89	0.53
1:E:199:ILE:N	1:E:207:PHE:O	2.29	0.53
1:A:66:HIS:HD2	1:B:184:GLU:HG3	1.74	0.53
1:E:256:ASP:HB2	1:F:282:GLN:O	2.09	0.53
1:F:233:ARG:HG3	1:F:236:ARG:HH22	1.74	0.53
1:A:66:HIS:CD2	1:B:184:GLU:HG3	2.43	0.53
2:H:23:DC:H2'	2:H:24:DG:C8	2.44	0.53
1:B:107:PRO:HB3	1:B:210:LEU:HD21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:260:GLU:CD	1:E:260:GLU:H	2.17	0.52
1:E:255:LEU:HD11	1:E:257:ILE:HD11	1.92	0.52
1:E:296:LYS:HD2	1:E:297:LYS:O	2.08	0.52
1:F:74:ARG:NH2	2:H:16:DG:H3'	2.24	0.52
1:A:116:TRP:NE1	1:A:120:ARG:O	2.41	0.52
2:C:4:DG:H2''	2:C:5:DG:C8	2.44	0.52
1:F:98:GLN:HE21	1:F:225:TYR:HA	1.75	0.52
1:B:117:ARG:HG2	1:B:120:ARG:HH11	1.74	0.52
1:E:98:GLN:HE22	1:E:228:VAL:HG21	1.75	0.52
1:E:104:ILE:HA	1:E:215:TYR:HB3	1.91	0.52
1:E:145:PRO:HG3	1:E:213:PRO:HD3	1.92	0.52
1:A:20:MET:HG3	1:B:45:ALA:CB	2.39	0.52
2:C:25:DC:N3	2:D:5:DG:N2	2.51	0.52
1:E:100:PRO:HB3	1:E:102:TYR:CZ	2.45	0.52
1:F:97:SER:HB2	1:F:101:ARG:CZ	2.39	0.52
1:E:292:MET:HB3	1:F:292:MET:HE2	1.91	0.52
1:F:162:LEU:O	1:F:166:SER:N	2.43	0.52
1:A:84:GLN:OE1	1:A:90:LYS:HD3	2.10	0.52
1:A:25:PHE:O	1:A:29:ARG:HB2	2.10	0.52
1:A:123:ILE:HD13	1:A:133:LYS:HB3	1.91	0.52
1:E:69:HIS:CE1	1:F:182:LEU:CD1	2.88	0.52
1:A:131:GLU:OE1	1:A:135:GLN:NE2	2.43	0.51
1:A:288:VAL:HG21	1:B:257:ILE:HG13	1.92	0.51
1:F:13:PRO:HG2	1:F:18:GLN:HG2	1.91	0.51
1:A:245:ARG:NH1	1:B:298:GLU:O	2.38	0.51
1:B:136:ILE:HG23	1:B:139:LYS:HD3	1.92	0.51
1:B:122:ARG:O	1:B:148:HIS:HB2	2.10	0.51
2:G:10:DG:H1	2:H:20:DC:N4	2.08	0.51
1:A:47:LYS:HA	1:A:50:ILE:HD12	1.92	0.51
1:A:266:LYS:HE2	1:A:267:ASP:OD1	2.11	0.51
1:E:7:LEU:HA	1:E:10:ARG:HB2	1.92	0.51
1:E:171:PRO:HG2	1:E:174:HIS:CG	2.46	0.51
1:A:236:ARG:NH2	1:B:297:LYS:HA	2.26	0.51
1:B:266:LYS:HG2	1:B:294:PHE:CE2	2.46	0.51
1:E:62:ARG:HD3	2:H:6:DC:H3'	1.92	0.51
1:B:239:ARG:O	1:B:243:GLU:N	2.32	0.50
1:E:39:LEU:HD22	1:F:43:ALA:HA	1.93	0.50
1:F:221:GLN:HE21	1:F:222:GLU:H	1.58	0.50
1:F:141:PRO:HG2	1:F:144:LEU:HD21	1.93	0.50
1:F:44:THR:OG1	1:F:93:LYS:O	2.28	0.50
2:D:9:DG:H2'	2:D:10:DG:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:SER:O	1:A:31:SER:N	2.29	0.50
1:E:97:SER:OG	1:E:98:GLN:N	2.43	0.50
1:F:203:TRP:HB3	1:F:205:MET:HE3	1.94	0.50
1:B:184:GLU:OE1	1:B:187:LYS:HD3	2.12	0.49
1:E:70:LEU:HD11	1:E:75:VAL:HG22	1.93	0.49
1:E:291:GLN:HB3	1:F:293:VAL:HG12	1.93	0.49
1:B:34:ARG:NH1	2:C:18:DC:OP1	2.45	0.49
1:E:269:LEU:HD12	1:E:272:ILE:HD11	1.93	0.49
1:F:33:HIS:NE2	1:F:97:SER:O	2.41	0.49
1:F:272:ILE:O	1:F:276:TRP:N	2.39	0.49
1:A:238:MET:O	1:A:242:ALA:N	2.45	0.49
1:A:285:GLY:HA3	1:B:256:ASP:CG	2.38	0.49
1:B:159:ILE:HG22	1:B:178:LEU:HD21	1.94	0.49
1:E:218:ALA:HB3	1:E:221:GLN:HA	1.94	0.49
1:A:245:ARG:HG3	1:A:246:PRO:HD2	1.95	0.49
1:E:40:ASP:O	1:E:44:THR:OG1	2.24	0.49
1:E:117:ARG:HG3	1:E:118:PRO:HD2	1.94	0.49
1:E:46:ALA:HB2	1:F:38:PHE:CE2	2.47	0.49
1:E:60:ASN:HD21	2:H:6:DC:H5'	1.78	0.49
1:E:198:ARG:CZ	1:E:206:PRO:HB3	2.43	0.49
1:F:129:THR:HG23	1:F:132:GLU:OE2	2.12	0.49
2:G:19:DC:H2''	2:G:20:DC:H5'	1.93	0.49
1:E:60:ASN:HB3	1:E:63:MET:HB3	1.95	0.49
1:E:245:ARG:C	1:E:247:ASN:H	2.20	0.49
1:A:288:VAL:O	1:B:254:GLU:HA	2.13	0.49
1:A:29:ARG:HA	1:B:68:HIS:HE1	1.78	0.49
1:B:199:ILE:O	1:B:207:PHE:N	2.41	0.49
1:A:60:ASN:HB3	1:A:63:MET:HB3	1.93	0.48
1:A:110:TRP:HD1	1:A:114:TYR:HB2	1.78	0.48
1:A:114:TYR:HB3	1:A:148:HIS:NE2	2.28	0.48
1:E:5:VAL:CG2	1:E:29:ARG:HH22	2.26	0.48
1:F:291:GLN:NE2	1:F:292:MET:H	2.10	0.48
1:A:155:PHE:CE2	1:A:187:LYS:HG3	2.48	0.48
1:A:236:ARG:HB2	1:B:22:TYR:CE2	2.48	0.48
1:A:292:MET:HE3	1:B:251:VAL:HB	1.94	0.48
1:B:110:TRP:CD1	1:B:114:TYR:HB2	2.48	0.48
1:E:179:SER:OG	2:H:19:DC:OP1	2.25	0.48
1:A:110:TRP:CD1	1:A:114:TYR:HB2	2.48	0.48
1:A:149:LEU:HD22	1:A:209:ALA:HB2	1.95	0.48
1:E:66:HIS:O	1:F:185:HIS:HA	2.13	0.48
1:F:16:MET:HA	1:F:19:ILE:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:PHE:HB3	1:B:248:THR:HA	1.95	0.48
1:B:156:LEU:O	1:B:160:GLU:N	2.35	0.48
2:H:10:DG:H2'	2:H:11:DG:C8	2.48	0.48
1:E:24:ALA:O	1:E:28:MET:N	2.36	0.47
1:F:135:GLN:OE1	1:F:135:GLN:N	2.40	0.47
1:B:40:ASP:O	1:B:44:THR:N	2.32	0.47
1:E:16:MET:HE2	1:F:98:GLN:HA	1.96	0.47
1:E:62:ARG:HG3	2:H:7:DG:OP2	2.14	0.47
1:E:201:SER:OG	1:E:205:MET:N	2.47	0.47
1:A:259:PRO:HA	1:A:262:MET:HG2	1.97	0.47
2:H:26:DC:H2''	2:H:27:DT:H71	1.95	0.47
1:B:106:PHE:HB3	1:B:107:PRO:HD3	1.96	0.47
1:F:46:ALA:O	1:F:50:ILE:HG13	2.14	0.47
1:A:81:GLU:HG3	1:A:90:LYS:HG2	1.97	0.47
1:A:237:MET:O	1:A:248:THR:HG21	2.14	0.47
1:E:19:ILE:HD11	1:F:228:VAL:HG13	1.96	0.47
1:F:125:GLY:O	1:F:126:THR:CB	2.62	0.47
1:A:17:ASP:O	1:A:21:LEU:N	2.41	0.47
1:B:114:TYR:O	1:B:148:HIS:N	2.48	0.47
1:E:105:GLN:HA	1:E:108:TYR:CD2	2.50	0.47
1:E:256:ASP:HB3	1:F:285:GLY:C	2.40	0.47
2:G:26:DC:H2''	2:G:27:DT:H72	1.96	0.47
1:A:16:MET:HA	1:A:19:ILE:HD12	1.97	0.47
2:C:13:DT:H2''	2:C:14:DC:H5'	1.96	0.47
1:E:13:PRO:HB2	1:E:17:ASP:CB	2.45	0.47
1:A:245:ARG:HB3	1:A:248:THR:HG1	1.80	0.47
1:A:290:LEU:HD23	1:B:253:GLU:HB2	1.96	0.47
1:E:68:HIS:HB2	1:E:70:LEU:HD22	1.97	0.47
1:E:115:PRO:HA	1:E:147:ALA:HA	1.97	0.47
1:E:287:PRO:HG2	1:F:296:LYS:HD3	1.96	0.47
1:F:116:TRP:NE1	1:F:120:ARG:O	2.47	0.47
1:A:20:MET:HG3	1:B:45:ALA:HB3	1.96	0.46
1:E:105:GLN:O	1:E:109:VAL:HG23	2.15	0.46
1:F:190:LEU:O	1:F:193:SER:OG	2.32	0.46
1:F:241:TRP:HB2	1:F:248:THR:HG22	1.97	0.46
1:A:236:ARG:NH1	1:A:240:ASP:OD2	2.48	0.46
1:B:202:PRO:HG2	1:B:203:TRP:CE3	2.50	0.46
1:E:131:GLU:O	1:E:135:GLN:HG2	2.15	0.46
1:E:99:GLU:HG2	1:E:104:ILE:HD11	1.97	0.46
1:E:163:HIS:O	1:E:166:SER:OG	2.31	0.46
1:E:212:ARG:HG3	1:E:213:PRO:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:53:THR:HA	1:E:56:GLU:HG2	1.97	0.46
1:E:142:SER:O	1:E:143:ASN:HB2	2.14	0.46
1:A:71:GLU:HG3	2:C:18:DC:C5	2.51	0.46
1:F:269:LEU:HA	1:F:272:ILE:HG12	1.96	0.46
1:E:110:TRP:CD1	1:E:114:TYR:HB2	2.51	0.46
1:F:81:GLU:HG3	1:F:90:LYS:HD3	1.98	0.46
1:F:71:GLU:OE1	2:H:18:DC:N4	2.43	0.45
1:E:84:GLN:O	1:E:88:GLU:HB2	2.17	0.45
1:E:256:ASP:HA	1:F:286:VAL:O	2.16	0.45
1:E:285:GLY:HA3	1:F:257:ILE:H	1.81	0.45
1:F:35:HIS:O	1:F:38:PHE:HB3	2.15	0.45
2:G:17:DA:H2''	2:G:18:DC:C6	2.52	0.45
1:A:106:PHE:CD2	1:A:162:LEU:HD13	2.52	0.45
1:E:62:ARG:HD2	2:H:7:DG:N7	2.31	0.45
1:E:228:VAL:HG12	1:F:15:ALA:HB1	1.98	0.45
1:F:136:ILE:O	1:F:139:LYS:HG2	2.16	0.45
1:A:33:HIS:HA	1:A:100:PRO:HG3	1.99	0.45
1:E:110:TRP:CZ3	1:E:196:VAL:HG13	2.52	0.45
1:E:268:GLU:O	1:E:272:ILE:HG23	2.17	0.45
1:A:236:ARG:O	1:A:240:ASP:N	2.46	0.45
1:B:263:GLN:HE21	1:B:267:ASP:CG	2.24	0.45
1:E:23:LEU:O	1:E:27:ALA:N	2.49	0.45
1:E:282:GLN:HB2	1:F:258:LEU:HG	1.98	0.45
1:A:130:SER:O	1:A:134:ARG:HG3	2.17	0.45
1:E:27:ALA:O	1:E:31:SER:HB2	2.17	0.45
1:E:272:ILE:HG13	1:E:273:ILE:HG12	1.99	0.45
2:G:15:DT:H2''	2:G:16:DG:H5'	1.99	0.45
1:E:133:LYS:O	1:E:137:GLU:HG3	2.16	0.44
1:B:109:VAL:O	1:B:113:LYS:N	2.43	0.44
1:B:260:GLU:H	1:B:260:GLU:CD	2.25	0.44
1:F:189:ARG:HA	1:F:189:ARG:HD3	1.74	0.44
1:A:10:ARG:NH1	1:B:86:LEU:O	2.50	0.44
1:A:292:MET:HG2	1:B:251:VAL:H	1.81	0.44
1:F:27:ALA:HA	1:F:31:SER:HB2	2.00	0.44
1:F:150:ILE:HG23	1:F:154:GLU:HB2	1.99	0.44
1:A:10:ARG:HD2	1:A:10:ARG:HA	1.87	0.44
1:E:280:TYR:O	1:F:257:ILE:HA	2.17	0.44
1:A:249:MET:HB3	1:B:294:PHE:HD2	1.81	0.44
1:B:67:LEU:HA	1:B:67:LEU:HD23	1.79	0.44
1:B:215:TYR:HB3	1:B:218:ALA:HB3	1.99	0.44
1:E:227:MET:HA	1:F:238:MET:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:PRO:O	1:B:76:LYS:N	2.44	0.44
1:E:100:PRO:HG2	1:E:103:LEU:HD12	1.98	0.44
1:B:249:MET:HE2	1:B:249:MET:HB2	1.75	0.43
1:B:292:MET:HE2	1:B:292:MET:HB2	1.89	0.43
1:E:293:VAL:O	1:F:290:LEU:HD12	2.18	0.43
1:A:223:ARG:NH2	1:B:241:TRP:O	2.47	0.43
1:A:298:GLU:N	1:B:236:ARG:HH12	2.16	0.43
2:G:24:DG:H1'	2:G:25:DC:H5'	1.99	0.43
1:F:81:GLU:O	1:F:85:ALA:N	2.47	0.43
1:F:83:ARG:NH1	1:F:88:GLU:OE1	2.51	0.43
2:G:27:DT:H2''	2:G:28:DG:H8	1.82	0.43
1:F:233:ARG:HA	1:F:236:ARG:NH1	2.32	0.43
1:A:227:MET:HB2	1:B:242:ALA:HB2	2.00	0.43
1:E:47:LYS:HA	1:E:50:ILE:HD12	2.00	0.43
1:A:223:ARG:O	1:A:227:MET:N	2.41	0.43
1:B:12:GLY:N	1:B:13:PRO:HD3	2.33	0.43
1:B:149:LEU:HB3	1:B:209:ALA:HB2	2.00	0.43
1:E:205:MET:HG3	1:E:206:PRO:HD2	2.00	0.43
1:E:70:LEU:CD1	1:E:75:VAL:HG22	2.48	0.43
1:E:98:GLN:HG2	1:E:221:GLN:HE22	1.83	0.43
1:A:286:VAL:O	1:B:256:ASP:HA	2.18	0.43
1:B:13:PRO:O	1:B:18:GLN:NE2	2.32	0.43
1:B:39:LEU:HD12	2:C:17:DA:H5''	2.00	0.43
1:B:150:ILE:HG12	1:B:151:THR:O	2.18	0.43
1:E:185:HIS:HA	1:F:66:HIS:HB3	2.00	0.43
1:E:257:ILE:H	1:F:286:VAL:H	1.67	0.43
1:E:269:LEU:HA	1:E:272:ILE:HG12	2.00	0.43
1:E:28:MET:O	1:E:32:GLY:HA2	2.19	0.42
1:F:272:ILE:HA	1:F:275:ALA:HB3	2.01	0.42
1:B:233:ARG:HG2	1:B:237:MET:HE2	2.01	0.42
1:F:253:GLU:HB3	1:F:255:LEU:HD22	2.01	0.42
2:H:5:DG:H2'	2:H:6:DC:O4'	2.19	0.42
1:A:100:PRO:O	1:A:104:ILE:HG13	2.20	0.42
1:A:160:GLU:HG2	1:A:178:LEU:HD23	2.01	0.42
1:E:110:TRP:HZ3	1:E:196:VAL:HG13	1.84	0.42
1:E:131:GLU:HA	1:E:134:ARG:HB2	2.01	0.42
1:A:47:LYS:HB3	1:A:78:ILE:HG23	2.01	0.42
1:A:81:GLU:O	1:A:85:ALA:N	2.52	0.42
1:B:128:LEU:HD23	1:B:128:LEU:HA	1.88	0.42
1:E:53:THR:O	1:E:57:GLN:HG2	2.20	0.42
1:E:100:PRO:O	1:E:104:ILE:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:VAL:N	1:F:8:ILE:HD13	2.35	0.42
1:F:26:SER:O	1:F:31:SER:HB2	2.20	0.42
1:A:288:VAL:HB	1:B:255:LEU:O	2.20	0.42
1:B:109:VAL:HB	1:B:158:LEU:HD21	2.01	0.42
1:E:111:MET:O	1:E:115:PRO:HB3	2.20	0.42
1:A:33:HIS:HE2	1:A:98:GLN:C	2.25	0.42
1:A:52:MET:HE2	1:B:5:VAL:HG21	2.00	0.42
2:D:25:DC:H2''	2:D:26:DC:C6	2.55	0.42
1:E:276:TRP:NE1	1:E:280:TYR:HE1	2.18	0.42
2:D:12:DG:H2'	2:D:13:DT:C6	2.54	0.42
1:F:47:LYS:HE2	1:F:74:ARG:NH2	2.35	0.42
1:A:38:PHE:CE2	1:B:46:ALA:HB2	2.55	0.41
1:A:238:MET:HA	1:A:241:TRP:HB3	2.02	0.41
1:A:247:ASN:HD21	1:B:262:MET:CG	2.33	0.41
1:B:11:LEU:HD23	1:B:11:LEU:HA	1.88	0.41
1:B:215:TYR:HD2	1:B:218:ALA:HB2	1.86	0.41
2:D:23:DC:H2'	2:D:24:DG:C8	2.54	0.41
1:F:180:GLU:HB2	2:G:20:DC:OP2	2.19	0.41
1:A:5:VAL:HB	1:A:6:ASP:H	1.63	0.41
1:A:11:LEU:HD23	1:A:11:LEU:HA	1.89	0.41
1:A:28:MET:O	1:A:189:ARG:NH2	2.53	0.41
1:B:152:SER:HB2	1:B:208:TYR:HE2	1.86	0.41
1:B:162:LEU:HD23	1:B:162:LEU:HA	1.91	0.41
1:E:262:MET:HB3	1:F:247:ASN:CG	2.46	0.41
1:A:223:ARG:HG3	1:B:244:LYS:HD2	2.02	0.41
1:A:292:MET:HG2	1:B:251:VAL:O	2.21	0.41
1:F:43:ALA:HB1	1:F:47:LYS:HE3	2.03	0.41
1:E:28:MET:HA	1:E:33:HIS:H	1.85	0.41
1:E:51:TYR:HD1	1:E:79:VAL:HG22	1.85	0.41
1:E:281:HIS:HA	1:F:256:ASP:O	2.20	0.41
1:F:114:TYR:CD2	1:F:150:ILE:HD11	2.55	0.41
1:A:81:GLU:HA	1:A:84:GLN:HB2	2.03	0.41
1:A:122:ARG:HB2	1:A:137:GLU:OE2	2.20	0.41
1:A:250:ARG:HH12	1:A:252:LEU:HB2	1.86	0.41
1:E:5:VAL:N	1:E:25:PHE:HE1	2.17	0.41
1:E:46:ALA:HB2	1:F:38:PHE:CD2	2.55	0.41
1:A:70:LEU:HD12	1:A:75:VAL:HG22	2.03	0.41
1:B:110:TRP:CD1	1:B:147:ALA:HB1	2.56	0.41
2:D:9:DG:H2'	2:D:10:DG:H8	1.85	0.41
1:E:137:GLU:HA	1:E:140:LEU:HG	2.02	0.41
1:F:160:GLU:HG2	1:F:178:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLY:HA3	1:A:101:ARG:HH22	1.85	0.41
1:A:198:ARG:HG2	1:A:208:TYR:CE1	2.56	0.41
1:B:52:MET:HE3	1:B:52:MET:HB3	1.93	0.41
1:B:55:LEU:HA	1:B:55:LEU:HD23	1.79	0.41
1:B:92:LEU:HD12	1:B:92:LEU:HA	1.91	0.41
2:C:22:DT:C2'	2:C:23:DC:H5'	2.51	0.41
1:E:25:PHE:HB3	1:F:239:ARG:NH2	2.36	0.41
1:E:182:LEU:O	1:E:186:ILE:HG13	2.21	0.41
1:F:282:GLN:HE21	1:F:282:GLN:HB3	1.57	0.41
2:H:3:DA:H2''	2:H:4:DG:C8	2.56	0.41
1:A:161:PHE:O	1:A:164:LYS:HB3	2.21	0.41
1:B:217:PRO:C	1:B:222:GLU:HG3	2.46	0.41
1:E:36:GLY:HA3	2:H:18:DC:OP1	2.21	0.41
1:E:296:LYS:HA	1:F:288:VAL:HA	2.02	0.41
1:F:100:PRO:HB3	1:F:102:TYR:CZ	2.55	0.41
1:A:117:ARG:HG3	1:E:101:ARG:HH22	1.86	0.40
1:A:129:THR:HG22	1:A:131:GLU:H	1.86	0.40
1:E:69:HIS:HE1	1:F:182:LEU:HD13	1.70	0.40
1:E:131:GLU:O	1:E:135:GLN:N	2.52	0.40
1:F:101:ARG:O	1:F:105:GLN:HG2	2.21	0.40
1:B:5:VAL:N	1:B:8:ILE:HD13	2.36	0.40
1:E:115:PRO:O	1:E:148:HIS:HD2	2.03	0.40
1:A:182:LEU:O	1:A:186:ILE:HG13	2.21	0.40
1:B:25:PHE:O	1:B:29:ARG:HB2	2.20	0.40
1:E:43:ALA:O	1:E:47:LYS:HG3	2.21	0.40
1:F:15:ALA:O	1:F:19:ILE:HG13	2.21	0.40
2:G:2:DC:H2''	2:G:3:DA:C8	2.56	0.40
2:G:3:DA:H2''	2:G:4:DG:C8	2.56	0.40
1:A:242:ALA:O	1:B:223:ARG:HG3	2.22	0.40
1:B:60:ASN:HD21	2:C:6:DC:H5''	1.86	0.40
1:E:272:ILE:HG21	1:F:276:TRP:CD1	2.56	0.40
2:G:27:DT:H2''	2:G:28:DG:C8	2.57	0.40
2:H:7:DG:C6	2:H:8:DA:C6	3.10	0.40
1:A:73:LYS:NZ	2:D:11:DG:O6	2.55	0.40
1:B:220:ASP:O	1:B:225:TYR:HB3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	292/302 (97%)	276 (94%)	16 (6%)	0	100	100
1	B	292/302 (97%)	278 (95%)	14 (5%)	0	100	100
1	E	292/302 (97%)	270 (92%)	22 (8%)	0	100	100
1	F	292/302 (97%)	265 (91%)	27 (9%)	0	100	100
All	All	1168/1208 (97%)	1089 (93%)	79 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	258/265 (97%)	244 (95%)	14 (5%)	20	50
1	B	258/265 (97%)	236 (92%)	22 (8%)	10	34
1	E	258/265 (97%)	239 (93%)	19 (7%)	13	40
1	F	258/265 (97%)	240 (93%)	18 (7%)	14	42
All	All	1032/1060 (97%)	959 (93%)	73 (7%)	13	42

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	75	VAL

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Mol	Chain	Res	Type
1	A	80	GLU
1	A	88	GLU
1	A	98	GLN
1	A	101	ARG
1	A	102	TYR
1	A	117	ARG
1	A	131	GLU
1	A	149	LEU
1	A	162	LEU
1	A	176	MET
1	A	201	SER
1	A	248	THR
1	B	5	VAL
1	B	21	LEU
1	B	90	LYS
1	B	92	LEU
1	B	97	SER
1	B	103	LEU
1	B	140	LEU
1	B	143	ASN
1	B	144	LEU
1	B	149	LEU
1	B	150	ILE
1	B	158	LEU
1	B	168	GLU
1	B	169	ASP
1	B	175	GLN
1	B	203	TRP
1	B	205	MET
1	B	223	ARG
1	B	252	LEU
1	B	255	LEU
1	B	256	ASP
1	B	284	ASP
1	E	6	ASP
1	E	20	MET
1	E	23	LEU
1	E	99	GLU
1	E	117	ARG
1	E	156	LEU
1	E	162	LEU
1	E	174	HIS

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Mol	Chain	Res	Type
1	E	176	MET
1	E	200	ASP
1	E	203	TRP
1	E	247	ASN
1	E	260	GLU
1	E	282	GLN
1	E	284	ASP
1	E	286	VAL
1	E	288	VAL
1	E	296	LYS
1	E	297	LYS
1	F	5	VAL
1	F	31	SER
1	F	56	GLU
1	F	62	ARG
1	F	80	GLU
1	F	117	ARG
1	F	129	THR
1	F	150	ILE
1	F	157	GLU
1	F	162	LEU
1	F	173	GLU
1	F	203	TRP
1	F	221	GLN
1	F	250	ARG
1	F	256	ASP
1	F	282	GLN
1	F	286	VAL
1	F	292	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	HIS
1	A	105	GLN
1	A	138	GLN
1	B	163	HIS
1	B	175	GLN
1	B	282	GLN
1	E	68	HIS
1	E	98	GLN
1	E	175	GLN

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Mol	Chain	Res	Type
1	E	264	GLN
1	E	282	GLN
1	F	84	GLN
1	F	98	GLN
1	F	175	GLN
1	F	221	GLN
1	F	282	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	G	101	-	4,4,4	0.25	0	6,6,6	0.12	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.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	294/302 (97%)	-0.87	0 100 100	85, 139, 194, 370	0
1	B	294/302 (97%)	-0.87	1 (0%) 90 81	92, 126, 190, 276	0
1	E	294/302 (97%)	-0.89	1 (0%) 90 81	69, 129, 216, 283	0
1	F	294/302 (97%)	-0.87	1 (0%) 90 81	61, 114, 180, 295	0
2	C	29/29 (100%)	-0.88	0 100 100	117, 154, 188, 206	0
2	D	29/29 (100%)	-0.79	0 100 100	123, 157, 172, 180	0
2	G	29/29 (100%)	-0.94	0 100 100	121, 162, 196, 208	0
2	H	29/29 (100%)	-0.89	0 100 100	110, 159, 197, 199	0
All	All	1292/1324 (97%)	-0.87	3 (0%) 91 85	61, 129, 196, 370	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	125	GLY	3.3
1	F	180	GLU	3.0
1	E	127	SER	2.6

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	G	101	5/5	0.99	0.07	82,82,82,82	5

6.5 Other polymers [i](#)

There are no such residues in this entry.