



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:47 PM UTC

PDB ID : 2GSZ / pdb_00002gsz
Title : Structure of A. aeolicus PilT with 6 monomers per asymmetric unit
Authors : Forest, K.T.; Satyshur, K.A.
Deposited on : 2006-04-27
Resolution : 4.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

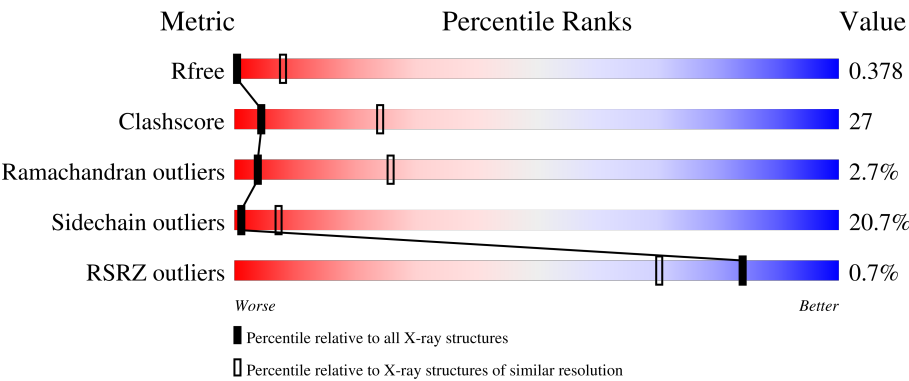
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 Å.

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



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

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	363	2% 43% 39% 13% 6%
1	B	363	38% 45% 11% 6%
1	C	363	% 43% 40% 11% 6%
1	D	363	39% 44% 11% 6%
1	E	363	% 40% 43% 12% 6%

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Mol	Chain	Length	Quality of chain
1	F	363	

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
2	SO4	B	375	-	-	X	-
2	SO4	C	375	-	-	X	-
2	SO4	E	375	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16344 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 twitching motility protein PilT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	B	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	C	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	D	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	E	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			
1	F	343	Total	C	N	O	S	Se	0	0	0
			2717	1731	471	505	1	9			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	MSE	MET	modified residue	GB 2983313
A	136	MSE	MET	modified residue	GB 2983313
A	156	MSE	MET	modified residue	GB 2983313
A	218	MSE	MET	modified residue	GB 2983313
A	318	MSE	MET	modified residue	GB 2983313
A	327	MSE	MET	modified residue	GB 2983313
A	330	MSE	MET	modified residue	GB 2983313
A	349	MSE	MET	modified residue	GB 2983313
A	361	MSE	MET	modified residue	GB 2983313
A	367	LEU	-	expression tag	GB 2983313
A	368	GLU	-	expression tag	GB 2983313
A	369	HIS	-	expression tag	GB 2983313
A	370	HIS	-	expression tag	GB 2983313
A	371	HIS	-	expression tag	GB 2983313
A	372	HIS	-	expression tag	GB 2983313
A	373	HIS	-	expression tag	GB 2983313
A	374	HIS	-	expression tag	GB 2983313

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Chain	Residue	Modelled	Actual	Comment	Reference
B	68	MSE	MET	modified residue	GB 2983313
B	136	MSE	MET	modified residue	GB 2983313
B	156	MSE	MET	modified residue	GB 2983313
B	218	MSE	MET	modified residue	GB 2983313
B	318	MSE	MET	modified residue	GB 2983313
B	327	MSE	MET	modified residue	GB 2983313
B	330	MSE	MET	modified residue	GB 2983313
B	349	MSE	MET	modified residue	GB 2983313
B	361	MSE	MET	modified residue	GB 2983313
B	367	LEU	-	expression tag	GB 2983313
B	368	GLU	-	expression tag	GB 2983313
B	369	HIS	-	expression tag	GB 2983313
B	370	HIS	-	expression tag	GB 2983313
B	371	HIS	-	expression tag	GB 2983313
B	372	HIS	-	expression tag	GB 2983313
B	373	HIS	-	expression tag	GB 2983313
B	374	HIS	-	expression tag	GB 2983313
C	68	MSE	MET	modified residue	GB 2983313
C	136	MSE	MET	modified residue	GB 2983313
C	156	MSE	MET	modified residue	GB 2983313
C	218	MSE	MET	modified residue	GB 2983313
C	318	MSE	MET	modified residue	GB 2983313
C	327	MSE	MET	modified residue	GB 2983313
C	330	MSE	MET	modified residue	GB 2983313
C	349	MSE	MET	modified residue	GB 2983313
C	361	MSE	MET	modified residue	GB 2983313
C	367	LEU	-	expression tag	GB 2983313
C	368	GLU	-	expression tag	GB 2983313
C	369	HIS	-	expression tag	GB 2983313
C	370	HIS	-	expression tag	GB 2983313
C	371	HIS	-	expression tag	GB 2983313
C	372	HIS	-	expression tag	GB 2983313
C	373	HIS	-	expression tag	GB 2983313
C	374	HIS	-	expression tag	GB 2983313
D	68	MSE	MET	modified residue	GB 2983313
D	136	MSE	MET	modified residue	GB 2983313
D	156	MSE	MET	modified residue	GB 2983313
D	218	MSE	MET	modified residue	GB 2983313
D	318	MSE	MET	modified residue	GB 2983313
D	327	MSE	MET	modified residue	GB 2983313
D	330	MSE	MET	modified residue	GB 2983313
D	349	MSE	MET	modified residue	GB 2983313

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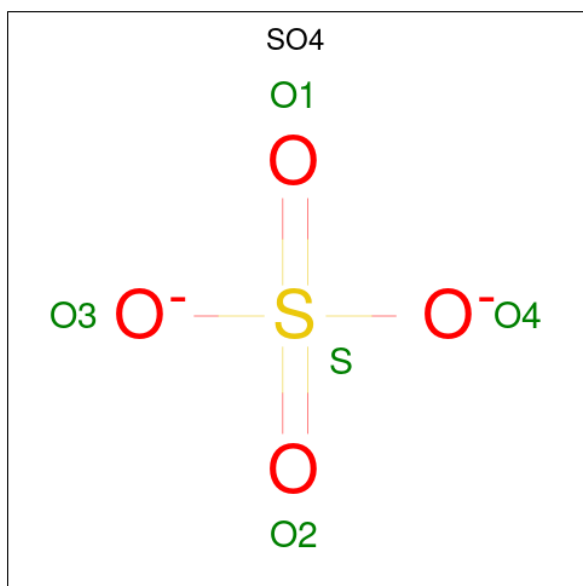
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D	361	MSE	MET	modified residue	GB 2983313
D	367	LEU	-	expression tag	GB 2983313
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D	369	HIS	-	expression tag	GB 2983313
D	370	HIS	-	expression tag	GB 2983313
D	371	HIS	-	expression tag	GB 2983313
D	372	HIS	-	expression tag	GB 2983313
D	373	HIS	-	expression tag	GB 2983313
D	374	HIS	-	expression tag	GB 2983313
E	68	MSE	MET	modified residue	GB 2983313
E	136	MSE	MET	modified residue	GB 2983313
E	156	MSE	MET	modified residue	GB 2983313
E	218	MSE	MET	modified residue	GB 2983313
E	318	MSE	MET	modified residue	GB 2983313
E	327	MSE	MET	modified residue	GB 2983313
E	330	MSE	MET	modified residue	GB 2983313
E	349	MSE	MET	modified residue	GB 2983313
E	361	MSE	MET	modified residue	GB 2983313
E	367	LEU	-	expression tag	GB 2983313
E	368	GLU	-	expression tag	GB 2983313
E	369	HIS	-	expression tag	GB 2983313
E	370	HIS	-	expression tag	GB 2983313
E	371	HIS	-	expression tag	GB 2983313
E	372	HIS	-	expression tag	GB 2983313
E	373	HIS	-	expression tag	GB 2983313
E	374	HIS	-	expression tag	GB 2983313
F	68	MSE	MET	modified residue	GB 2983313
F	136	MSE	MET	modified residue	GB 2983313
F	156	MSE	MET	modified residue	GB 2983313
F	218	MSE	MET	modified residue	GB 2983313
F	318	MSE	MET	modified residue	GB 2983313
F	327	MSE	MET	modified residue	GB 2983313
F	330	MSE	MET	modified residue	GB 2983313
F	349	MSE	MET	modified residue	GB 2983313
F	361	MSE	MET	modified residue	GB 2983313
F	367	LEU	-	expression tag	GB 2983313
F	368	GLU	-	expression tag	GB 2983313
F	369	HIS	-	expression tag	GB 2983313
F	370	HIS	-	expression tag	GB 2983313
F	371	HIS	-	expression tag	GB 2983313
F	372	HIS	-	expression tag	GB 2983313
F	373	HIS	-	expression tag	GB 2983313

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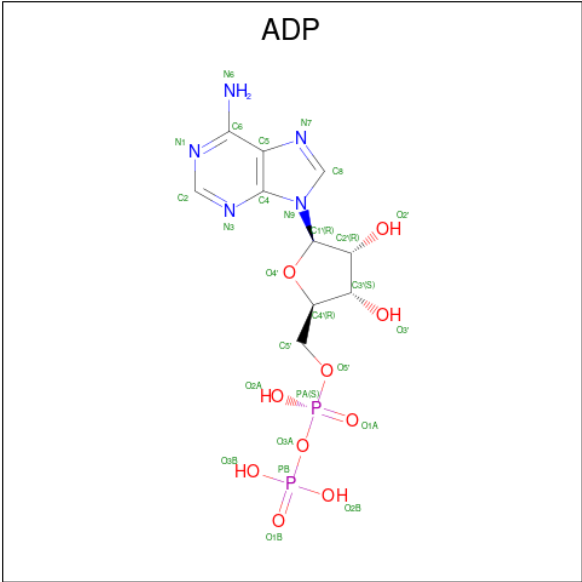
Chain	Residue	Modelled	Actual	Comment	Reference
F	374	HIS	-	expression tag	GB 2983313

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

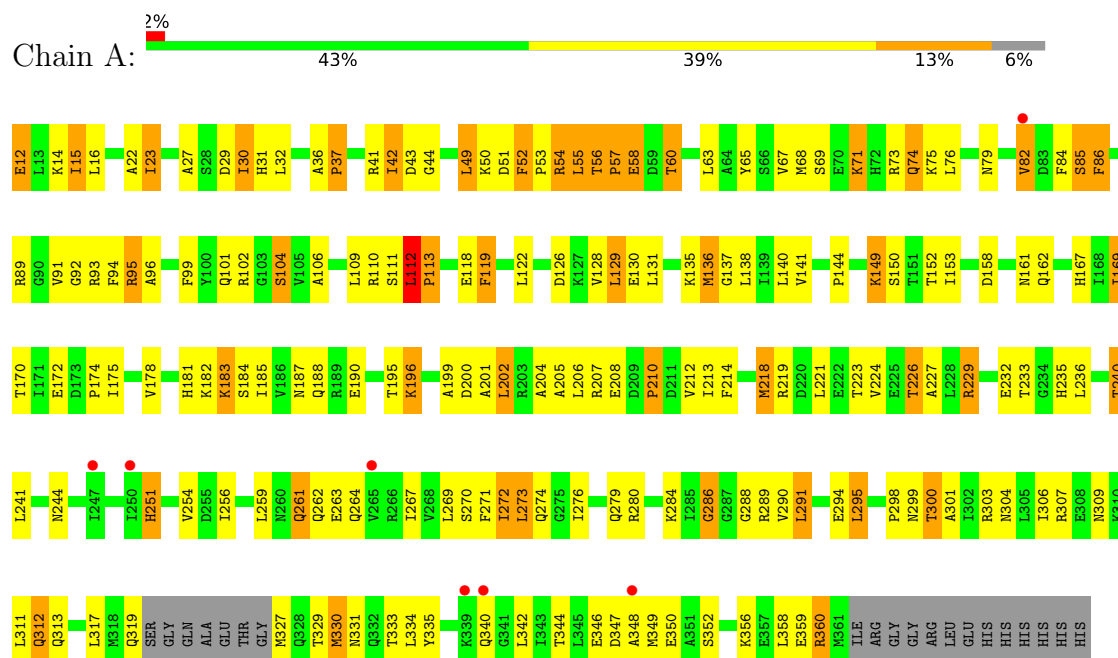


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	F	1	27	10	5	10	2	0	0

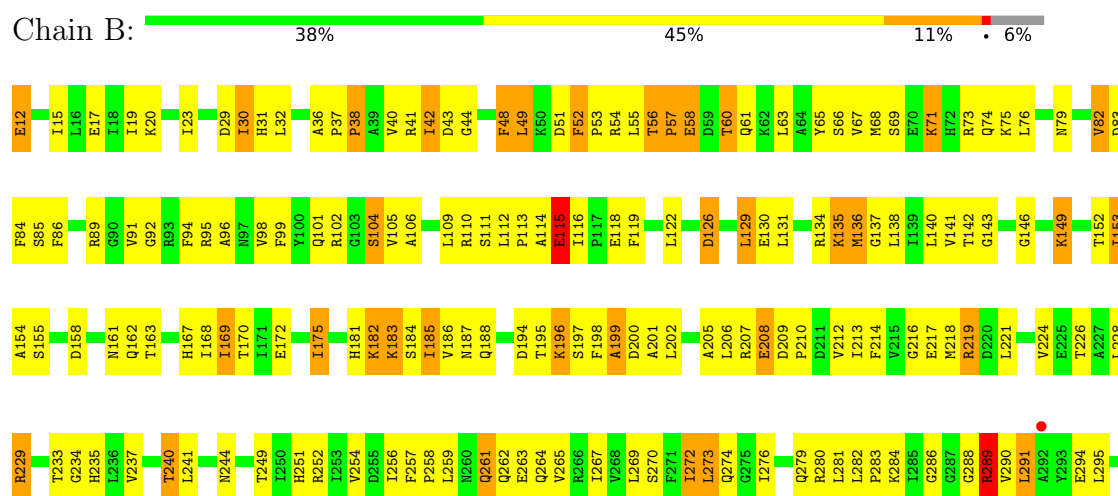
3 Residue-property plots

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.

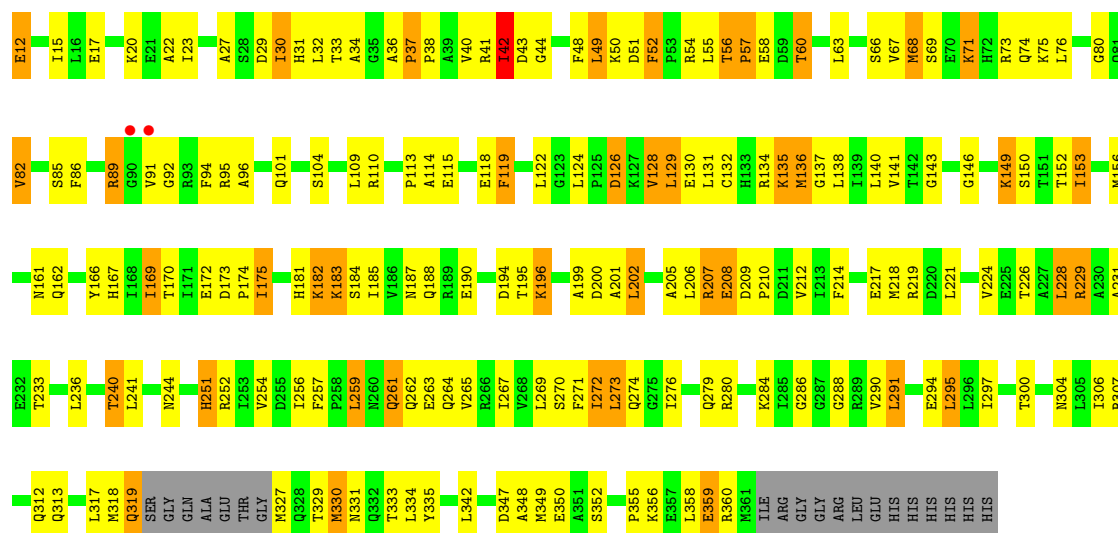
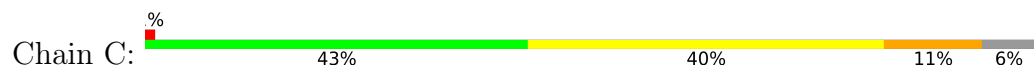
• Molecule 1: twitching motility protein PilT



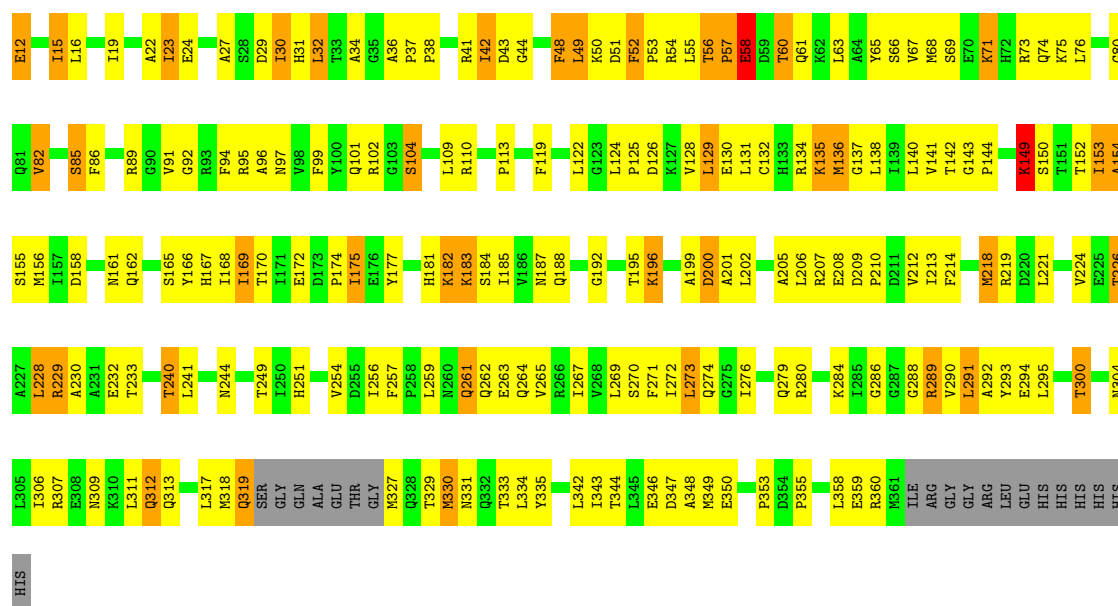
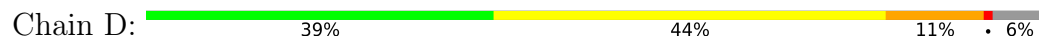
• Molecule 1: twitching motility protein PilT



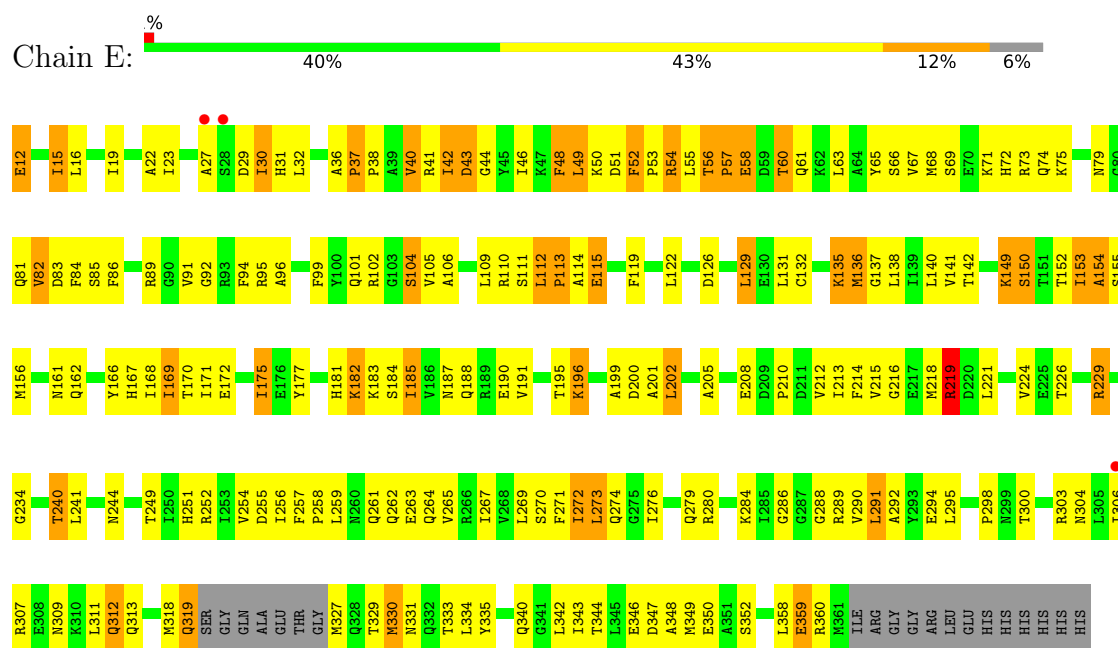
- Molecule 1: twitching motility protein PilT



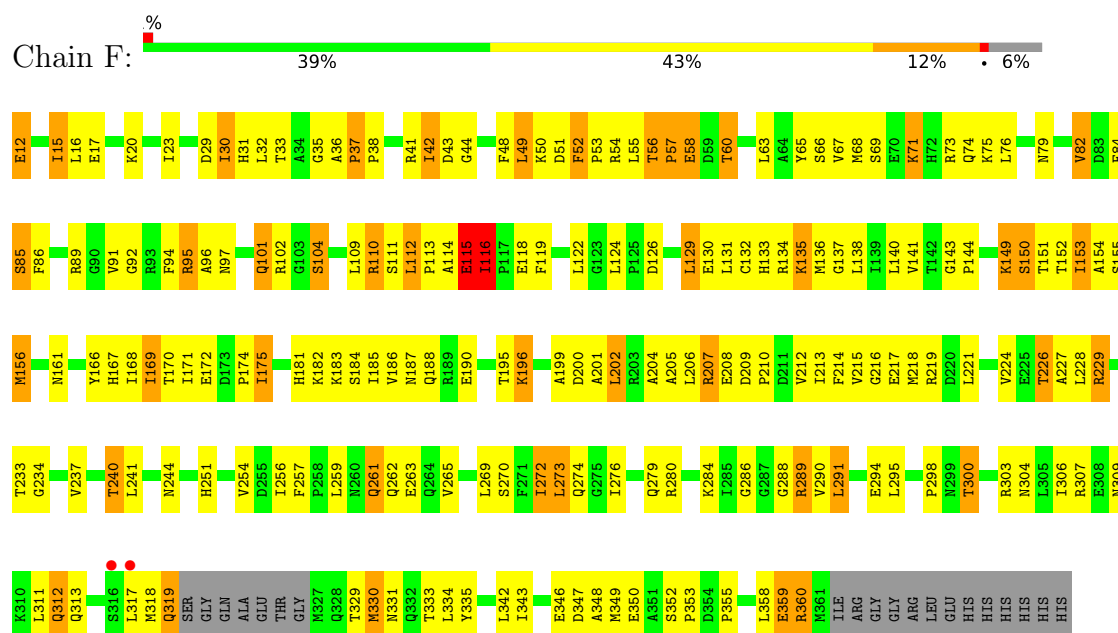
- Molecule 1: twitching motility protein PilT



- Molecule 1: twitching motility protein PilT



• Molecule 1: twitching motility protein PilT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	206.11Å 105.24Å 123.02Å 90.00° 111.06° 90.00°	Depositor
Resolution (Å)	25.00 – 4.20 25.00 – 4.20	Depositor EDS
% Data completeness (in resolution range)	94.8 (25.00-4.20) 94.2 (25.00-4.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.91 (at 4.27Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.343 , 0.406 0.321 , 0.378	Depositor DCC
R_{free} test set	859 reflections (4.37%)	wwPDB-VP
Wilson B-factor (Å ²)	115.0	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 9.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	16344	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	1.10	3/2753 (0.1%)	1.17	14/3702 (0.4%)
1	B	1.07	6/2753 (0.2%)	1.19	8/3702 (0.2%)
1	C	1.01	3/2753 (0.1%)	1.17	17/3702 (0.5%)
1	D	1.03	4/2753 (0.1%)	1.18	13/3702 (0.4%)
1	E	1.06	3/2753 (0.1%)	1.22	10/3702 (0.3%)
1	F	1.04	3/2753 (0.1%)	1.21	26/3702 (0.7%)
All	All	1.05	22/16518 (0.1%)	1.19	88/22212 (0.4%)

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
1	B	0	1
1	F	0	2
All	All	0	3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	136	MSE	SE-CE	9.39	2.23	1.95
1	C	136	MSE	SE-CE	7.96	2.19	1.95
1	B	115	GLU	CD-OE1	7.80	1.40	1.25
1	A	218	MSE	SE-CE	7.62	2.18	1.95
1	A	136	MSE	SE-CE	7.57	2.18	1.95
1	F	215	VAL	C-O	-6.78	1.17	1.24
1	B	115	GLU	CD-OE2	6.59	1.37	1.25
1	B	163	THR	CA-CB	6.40	1.63	1.53
1	E	136	MSE	SE-CE	6.38	2.14	1.95
1	B	136	MSE	SE-CE	6.37	2.14	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	349	MSE	SE-CE	6.28	2.14	1.95
1	E	349	MSE	SE-CE	6.24	2.14	1.95
1	F	156	MSE	SE-CE	6.15	2.13	1.95
1	D	218	MSE	SE-CE	6.11	2.13	1.95
1	A	106	ALA	CA-CB	-5.67	1.44	1.53
1	C	42	ILE	CA-CB	5.59	1.61	1.53
1	C	68	MSE	SE-CE	5.33	2.11	1.95
1	D	300	THR	CA-CB	5.31	1.62	1.53
1	E	112	LEU	CG-CD2	5.26	1.70	1.52
1	F	116	ILE	N-CA	5.19	1.52	1.46
1	B	237	VAL	CA-CB	-5.08	1.47	1.53
1	B	318	MSE	CG-SE	5.03	2.10	1.95

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	219	ARG	CG-CD-NE	11.90	138.18	112.00
1	F	115	GLU	N-CA-C	-10.21	94.19	109.81
1	D	289	ARG	NE-CZ-NH2	9.91	128.12	119.20
1	D	289	ARG	NE-CZ-NH1	-9.06	112.44	121.50
1	F	115	GLU	CA-C-N	8.70	138.22	122.13
1	F	115	GLU	C-N-CA	8.70	138.22	122.13
1	F	286	GLY	N-CA-C	8.42	117.87	110.21
1	D	289	ARG	CD-NE-CZ	8.22	135.91	124.40
1	F	116	ILE	N-CA-C	7.65	125.40	108.88
1	B	143	GLY	CA-C-N	7.44	127.36	119.85
1	B	143	GLY	C-N-CA	7.44	127.36	119.85
1	E	89	ARG	CB-CG-CD	7.32	128.12	111.30
1	A	60	THR	N-CA-C	-7.26	104.30	113.01
1	C	143	GLY	CA-C-N	7.09	127.01	119.85
1	C	143	GLY	C-N-CA	7.09	127.01	119.85
1	A	37	PRO	CA-C-N	6.94	126.98	119.90
1	A	37	PRO	C-N-CA	6.94	126.98	119.90
1	A	112	LEU	CA-C-N	6.80	128.34	119.84
1	A	112	LEU	C-N-CA	6.80	128.34	119.84
1	F	112	LEU	CA-C-N	6.76	128.28	119.84
1	F	112	LEU	C-N-CA	6.76	128.28	119.84
1	A	251	HIS	N-CA-C	-6.72	103.20	111.40
1	B	60	THR	N-CA-C	-6.70	104.37	112.54
1	D	181	HIS	N-CA-C	6.70	119.84	107.99
1	A	286	GLY	N-CA-C	6.59	116.20	110.21
1	A	356	LYS	N-CA-C	6.58	118.11	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	GLN	N-CA-C	-6.56	103.40	111.40
1	B	289	ARG	CB-CA-C	-6.42	102.28	112.05
1	E	219	ARG	CD-NE-CZ	6.38	133.33	124.40
1	E	181	HIS	N-CA-C	6.35	119.06	108.20
1	C	356	LYS	N-CA-C	6.33	117.85	111.07
1	A	181	HIS	N-CA-C	6.32	119.50	107.75
1	E	60	THR	N-CA-C	-6.32	104.84	112.54
1	B	181	HIS	N-CA-C	6.20	119.28	107.75
1	E	37	PRO	CA-C-N	6.12	127.49	119.84
1	E	37	PRO	C-N-CA	6.12	127.49	119.84
1	F	60	THR	N-CA-C	-6.11	105.08	112.54
1	F	181	HIS	N-CA-C	6.11	119.12	107.75
1	D	143	GLY	CA-C-N	5.96	125.87	119.85
1	D	143	GLY	C-N-CA	5.96	125.87	119.85
1	B	356	LYS	N-CA-C	5.95	118.25	111.11
1	B	216	GLY	N-CA-C	5.95	119.87	112.73
1	D	128	VAL	CB-CA-C	-5.94	104.09	111.94
1	C	60	THR	N-CA-C	-5.91	105.33	112.54
1	E	89	ARG	CG-CD-NE	5.82	124.80	112.00
1	E	216	GLY	N-CA-C	5.79	119.89	112.83
1	C	181	HIS	N-CA-C	5.77	118.06	108.20
1	D	149	LYS	N-CA-C	-5.72	106.13	113.23
1	F	186	VAL	CB-CA-C	-5.69	103.59	110.99
1	C	89	ARG	CA-C-N	5.67	126.39	120.03
1	C	89	ARG	C-N-CA	5.67	126.39	120.03
1	B	186	VAL	N-CA-C	5.66	116.27	107.28
1	A	360	ARG	N-CA-C	-5.65	105.22	111.71
1	D	349	MSE	N-CA-C	-5.57	107.06	112.97
1	F	143	GLY	CA-C-N	5.56	125.47	119.85
1	F	143	GLY	C-N-CA	5.56	125.47	119.85
1	F	207	ARG	N-CA-C	-5.53	107.19	114.04
1	F	216	GLY	N-CA-C	5.50	119.33	112.73
1	D	34	ALA	N-CA-C	5.49	117.12	111.03
1	A	119	PHE	N-CA-C	5.46	117.99	111.71
1	F	289	ARG	CB-CA-C	-5.34	103.45	111.73
1	C	37	PRO	CA-C-N	5.31	126.47	119.84
1	C	37	PRO	C-N-CA	5.31	126.47	119.84
1	D	158	ASP	N-CA-C	5.29	117.05	111.28
1	D	60	THR	N-CA-C	-5.24	106.14	112.54
1	A	136	MSE	N-CA-C	5.24	116.40	108.07
1	C	207	ARG	N-CA-C	-5.23	107.56	114.04
1	C	297	ILE	CA-C-N	5.20	126.02	119.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	297	ILE	C-N-CA	5.20	126.02	119.98
1	C	128	VAL	CB-CA-C	-5.20	105.16	111.87
1	F	101	GLN	CA-C-N	-5.20	115.22	123.12
1	F	101	GLN	C-N-CA	-5.20	115.22	123.12
1	C	136	MSE	N-CA-C	5.18	116.31	108.07
1	C	119	PHE	N-CA-C	5.14	117.63	111.71
1	F	110	ARG	CA-C-N	-5.10	115.00	122.19
1	F	110	ARG	C-N-CA	-5.10	115.00	122.19
1	C	251	HIS	N-CA-C	-5.10	105.18	111.40
1	A	349	MSE	N-CA-C	-5.07	107.60	112.97
1	C	115	GLU	N-CA-C	5.05	116.09	108.46
1	E	113	PRO	N-CA-C	5.05	120.11	111.68
1	F	186	VAL	N-CA-C	5.03	115.28	107.28
1	F	124	LEU	CA-C-N	5.03	125.03	120.21
1	F	124	LEU	C-N-CA	5.03	125.03	120.21
1	F	360	ARG	N-CA-C	-5.03	105.93	111.71
1	F	35	GLY	N-CA-C	5.01	120.18	114.67
1	D	58	GLU	N-CA-C	-5.00	107.00	113.01
1	F	37	PRO	CA-C-N	5.00	126.09	119.84
1	F	37	PRO	C-N-CA	5.00	126.09	119.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	115	GLU	Peptide
1	F	114	ALA	Peptide
1	F	115	GLU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2717	0	2798	166	2
1	B	2717	0	2798	160	4
1	C	2717	0	2798	138	0
1	D	2717	0	2797	170	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2717	0	2798	188	0
1	F	2717	0	2798	159	0
2	B	5	0	0	6	0
2	C	5	0	0	4	0
2	E	5	0	0	3	0
3	F	27	0	12	7	0
All	All	16344	0	16799	879	5

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 27.

All (879) 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:136:MSE:SE	1:E:136:MSE:CE	2.14	1.44
1:B:136:MSE:SE	1:B:136:MSE:CE	2.14	1.44
1:A:136:MSE:CE	1:A:136:MSE:SE	2.18	1.42
1:A:218:MSE:CE	1:A:218:MSE:SE	2.18	1.41
1:C:136:MSE:SE	1:C:136:MSE:CE	2.19	1.41
1:D:136:MSE:SE	1:D:136:MSE:CE	2.23	1.35
1:A:304:ASN:OD1	1:B:259:LEU:HD21	1.29	1.26
1:A:71:LYS:NZ	1:A:196:LYS:HE2	1.53	1.24
1:E:229:ARG:NH1	1:F:144:PRO:HB2	1.52	1.22
1:C:264:GLN:HE22	1:D:353:PRO:HA	1.09	1.17
1:D:307:ARG:HD3	1:E:258:PRO:CA	1.77	1.15
1:C:264:GLN:NE2	1:D:353:PRO:HA	1.62	1.13
1:A:149:LYS:H	1:A:149:LYS:HD3	1.06	1.12
1:F:259:LEU:HA	1:F:262:GLN:HB2	1.31	1.12
1:B:149:LYS:HD3	1:B:149:LYS:H	1.12	1.11
1:D:307:ARG:CD	1:E:258:PRO:HA	1.81	1.10
1:A:232:GLU:O	1:B:219:ARG:HG3	1.52	1.09
1:E:149:LYS:HD3	1:E:149:LYS:H	1.12	1.09
1:B:259:LEU:HA	1:B:262:GLN:HB2	1.38	1.06
1:E:259:LEU:HA	1:E:262:GLN:HB2	1.36	1.06
1:D:149:LYS:H	1:D:149:LYS:HD3	1.18	1.06
1:A:136:MSE:SE	1:B:252:ARG:HH22	1.89	1.04
1:A:136:MSE:SE	1:B:252:ARG:NH2	2.41	1.04
1:A:71:LYS:HZ2	1:A:196:LYS:HE2	1.06	1.03
1:C:149:LYS:H	1:C:149:LYS:HD3	1.17	1.03
1:B:149:LYS:NZ	2:B:375:SO4:S	2.31	1.03
1:D:307:ARG:HD3	1:E:258:PRO:HA	1.08	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:ASP:OD1	1:B:281:LEU:O	1.78	1.02
1:D:259:LEU:HA	1:D:262:GLN:HB2	1.36	1.01
1:C:259:LEU:HA	1:C:262:GLN:HB2	1.41	0.98
1:D:233:THR:CB	1:E:219:ARG:HD2	1.92	0.97
1:C:331:ASN:HA	1:C:334:LEU:HD12	1.46	0.97
1:E:94:PHE:CD2	1:E:111:SER:HA	1.98	0.97
1:A:259:LEU:HA	1:A:262:GLN:HB2	1.43	0.97
1:E:267:ILE:HD13	1:F:355:PRO:HG2	1.44	0.96
1:A:331:ASN:HA	1:A:334:LEU:HD12	1.50	0.94
1:A:304:ASN:OD1	1:B:259:LEU:CD2	2.15	0.93
1:F:71:LYS:HZ2	1:F:196:LYS:HE2	1.32	0.93
1:B:331:ASN:HA	1:B:334:LEU:HD12	1.47	0.93
1:A:307:ARG:HD3	1:B:258:PRO:HG3	1.49	0.92
1:E:196:LYS:HE3	1:E:196:LYS:HA	1.53	0.91
1:A:271:PHE:CE1	1:B:256:ILE:HG22	2.06	0.91
1:F:71:LYS:NZ	1:F:196:LYS:HE2	1.83	0.90
1:E:331:ASN:HA	1:E:334:LEU:HD12	1.54	0.90
1:F:149:LYS:H	1:F:149:LYS:HD3	1.34	0.89
1:C:196:LYS:HE3	1:C:196:LYS:HA	1.52	0.89
1:D:331:ASN:HA	1:D:334:LEU:HD12	1.53	0.89
1:F:149:LYS:H	1:F:149:LYS:CD	1.88	0.87
1:D:136:MSE:SE	1:E:252:ARG:NH2	2.58	0.86
1:C:149:LYS:H	1:C:149:LYS:CD	1.89	0.86
1:D:233:THR:HB	1:E:219:ARG:HD2	1.56	0.86
1:F:331:ASN:HA	1:F:334:LEU:HD12	1.58	0.85
1:D:149:LYS:H	1:D:149:LYS:CD	1.89	0.85
1:E:271:PHE:CE2	1:F:350:GLU:OE1	2.29	0.85
1:A:149:LYS:H	1:A:149:LYS:CD	1.89	0.84
1:A:149:LYS:HD3	1:A:149:LYS:N	1.88	0.84
1:D:94:PHE:HD2	1:D:110:ARG:O	1.60	0.84
1:F:196:LYS:HE3	1:F:196:LYS:HA	1.59	0.84
1:A:271:PHE:CZ	1:B:256:ILE:HG22	2.12	0.84
1:C:42:ILE:O	1:C:43:ASP:HB2	1.77	0.84
1:F:149:LYS:NZ	3:F:500:ADP:PB	2.51	0.84
1:E:149:LYS:HD3	1:E:149:LYS:N	1.93	0.83
1:A:304:ASN:CG	1:B:259:LEU:HD21	2.02	0.83
1:C:267:ILE:CD1	1:D:355:PRO:HG2	2.08	0.83
1:E:38:PRO:HD3	1:E:56:THR:OG1	1.79	0.82
1:B:149:LYS:HD3	1:B:149:LYS:N	1.93	0.82
1:D:196:LYS:HA	1:D:196:LYS:HE3	1.61	0.82
1:F:149:LYS:HZ2	3:F:500:ADP:PB	2.02	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:94:PHE:HD2	1:E:111:SER:HA	1.42	0.82
1:A:122:LEU:O	1:A:291:LEU:HD23	1.80	0.81
1:A:304:ASN:HD21	1:B:259:LEU:HD23	1.44	0.81
1:F:85:SER:OG	1:F:190:GLU:OE1	1.98	0.81
1:A:71:LYS:HZ3	1:A:196:LYS:HE2	1.46	0.80
1:A:94:PHE:HD2	1:A:110:ARG:O	1.64	0.80
1:F:170:THR:OG1	1:F:188:GLN:HG2	1.81	0.80
1:B:161:ASN:HA	1:B:184:SER:OG	1.82	0.80
1:C:149:LYS:HD3	1:C:149:LYS:N	1.95	0.80
1:D:38:PRO:HD3	1:D:56:THR:OG1	1.82	0.80
1:E:229:ARG:HH12	1:F:144:PRO:HB2	1.46	0.80
1:E:149:LYS:H	1:E:149:LYS:CD	1.94	0.79
1:D:167:HIS:CE1	1:D:169:ILE:HD12	2.17	0.79
1:E:269:LEU:O	1:E:273:LEU:HB2	1.81	0.79
1:D:170:THR:HG22	1:D:214:PHE:HB3	1.65	0.79
1:B:94:PHE:HD2	1:B:110:ARG:O	1.66	0.79
1:D:170:THR:OG1	1:D:188:GLN:HG2	1.83	0.79
1:D:60:THR:HA	1:D:63:LEU:HD12	1.65	0.79
1:F:138:LEU:HD22	1:F:140:LEU:HD21	1.65	0.78
1:C:149:LYS:NZ	2:C:375:SO4:S	2.56	0.78
1:D:42:ILE:O	1:D:43:ASP:HB2	1.82	0.78
1:B:60:THR:HA	1:B:63:LEU:HD12	1.66	0.78
1:C:149:LYS:NZ	2:C:375:SO4:O1	2.16	0.78
1:C:170:THR:HG22	1:C:214:PHE:HB3	1.66	0.77
1:E:229:ARG:NH1	1:F:144:PRO:CB	2.43	0.77
1:B:149:LYS:H	1:B:149:LYS:CD	1.93	0.77
1:E:267:ILE:HD13	1:F:355:PRO:CG	2.15	0.77
1:E:335:TYR:HB2	1:E:358:LEU:HD11	1.67	0.77
1:C:170:THR:OG1	1:C:188:GLN:HG2	1.85	0.77
1:E:94:PHE:HE2	1:E:111:SER:HG	1.28	0.77
1:B:42:ILE:O	1:B:43:ASP:HB2	1.85	0.77
1:B:170:THR:OG1	1:B:188:GLN:HG2	1.85	0.76
1:A:60:THR:HA	1:A:63:LEU:HD12	1.67	0.76
1:C:60:THR:HA	1:C:63:LEU:HD12	1.66	0.76
1:A:307:ARG:HD3	1:B:258:PRO:CG	2.14	0.76
1:C:38:PRO:HD3	1:C:56:THR:OG1	1.86	0.76
1:B:284:LYS:HE3	1:B:342:LEU:HD23	1.67	0.76
1:B:335:TYR:HB2	1:B:358:LEU:HD11	1.67	0.76
1:A:196:LYS:HE3	1:A:196:LYS:HA	1.68	0.76
1:A:161:ASN:HA	1:A:184:SER:OG	1.86	0.76
1:E:170:THR:OG1	1:E:188:GLN:HG2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:VAL:HG13	1:A:92:GLY:H	1.52	0.75
1:C:264:GLN:NE2	1:D:353:PRO:CA	2.46	0.75
1:F:42:ILE:O	1:F:43:ASP:HB2	1.86	0.75
1:F:122:LEU:O	1:F:291:LEU:HD23	1.86	0.75
1:A:42:ILE:O	1:A:43:ASP:HB2	1.86	0.75
1:B:122:LEU:O	1:B:291:LEU:HD23	1.87	0.74
1:C:94:PHE:HD2	1:C:110:ARG:O	1.70	0.74
1:E:172:GLU:HG2	1:E:214:PHE:HE2	1.52	0.74
1:C:335:TYR:HB2	1:C:358:LEU:HD11	1.69	0.74
1:E:94:PHE:HD2	1:E:110:ARG:O	1.71	0.74
1:F:141:VAL:HG12	1:F:141:VAL:O	1.88	0.74
1:F:149:LYS:NZ	3:F:500:ADP:O1B	2.20	0.74
1:D:271:PHE:HE1	1:E:255:ASP:HB3	1.52	0.74
1:F:161:ASN:HA	1:F:184:SER:OG	1.87	0.74
1:C:138:LEU:HD22	1:C:140:LEU:HD21	1.70	0.74
1:D:136:MSE:SE	1:E:252:ARG:HH21	2.20	0.74
1:A:58:GLU:O	1:A:58:GLU:HG2	1.88	0.73
1:C:161:ASN:HA	1:C:184:SER:OG	1.87	0.73
1:C:267:ILE:HD13	1:D:355:PRO:HG2	1.70	0.73
1:A:170:THR:OG1	1:A:188:GLN:HG2	1.87	0.73
1:E:91:VAL:HG13	1:E:92:GLY:H	1.53	0.73
1:C:267:ILE:HD13	1:D:355:PRO:CG	2.18	0.73
1:C:205:ALA:HA	1:C:208:GLU:OE2	1.88	0.73
1:E:12:GLU:HA	1:E:52:PHE:CE1	2.23	0.73
1:D:149:LYS:HD3	1:D:149:LYS:N	1.94	0.73
1:D:172:GLU:HG2	1:D:214:PHE:HE2	1.53	0.73
1:F:269:LEU:O	1:F:273:LEU:HB2	1.89	0.73
1:E:94:PHE:HE2	1:E:111:SER:OG	1.72	0.72
1:C:271:PHE:CD1	1:D:346:GLU:HG3	2.23	0.72
1:F:38:PRO:HD3	1:F:56:THR:OG1	1.88	0.72
1:E:161:ASN:HA	1:E:184:SER:OG	1.88	0.72
1:C:122:LEU:O	1:C:291:LEU:HD23	1.90	0.72
1:C:63:LEU:O	1:C:66:SER:OG	2.08	0.72
1:D:30:ILE:CD1	1:D:32:LEU:HD21	2.20	0.71
1:D:161:ASN:HA	1:D:184:SER:OG	1.89	0.71
1:F:335:TYR:HB2	1:F:358:LEU:HD11	1.72	0.71
1:C:49:LEU:C	1:C:51:ASP:H	1.97	0.71
1:E:170:THR:HG22	1:E:214:PHE:HB3	1.72	0.71
1:D:269:LEU:O	1:D:273:LEU:HB2	1.91	0.71
1:E:94:PHE:CE2	1:E:111:SER:HA	2.25	0.70
1:B:76:LEU:HG	1:B:76:LEU:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:LEU:O	1:B:273:LEU:HB2	1.92	0.70
1:A:71:LYS:NZ	1:A:196:LYS:CE	2.45	0.70
1:F:119:PHE:CD1	1:F:129:LEU:HG	2.26	0.70
1:B:138:LEU:HD22	1:B:140:LEU:HD21	1.74	0.70
1:E:42:ILE:O	1:E:43:ASP:HB2	1.90	0.70
1:F:49:LEU:C	1:F:51:ASP:H	2.00	0.70
1:F:218:MSE:HE3	1:F:224:VAL:HG22	1.74	0.69
1:F:284:LYS:HE3	1:F:342:LEU:HD23	1.73	0.69
1:B:91:VAL:HG13	1:B:92:GLY:H	1.56	0.69
1:E:122:LEU:O	1:E:291:LEU:HD23	1.92	0.69
1:E:60:THR:HA	1:E:63:LEU:HD12	1.75	0.69
1:A:279:GLN:O	1:A:280:ARG:HG3	1.93	0.69
1:D:94:PHE:CD2	1:D:110:ARG:O	2.45	0.69
1:E:229:ARG:CZ	1:F:144:PRO:HB2	2.22	0.69
1:A:271:PHE:CZ	1:B:256:ILE:CG2	2.76	0.68
1:A:240:THR:C	1:A:241:LEU:HD12	2.19	0.68
1:A:138:LEU:HD22	1:A:140:LEU:HD21	1.76	0.68
1:D:307:ARG:HD3	1:E:258:PRO:CB	2.22	0.68
1:C:172:GLU:HG2	1:C:214:PHE:HE2	1.58	0.68
1:C:284:LYS:HE3	1:C:342:LEU:HD23	1.75	0.68
1:A:170:THR:HG22	1:A:214:PHE:HB3	1.75	0.68
1:A:195:THR:HG21	1:A:201:ALA:HB2	1.75	0.68
1:D:233:THR:HA	1:E:219:ARG:NE	2.09	0.68
1:E:172:GLU:HG2	1:E:214:PHE:CE2	2.28	0.68
1:E:96:ALA:HA	1:E:109:LEU:HD23	1.76	0.67
1:A:137:GLY:HA2	1:A:272:ILE:HG13	1.74	0.67
1:C:218:MSE:HE3	1:C:224:VAL:HG22	1.74	0.67
1:F:149:LYS:CD	1:F:149:LYS:N	2.58	0.67
1:A:188:GLN:H	1:B:101:GLN:HE21	1.41	0.67
1:B:218:MSE:HE3	1:B:224:VAL:HG22	1.76	0.67
1:F:12:GLU:HA	1:F:52:PHE:CE1	2.30	0.67
1:D:30:ILE:HD13	1:D:32:LEU:HD21	1.76	0.67
1:F:60:THR:HA	1:F:63:LEU:HD12	1.74	0.67
1:E:137:GLY:HA2	1:E:272:ILE:HG13	1.76	0.67
1:D:119:PHE:CD1	1:D:129:LEU:HG	2.30	0.67
1:D:335:TYR:HB2	1:D:358:LEU:HD11	1.76	0.67
1:D:122:LEU:O	1:D:291:LEU:HD23	1.95	0.66
1:D:284:LYS:HE3	1:D:342:LEU:HD23	1.76	0.66
1:C:208:GLU:HG2	1:D:99:PHE:CE1	2.30	0.66
1:A:335:TYR:HB2	1:A:358:LEU:HD11	1.77	0.66
1:C:273:LEU:HD11	1:C:276:ILE:HG13	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:GLU:HA	1:B:52:PHE:CE1	2.30	0.66
1:D:91:VAL:HG13	1:D:92:GLY:H	1.61	0.66
1:D:218:MSE:HE3	1:D:224:VAL:HG22	1.77	0.66
1:D:172:GLU:HG2	1:D:214:PHE:CE2	2.30	0.66
1:D:233:THR:HA	1:E:219:ARG:HE	1.60	0.66
1:B:149:LYS:O	1:B:153:ILE:HG12	1.96	0.66
1:D:149:LYS:CD	1:D:149:LYS:N	2.52	0.65
1:A:269:LEU:O	1:A:273:LEU:HB2	1.97	0.65
1:E:138:LEU:HD22	1:E:140:LEU:HD21	1.77	0.65
1:B:38:PRO:HD3	1:B:56:THR:OG1	1.97	0.65
1:B:149:LYS:HD3	2:B:375:SO4:O4	1.96	0.65
1:F:91:VAL:HG13	1:F:92:GLY:H	1.62	0.65
1:F:137:GLY:HA2	1:F:272:ILE:HG13	1.77	0.65
1:A:307:ARG:HD3	1:B:258:PRO:CB	2.26	0.65
1:D:273:LEU:HD11	1:D:276:ILE:HG13	1.79	0.65
1:A:271:PHE:CE1	1:B:256:ILE:CG2	2.79	0.65
1:A:12:GLU:HA	1:A:52:PHE:CE1	2.32	0.65
1:A:85:SER:OG	1:A:190:GLU:OE1	2.12	0.65
1:B:172:GLU:HG2	1:B:214:PHE:HE2	1.62	0.65
1:B:196:LYS:HE3	1:B:196:LYS:HA	1.77	0.65
1:C:264:GLN:NE2	1:D:353:PRO:O	2.29	0.64
1:A:49:LEU:C	1:A:51:ASP:H	2.05	0.64
1:D:188:GLN:H	1:E:101:GLN:HE21	1.45	0.64
1:D:224:VAL:HG21	1:D:256:ILE:HD11	1.80	0.64
1:E:69:SER:O	1:E:73:ARG:HG3	1.97	0.64
1:E:49:LEU:C	1:E:51:ASP:H	2.06	0.64
1:B:119:PHE:CD1	1:B:129:LEU:HG	2.33	0.64
1:F:94:PHE:HD2	1:F:110:ARG:O	1.80	0.64
1:D:138:LEU:HD22	1:D:140:LEU:HD21	1.80	0.64
1:D:304:ASN:OD1	1:E:259:LEU:HD11	1.98	0.64
1:C:149:LYS:CD	1:C:149:LYS:N	2.55	0.64
1:F:132:CYS:SG	1:F:156:MSE:HB3	2.37	0.64
1:F:269:LEU:HG	1:F:273:LEU:HD23	1.80	0.64
1:C:12:GLU:HA	1:C:52:PHE:CE1	2.33	0.63
1:D:71:LYS:HD3	1:D:192:GLY:O	1.98	0.63
1:E:150:SER:OG	2:E:375:SO4:O2	2.16	0.63
1:E:271:PHE:HE1	1:F:346:GLU:HG3	1.64	0.63
1:E:136:MSE:HE2	1:E:234:GLY:HA2	1.81	0.63
1:F:273:LEU:HD11	1:F:276:ILE:HG13	1.79	0.63
1:E:284:LYS:H	1:E:288:GLY:HA2	1.64	0.63
1:E:119:PHE:CD1	1:E:129:LEU:HG	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:HIS:ND1	1:A:210:PRO:HA	2.14	0.63
1:B:167:HIS:ND1	1:B:210:PRO:HA	2.13	0.63
1:D:167:HIS:HE1	1:D:169:ILE:HD12	1.62	0.63
1:F:76:LEU:O	1:F:76:LEU:HG	1.99	0.63
1:B:273:LEU:HD11	1:B:276:ILE:HG13	1.81	0.62
1:E:30:ILE:CD1	1:E:32:LEU:HD21	2.30	0.62
1:A:273:LEU:HD11	1:A:276:ILE:HG13	1.82	0.62
1:A:269:LEU:HG	1:A:273:LEU:HD23	1.80	0.62
1:A:284:LYS:HE3	1:A:342:LEU:HD23	1.82	0.62
1:B:94:PHE:CD2	1:B:110:ARG:O	2.50	0.62
1:F:195:THR:HG22	1:F:196:LYS:H	1.65	0.62
1:A:119:PHE:CD1	1:A:129:LEU:HG	2.35	0.62
1:B:170:THR:HG22	1:B:214:PHE:HB3	1.80	0.62
1:F:149:LYS:O	1:F:153:ILE:HG12	2.00	0.62
1:C:195:THR:HG21	1:C:201:ALA:HB2	1.82	0.62
1:E:36:ALA:HB1	1:E:37:PRO:HD2	1.82	0.61
1:A:71:LYS:HD2	1:A:196:LYS:HZ3	1.63	0.61
1:C:187:ASN:HA	1:D:101:GLN:HE21	1.65	0.61
1:C:269:LEU:O	1:C:273:LEU:HB2	1.99	0.61
1:F:294:GLU:HB2	1:F:330:MSE:HG2	1.82	0.61
1:C:264:GLN:CD	1:D:353:PRO:O	2.44	0.61
1:B:137:GLY:HA2	1:B:272:ILE:HG13	1.82	0.61
1:C:172:GLU:HG2	1:C:214:PHE:CE2	2.36	0.61
1:D:195:THR:HG22	1:D:196:LYS:H	1.66	0.61
1:F:149:LYS:HD3	1:F:149:LYS:N	2.10	0.61
1:E:264:GLN:HE21	1:F:353:PRO:HA	1.66	0.61
1:F:149:LYS:HZ3	3:F:500:ADP:PB	2.23	0.61
1:C:141:VAL:HG12	1:C:141:VAL:O	2.01	0.60
1:B:205:ALA:HA	1:B:208:GLU:OE2	2.00	0.60
1:D:67:VAL:HG13	1:D:86:PHE:CD1	2.35	0.60
1:D:137:GLY:HA2	1:D:272:ILE:HG13	1.83	0.60
1:A:99:PHE:CE1	1:F:208:GLU:HG2	2.36	0.60
1:B:149:LYS:N	1:B:149:LYS:CD	2.61	0.60
1:A:218:MSE:HE3	1:A:224:VAL:HG22	1.83	0.60
1:F:67:VAL:HG13	1:F:86:PHE:CD1	2.36	0.60
1:F:150:SER:OG	3:F:500:ADP:O3B	2.20	0.59
1:F:318:MSE:C	1:F:319:GLN:HG3	2.26	0.59
1:B:172:GLU:HG2	1:B:214:PHE:CE2	2.37	0.59
1:C:284:LYS:H	1:C:288:GLY:HA2	1.67	0.59
1:D:195:THR:HG21	1:D:201:ALA:HB2	1.84	0.59
1:E:224:VAL:HG21	1:E:256:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:THR:OG1	1:E:219:ARG:HD2	2.02	0.59
1:B:96:ALA:HA	1:B:109:LEU:HD23	1.84	0.59
1:D:12:GLU:HA	1:D:52:PHE:CE1	2.38	0.59
1:D:49:LEU:C	1:D:51:ASP:H	2.10	0.59
1:E:264:GLN:NE2	1:F:353:PRO:HA	2.17	0.59
1:F:141:VAL:HG12	1:F:149:LYS:HB3	1.84	0.59
1:A:271:PHE:CD1	1:B:256:ILE:HG22	2.38	0.58
1:A:304:ASN:HD21	1:B:259:LEU:CD2	2.13	0.58
1:E:114:ALA:O	1:E:115:GLU:HB3	2.01	0.58
1:A:71:LYS:CD	1:A:196:LYS:NZ	2.67	0.58
1:A:195:THR:HG22	1:A:196:LYS:H	1.68	0.58
1:B:162:GLN:HG2	1:B:182:LYS:HG2	1.85	0.58
1:C:69:SER:O	1:C:73:ARG:HG3	2.03	0.58
1:C:162:GLN:HG2	1:C:182:LYS:HG2	1.85	0.58
1:E:304:ASN:HD22	1:E:307:ARG:HH11	1.49	0.58
1:F:167:HIS:ND1	1:F:210:PRO:HA	2.19	0.58
1:D:205:ALA:HA	1:D:208:GLU:OE2	2.02	0.58
1:D:63:LEU:O	1:D:66:SER:OG	2.20	0.58
1:F:224:VAL:HG21	1:F:256:ILE:HD11	1.85	0.58
1:D:208:GLU:HG2	1:E:99:PHE:CE1	2.38	0.58
1:E:273:LEU:HD11	1:E:276:ILE:HG13	1.85	0.58
1:E:141:VAL:O	1:E:141:VAL:HG12	2.03	0.58
1:F:131:LEU:HD21	1:F:274:GLN:O	2.04	0.58
1:A:94:PHE:CD2	1:A:110:ARG:O	2.53	0.58
1:A:136:MSE:SE	1:B:252:ARG:HH21	2.34	0.58
1:A:304:ASN:CG	1:B:259:LEU:CD2	2.72	0.58
1:C:170:THR:HG1	1:C:188:GLN:HG2	1.68	0.58
1:A:101:GLN:HE21	1:F:187:ASN:HA	1.69	0.58
1:D:259:LEU:CA	1:D:262:GLN:HB2	2.24	0.58
1:E:94:PHE:HE2	1:E:111:SER:CB	2.16	0.58
1:E:166:TYR:O	1:E:184:SER:HB2	2.04	0.58
1:A:71:LYS:HD3	1:A:196:LYS:HZ1	1.69	0.57
1:A:304:ASN:ND2	1:B:259:LEU:CD2	2.67	0.57
1:E:271:PHE:CE1	1:F:346:GLU:HG3	2.40	0.57
1:F:349:MSE:SE	1:F:355:PRO:HA	2.54	0.57
1:C:304:ASN:HD22	1:C:307:ARG:HH11	1.52	0.57
1:F:358:LEU:C	1:F:360:ARG:H	2.13	0.57
1:C:56:THR:HG22	1:C:57:PRO:HD2	1.86	0.57
1:D:141:VAL:HG12	1:D:149:LYS:HB3	1.87	0.57
1:E:94:PHE:CD2	1:E:110:ARG:O	2.54	0.57
1:F:304:ASN:HD22	1:F:307:ARG:HH11	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:GLU:HG2	1:A:214:PHE:CE2	2.39	0.57
1:B:304:ASN:HD22	1:B:307:ARG:HH11	1.52	0.57
1:E:284:LYS:HE3	1:E:342:LEU:HD23	1.87	0.57
1:B:67:VAL:HG13	1:B:86:PHE:CD1	2.40	0.57
1:E:240:THR:C	1:E:241:LEU:HD12	2.30	0.57
1:F:49:LEU:C	1:F:51:ASP:N	2.63	0.57
1:A:304:ASN:ND2	1:B:259:LEU:HD23	2.18	0.56
1:B:224:VAL:HG21	1:B:256:ILE:HD11	1.86	0.56
1:E:131:LEU:HD21	1:E:274:GLN:O	2.06	0.56
1:E:294:GLU:HB2	1:E:330:MSE:HG2	1.87	0.56
1:C:279:GLN:O	1:C:280:ARG:HG3	2.05	0.56
1:C:91:VAL:HG13	1:C:92:GLY:H	1.70	0.56
1:D:167:HIS:ND1	1:D:210:PRO:HA	2.20	0.56
1:D:233:THR:HA	1:E:219:ARG:CD	2.36	0.56
1:E:67:VAL:HG13	1:E:86:PHE:CD1	2.40	0.56
1:E:218:MSE:HE3	1:E:224:VAL:HG22	1.86	0.56
1:A:205:ALA:HA	1:A:208:GLU:OE2	2.06	0.56
1:B:169:ILE:HG13	1:B:187:ASN:HB2	1.87	0.55
1:F:204:ALA:O	1:F:205:ALA:C	2.49	0.55
1:B:63:LEU:O	1:B:66:SER:OG	2.23	0.55
1:B:194:ASP:O	1:C:80:GLY:HA3	2.04	0.55
1:D:132:CYS:SG	1:D:156:MSE:HB3	2.47	0.55
1:C:94:PHE:CD2	1:C:110:ARG:O	2.55	0.55
1:D:96:ALA:HA	1:D:109:LEU:HD23	1.88	0.55
1:E:68:MSE:HE3	1:E:82:VAL:HG21	1.88	0.55
1:B:284:LYS:H	1:B:288:GLY:HA2	1.71	0.55
1:C:67:VAL:HG13	1:C:86:PHE:CD1	2.41	0.55
1:D:36:ALA:HB1	1:D:37:PRO:HD2	1.89	0.55
1:F:95:ARG:NH1	1:F:174:PRO:HD3	2.21	0.55
1:D:294:GLU:HB2	1:D:330:MSE:HG2	1.89	0.55
1:A:307:ARG:HD3	1:B:258:PRO:HB3	1.86	0.55
1:B:195:THR:HG21	1:B:201:ALA:HB2	1.89	0.55
1:C:141:VAL:HG12	1:C:149:LYS:HB3	1.88	0.55
1:E:270:SER:HB3	1:E:306:ILE:HB	1.88	0.55
1:B:269:LEU:HG	1:B:273:LEU:HD23	1.89	0.55
1:B:279:GLN:O	1:B:280:ARG:HG3	2.07	0.55
1:D:162:GLN:HG2	1:D:182:LYS:HG2	1.89	0.55
1:D:56:THR:HG22	1:D:57:PRO:HD2	1.89	0.55
1:F:279:GLN:O	1:F:280:ARG:HG3	2.07	0.55
1:C:49:LEU:C	1:C:51:ASP:N	2.62	0.55
1:A:76:LEU:O	1:A:76:LEU:HG	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:267:ILE:CD1	1:D:355:PRO:CG	2.81	0.54
1:D:31:HIS:C	1:D:32:LEU:HD23	2.32	0.54
1:A:141:VAL:HG12	1:A:141:VAL:O	2.06	0.54
1:B:240:THR:C	1:B:241:LEU:HD12	2.32	0.54
1:D:229:ARG:O	1:D:233:THR:HG22	2.06	0.54
1:E:149:LYS:O	1:E:153:ILE:HG12	2.06	0.54
1:E:271:PHE:CD2	1:F:350:GLU:OE1	2.59	0.54
1:F:170:THR:HG22	1:F:214:PHE:HB3	1.89	0.54
1:A:67:VAL:HG13	1:A:86:PHE:CD1	2.41	0.54
1:B:131:LEU:HD21	1:B:274:GLN:O	2.07	0.54
1:D:207:ARG:HD2	1:E:83:ASP:OD1	2.07	0.54
1:E:269:LEU:HG	1:E:273:LEU:HD23	1.90	0.54
1:F:169:ILE:HG13	1:F:187:ASN:HB2	1.89	0.54
1:F:240:THR:C	1:F:241:LEU:HD12	2.31	0.54
1:A:71:LYS:HZ3	1:A:196:LYS:CE	2.14	0.54
1:E:56:THR:HG22	1:E:57:PRO:HD2	1.90	0.54
1:C:196:LYS:HE3	1:C:196:LYS:CA	2.32	0.54
1:D:122:LEU:HD21	1:D:152:THR:HA	1.89	0.54
1:A:131:LEU:HD21	1:A:274:GLN:O	2.08	0.54
1:E:187:ASN:HA	1:F:101:GLN:HE21	1.72	0.54
1:E:309:ASN:O	1:E:311:LEU:HG	2.08	0.54
1:A:56:THR:HG22	1:A:57:PRO:HD2	1.90	0.54
1:B:49:LEU:C	1:B:51:ASP:H	2.14	0.54
1:B:259:LEU:CA	1:B:262:GLN:HB2	2.25	0.54
1:E:15:ILE:HG23	1:E:16:LEU:H	1.73	0.54
1:E:168:ILE:HG23	1:E:212:VAL:HB	1.90	0.54
1:F:119:PHE:CE1	1:F:129:LEU:HG	2.43	0.54
1:B:210:PRO:HG2	1:B:213:ILE:HD11	1.89	0.54
1:C:22:ALA:O	1:C:27:ALA:CB	2.56	0.54
1:D:232:GLU:O	1:E:219:ARG:HD3	2.08	0.54
1:D:233:THR:CA	1:E:219:ARG:HD2	2.37	0.54
1:F:195:THR:HG21	1:F:201:ALA:HB2	1.89	0.54
1:A:71:LYS:HD2	1:A:196:LYS:NZ	2.22	0.54
1:A:270:SER:HB3	1:A:306:ILE:HB	1.89	0.54
1:C:137:GLY:HA2	1:C:272:ILE:HG13	1.89	0.54
1:F:138:LEU:HD22	1:F:140:LEU:CD2	2.36	0.54
1:D:240:THR:C	1:D:241:LEU:HD12	2.33	0.53
1:D:304:ASN:HD22	1:D:307:ARG:HH11	1.57	0.53
1:E:259:LEU:HD23	1:E:259:LEU:H	1.71	0.53
1:F:205:ALA:HA	1:F:208:GLU:OE2	2.07	0.53
1:A:169:ILE:HG13	1:A:187:ASN:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:PHE:HB3	1:B:53:PRO:HD3	1.88	0.53
1:F:202:LEU:O	1:F:205:ALA:N	2.42	0.53
1:C:149:LYS:HD3	2:C:375:SO4:O3	2.08	0.53
1:D:271:PHE:CE1	1:E:255:ASP:HB3	2.40	0.53
1:E:167:HIS:ND1	1:E:210:PRO:HA	2.24	0.53
1:A:96:ALA:HA	1:A:109:LEU:HD23	1.90	0.53
1:B:65:TYR:HD1	1:B:73:ARG:NH1	2.07	0.53
1:C:270:SER:HB3	1:C:306:ILE:HB	1.90	0.53
1:E:49:LEU:C	1:E:51:ASP:N	2.65	0.53
1:A:172:GLU:HG2	1:A:214:PHE:HE2	1.71	0.53
1:F:153:ILE:O	1:F:154:ALA:C	2.52	0.53
1:E:149:LYS:N	1:E:149:LYS:CD	2.62	0.53
1:F:71:LYS:HZ2	1:F:196:LYS:CE	2.15	0.53
1:F:136:MSE:HE2	1:F:234:GLY:HA2	1.90	0.53
1:C:42:ILE:O	1:C:43:ASP:CB	2.53	0.53
1:C:119:PHE:CD1	1:C:129:LEU:HG	2.43	0.53
1:F:71:LYS:NZ	1:F:196:LYS:CE	2.64	0.53
1:E:149:LYS:NZ	2:E:375:SO4:O1	2.42	0.53
1:F:151:THR:OG1	3:F:500:ADP:O1A	2.24	0.53
1:F:166:TYR:O	1:F:184:SER:HB2	2.09	0.53
1:C:122:LEU:HD21	1:C:152:THR:HA	1.90	0.53
1:E:169:ILE:HG13	1:E:187:ASN:HB2	1.90	0.53
1:F:63:LEU:O	1:F:66:SER:OG	2.27	0.53
1:F:86:PHE:H	1:F:86:PHE:HD2	1.56	0.53
1:D:304:ASN:OD1	1:E:259:LEU:CD1	2.56	0.53
1:B:146:GLY:N	2:B:375:SO4:O3	2.38	0.52
1:D:131:LEU:HD21	1:D:274:GLN:O	2.09	0.52
1:E:30:ILE:HD13	1:E:32:LEU:HD21	1.89	0.52
1:A:65:TYR:CD1	1:A:73:ARG:HD2	2.43	0.52
1:A:122:LEU:HD21	1:A:152:THR:HA	1.91	0.52
1:D:76:LEU:HG	1:D:76:LEU:O	2.09	0.52
1:E:132:CYS:SG	1:E:156:MSE:HB3	2.49	0.52
1:F:94:PHE:CD2	1:F:111:SER:HA	2.44	0.52
1:A:358:LEU:C	1:A:360:ARG:H	2.17	0.52
1:B:69:SER:O	1:B:73:ARG:HG3	2.09	0.52
1:B:185:ILE:HD11	1:C:33:THR:HB	1.91	0.52
1:D:269:LEU:HG	1:D:273:LEU:HD23	1.91	0.52
1:C:229:ARG:O	1:C:233:THR:HG22	2.08	0.52
1:F:96:ALA:HA	1:F:109:LEU:HD23	1.92	0.52
1:C:138:LEU:HD22	1:C:140:LEU:CD2	2.39	0.52
1:E:358:LEU:C	1:E:360:ARG:H	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:GLU:HB2	1:C:330:MSE:HG2	1.92	0.52
1:F:153:ILE:O	1:F:155:SER:N	2.43	0.52
1:A:195:THR:HG22	1:A:196:LYS:N	2.24	0.52
1:A:207:ARG:HD2	1:B:83:ASP:OD1	2.10	0.52
1:B:68:MSE:SE	1:B:98:VAL:HG21	2.60	0.52
1:B:149:LYS:NZ	2:B:375:SO4:O3	2.38	0.52
1:C:131:LEU:HD21	1:C:274:GLN:O	2.10	0.52
1:D:169:ILE:HG13	1:D:187:ASN:HB2	1.90	0.52
1:D:200:ASP:HB2	1:E:81:GLN:HE22	1.74	0.52
1:E:205:ALA:HA	1:E:208:GLU:OE2	2.10	0.52
1:A:86:PHE:H	1:A:86:PHE:HD2	1.57	0.52
1:D:49:LEU:C	1:D:51:ASP:N	2.68	0.52
1:D:149:LYS:O	1:D:153:ILE:HG12	2.09	0.52
1:A:208:GLU:HG2	1:B:99:PHE:CE1	2.45	0.52
1:B:56:THR:HG22	1:B:57:PRO:HD2	1.90	0.52
1:E:22:ALA:O	1:E:27:ALA:CB	2.58	0.52
1:F:270:SER:HB3	1:F:306:ILE:HB	1.92	0.52
1:C:76:LEU:O	1:C:76:LEU:HG	2.10	0.52
1:C:170:THR:HB	1:C:214:PHE:HD2	1.75	0.52
1:F:331:ASN:ND2	1:F:352:SER:OG	2.43	0.51
1:B:105:VAL:HG12	1:B:106:ALA:N	2.25	0.51
1:B:264:GLN:HA	1:B:267:ILE:HD12	1.90	0.51
1:F:196:LYS:HE3	1:F:196:LYS:CA	2.38	0.51
1:A:309:ASN:O	1:A:311:LEU:HG	2.10	0.51
1:C:271:PHE:CD1	1:D:346:GLU:CG	2.91	0.51
1:D:85:SER:OG	1:D:174:PRO:HB2	2.11	0.51
1:C:224:VAL:HG21	1:C:256:ILE:HD11	1.93	0.51
1:C:240:THR:C	1:C:241:LEU:HD12	2.35	0.51
1:F:68:MSE:HE3	1:F:82:VAL:HG21	1.92	0.51
1:A:85:SER:OG	1:A:174:PRO:HB2	2.10	0.51
1:D:30:ILE:CD1	1:D:32:LEU:CD2	2.87	0.51
1:A:84:PHE:CE2	1:A:96:ALA:HB3	2.46	0.51
1:C:169:ILE:HG13	1:C:187:ASN:HB2	1.91	0.51
1:A:187:ASN:HA	1:B:101:GLN:HE21	1.76	0.50
1:E:267:ILE:CD1	1:F:355:PRO:HG2	2.29	0.50
1:F:102:ARG:C	1:F:104:SER:H	2.19	0.50
1:B:187:ASN:HA	1:C:101:GLN:HE21	1.76	0.50
1:C:167:HIS:CE1	1:C:169:ILE:HD12	2.47	0.50
1:F:172:GLU:HG2	1:F:214:PHE:CE2	2.46	0.50
1:A:144:PRO:HB2	1:F:229:ARG:NH1	2.27	0.50
1:D:69:SER:O	1:D:73:ARG:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:200:ASP:HB2	1:E:81:GLN:NE2	2.26	0.50
1:D:347:ASP:O	1:D:350:GLU:HB3	2.11	0.50
1:E:279:GLN:O	1:E:280:ARG:HG3	2.10	0.50
1:E:122:LEU:HD21	1:E:152:THR:HA	1.92	0.50
1:C:130:GLU:HG2	1:C:134:ARG:HH21	1.77	0.50
1:D:113:PRO:HB2	1:D:177:TYR:CE1	2.46	0.50
1:E:52:PHE:HB3	1:E:53:PRO:HD3	1.93	0.50
1:B:294:GLU:HB2	1:B:330:MSE:HG2	1.92	0.50
1:C:264:GLN:HA	1:C:267:ILE:HD12	1.93	0.50
1:D:195:THR:HG22	1:D:196:LYS:N	2.24	0.50
1:E:15:ILE:HG23	1:E:16:LEU:N	2.27	0.50
1:A:54:ARG:O	1:A:55:LEU:C	2.53	0.50
1:B:94:PHE:CD2	1:B:111:SER:HA	2.47	0.50
1:C:175:ILE:HD11	1:C:190:GLU:HB2	1.92	0.50
1:D:279:GLN:O	1:D:280:ARG:HG3	2.11	0.50
1:E:105:VAL:HG12	1:E:106:ALA:N	2.27	0.50
1:E:171:ILE:HD11	1:E:202:LEU:HA	1.93	0.50
1:F:52:PHE:O	1:F:53:PRO:C	2.55	0.50
1:F:149:LYS:HD3	3:F:500:ADP:O3B	2.12	0.50
1:F:168:ILE:HG23	1:F:212:VAL:HB	1.93	0.50
1:B:142:THR:HG21	1:B:249:THR:OG1	2.12	0.50
1:E:48:PHE:CD1	1:E:48:PHE:N	2.80	0.50
1:E:284:LYS:HG2	1:E:286:GLY:H	1.76	0.50
1:F:135:LYS:HD3	1:F:135:LYS:H	1.77	0.50
1:A:41:ARG:HD3	1:A:44:GLY:HA2	1.94	0.50
1:B:195:THR:HG22	1:B:196:LYS:H	1.76	0.50
1:C:166:TYR:O	1:C:184:SER:HB2	2.12	0.50
1:D:168:ILE:HG23	1:D:212:VAL:HB	1.94	0.50
1:E:167:HIS:CE1	1:E:169:ILE:HD12	2.47	0.50
1:A:294:GLU:HB2	1:A:330:MSE:HG2	1.93	0.49
1:B:358:LEU:C	1:B:360:ARG:H	2.20	0.49
1:C:358:LEU:C	1:C:360:ARG:H	2.19	0.49
1:A:102:ARG:C	1:A:104:SER:H	2.19	0.49
1:A:158:ASP:O	1:A:161:ASN:HB3	2.13	0.49
1:D:229:ARG:O	1:D:233:THR:CG2	2.60	0.49
1:E:36:ALA:HB1	1:E:37:PRO:CD	2.41	0.49
1:F:122:LEU:HD21	1:F:152:THR:HA	1.94	0.49
1:A:36:ALA:HB1	1:A:37:PRO:HD2	1.94	0.49
1:D:41:ARG:HD3	1:D:44:GLY:HA2	1.94	0.49
1:A:233:THR:HB	1:B:219:ARG:HG2	1.94	0.49
1:A:331:ASN:ND2	1:A:352:SER:OG	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:ASP:O	1:D:80:GLY:HA3	2.12	0.49
1:E:195:THR:HG22	1:E:196:LYS:H	1.78	0.49
1:B:135:LYS:H	1:B:135:LYS:HD3	1.78	0.49
1:B:167:HIS:CE1	1:B:169:ILE:HD12	2.48	0.49
1:B:122:LEU:HD21	1:B:152:THR:HA	1.94	0.49
1:B:218:MSE:HE2	1:B:241:LEU:HD11	1.94	0.49
1:E:31:HIS:C	1:E:32:LEU:HD23	2.38	0.49
1:E:210:PRO:HG2	1:E:213:ILE:HD11	1.93	0.49
1:F:210:PRO:HG2	1:F:213:ILE:HD11	1.94	0.49
1:A:22:ALA:O	1:A:27:ALA:CB	2.60	0.49
1:E:284:LYS:N	1:E:288:GLY:HA2	2.28	0.49
1:A:49:LEU:C	1:A:51:ASP:N	2.68	0.48
1:A:299:ASN:O	1:A:301:ALA:N	2.46	0.48
1:A:224:VAL:HG21	1:A:256:ILE:HD11	1.95	0.48
1:B:31:HIS:C	1:B:32:LEU:HD23	2.38	0.48
1:B:94:PHE:HD2	1:B:111:SER:HA	1.77	0.48
1:C:22:ALA:O	1:C:27:ALA:HB3	2.13	0.48
1:C:349:MSE:SE	1:C:355:PRO:HA	2.63	0.48
1:F:52:PHE:HB3	1:F:53:PRO:HD3	1.94	0.48
1:A:284:LYS:H	1:A:288:GLY:HA2	1.78	0.48
1:B:36:ALA:HB1	1:B:37:PRO:HD2	1.95	0.48
1:B:331:ASN:ND2	1:B:352:SER:OG	2.47	0.48
1:E:347:ASP:O	1:E:350:GLU:HB3	2.14	0.48
1:F:254:VAL:HG12	1:F:262:GLN:HG2	1.94	0.48
1:A:202:LEU:O	1:A:205:ALA:N	2.46	0.48
1:E:195:THR:HG21	1:E:201:ALA:HB2	1.95	0.48
1:E:254:VAL:HG12	1:E:262:GLN:HG2	1.95	0.48
1:F:172:GLU:HG2	1:F:214:PHE:HE2	1.77	0.48
1:A:240:THR:O	1:A:241:LEU:HD12	2.12	0.48
1:A:284:LYS:HG2	1:A:286:GLY:H	1.79	0.48
1:C:96:ALA:HA	1:C:109:LEU:HD23	1.96	0.48
1:C:132:CYS:SG	1:C:156:MSE:HB3	2.54	0.48
1:D:38:PRO:HD3	1:D:56:THR:HG1	1.79	0.48
1:D:119:PHE:CE1	1:D:129:LEU:HG	2.48	0.48
1:E:264:GLN:HA	1:E:267:ILE:HD12	1.95	0.48
1:F:229:ARG:O	1:F:233:THR:HG22	2.13	0.48
1:A:52:PHE:HB3	1:A:53:PRO:HD3	1.96	0.48
1:B:168:ILE:HG23	1:B:212:VAL:HB	1.95	0.48
1:C:218:MSE:HE2	1:C:241:LEU:HD11	1.95	0.48
1:E:149:LYS:NZ	2:E:375:SO4:O3	2.28	0.48
1:F:31:HIS:C	1:F:32:LEU:HD23	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:36:ALA:HB1	1:F:37:PRO:HD2	1.94	0.48
1:F:69:SER:O	1:F:73:ARG:HG3	2.14	0.48
1:A:312:GLN:CD	1:A:312:GLN:H	2.21	0.48
1:B:86:PHE:CE2	1:B:94:PHE:HB2	2.49	0.48
1:C:86:PHE:H	1:C:86:PHE:HD2	1.62	0.48
1:E:63:LEU:O	1:E:66:SER:OG	2.29	0.48
1:F:171:ILE:HD11	1:F:202:LEU:HA	1.95	0.48
1:E:52:PHE:O	1:E:53:PRO:C	2.57	0.47
1:E:129:LEU:HD23	1:E:129:LEU:HA	1.56	0.47
1:A:93:ARG:CZ	1:A:178:VAL:HG23	2.45	0.47
1:B:284:LYS:HG2	1:B:286:GLY:H	1.78	0.47
1:D:257:PHE:CZ	1:D:265:VAL:HG21	2.49	0.47
1:E:196:LYS:HA	1:E:196:LYS:CE	2.36	0.47
1:A:344:THR:C	1:A:346:GLU:H	2.23	0.47
1:D:42:ILE:O	1:D:43:ASP:CB	2.56	0.47
1:A:254:VAL:HG12	1:A:262:GLN:HG2	1.96	0.47
1:A:271:PHE:CE2	1:B:256:ILE:HG22	2.49	0.47
1:C:264:GLN:NE2	1:D:353:PRO:C	2.72	0.47
1:D:175:ILE:H	1:D:175:ILE:HG13	1.53	0.47
1:E:333:THR:O	1:E:333:THR:HG22	2.14	0.47
1:B:343:ILE:HD12	1:B:348:ALA:HB2	1.96	0.47
1:C:149:LYS:O	1:C:153:ILE:HG12	2.14	0.47
1:C:267:ILE:HD13	1:D:355:PRO:HG3	1.94	0.47
1:A:182:LYS:HB3	1:A:183:LYS:H	1.58	0.47
1:A:229:ARG:O	1:A:233:THR:CG2	2.62	0.47
1:B:136:MSE:HE2	1:B:234:GLY:HA2	1.96	0.47
1:D:52:PHE:HB3	1:D:53:PRO:HD3	1.95	0.47
1:D:271:PHE:CE2	1:E:252:ARG:NH1	2.82	0.47
1:E:265:VAL:O	1:E:269:LEU:HB2	2.15	0.47
1:A:204:ALA:O	1:A:205:ALA:C	2.55	0.47
1:B:48:PHE:CD1	1:B:48:PHE:N	2.82	0.47
1:C:188:GLN:H	1:D:101:GLN:HE21	1.62	0.47
1:D:86:PHE:CE2	1:D:94:PHE:HB2	2.49	0.47
1:D:210:PRO:HG2	1:D:213:ILE:HD11	1.95	0.47
1:E:162:GLN:HG2	1:E:182:LYS:HG2	1.97	0.47
1:F:56:THR:HG22	1:F:57:PRO:HD2	1.96	0.47
1:F:94:PHE:HD2	1:F:111:SER:HA	1.78	0.47
1:B:130:GLU:HG2	1:B:134:ARG:HH21	1.79	0.47
1:E:41:ARG:HD3	1:E:44:GLY:HA2	1.96	0.47
1:A:304:ASN:HD22	1:A:307:ARG:HH11	1.61	0.47
1:C:135:LYS:H	1:C:135:LYS:HD3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:ALA:O	1:D:27:ALA:CB	2.63	0.47
1:E:196:LYS:HE3	1:E:196:LYS:CA	2.37	0.47
1:B:270:SER:HB3	1:B:306:ILE:HB	1.96	0.47
1:F:86:PHE:CE2	1:F:94:PHE:HB2	2.49	0.47
1:F:95:ARG:HB2	1:F:112:LEU:HG	1.96	0.47
1:F:229:ARG:O	1:F:233:THR:CG2	2.63	0.47
1:B:304:ASN:ND2	1:B:307:ARG:HH11	2.12	0.46
1:C:41:ARG:HD3	1:C:44:GLY:HA2	1.97	0.46
1:A:202:LEU:O	1:A:205:ALA:HB3	2.14	0.46
1:B:141:VAL:HG12	1:B:141:VAL:O	2.15	0.46
1:C:30:ILE:CD1	1:C:32:LEU:HD21	2.45	0.46
1:B:229:ARG:CZ	1:B:229:ARG:HB3	2.46	0.46
1:C:182:LYS:HB3	1:C:183:LYS:H	1.51	0.46
1:D:86:PHE:H	1:D:86:PHE:HD2	1.63	0.46
1:D:141:VAL:HG12	1:D:141:VAL:O	2.15	0.46
1:A:128:VAL:C	1:A:130:GLU:N	2.71	0.46
1:A:229:ARG:O	1:A:233:THR:HG22	2.15	0.46
1:F:94:PHE:CD2	1:F:110:ARG:O	2.66	0.46
1:B:141:VAL:HB	1:B:153:ILE:HD11	1.97	0.46
1:A:340:GLN:HB3	1:A:342:LEU:HD12	1.97	0.46
1:E:331:ASN:ND2	1:E:352:SER:OG	2.49	0.46
1:F:284:LYS:H	1:F:288:GLY:HA2	1.80	0.46
1:A:261:GLN:O	1:A:262:GLN:C	2.57	0.46
1:B:138:LEU:HD22	1:B:140:LEU:CD2	2.44	0.46
1:C:36:ALA:HB1	1:C:37:PRO:HD2	1.98	0.46
1:D:343:ILE:HD12	1:D:348:ALA:HB2	1.98	0.46
1:A:15:ILE:HG23	1:A:16:LEU:N	2.30	0.46
1:B:254:VAL:HG12	1:B:262:GLN:HG2	1.97	0.46
1:C:267:ILE:HD11	1:D:355:PRO:HG2	1.92	0.46
1:E:257:PHE:CZ	1:E:265:VAL:HG21	2.50	0.46
1:E:304:ASN:ND2	1:E:307:ARG:HH11	2.13	0.46
1:A:149:LYS:O	1:A:153:ILE:HG12	2.16	0.46
1:A:226:THR:O	1:A:227:ALA:C	2.58	0.46
1:D:318:MSE:C	1:D:319:GLN:HG3	2.41	0.46
1:C:229:ARG:O	1:C:233:THR:CG2	2.64	0.45
1:C:257:PHE:CZ	1:C:265:VAL:HG21	2.51	0.45
1:D:154:ALA:HB2	1:D:177:TYR:CD2	2.52	0.45
1:A:14:LYS:O	1:A:15:ILE:C	2.58	0.45
1:D:153:ILE:O	1:D:154:ALA:C	2.60	0.45
1:F:257:PHE:CZ	1:F:265:VAL:HG21	2.51	0.45
1:B:182:LYS:HB3	1:B:183:LYS:H	1.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:331:ASN:ND2	1:C:352:SER:OG	2.49	0.45
1:D:15:ILE:HG23	1:D:16:LEU:H	1.80	0.45
1:E:218:MSE:HE2	1:E:241:LEU:HD11	1.98	0.45
1:C:318:MSE:C	1:C:319:GLN:HG3	2.41	0.45
1:D:136:MSE:SE	1:E:252:ARG:HH22	2.42	0.45
1:E:42:ILE:O	1:E:43:ASP:CB	2.57	0.45
1:A:69:SER:O	1:A:73:ARG:HG3	2.16	0.45
1:B:17:GLU:HA	1:B:20:LYS:HB2	1.99	0.45
1:B:49:LEU:C	1:B:51:ASP:N	2.74	0.45
1:B:58:GLU:O	1:B:58:GLU:HG2	2.17	0.45
1:C:31:HIS:C	1:C:32:LEU:HD23	2.42	0.45
1:E:61:GLN:O	1:E:65:TYR:HB2	2.17	0.45
1:A:71:LYS:CD	1:A:196:LYS:HZ1	2.29	0.45
1:A:259:LEU:CA	1:A:262:GLN:HB2	2.32	0.45
1:B:86:PHE:HD2	1:B:86:PHE:H	1.63	0.45
1:B:126:ASP:N	1:B:126:ASP:OD2	2.49	0.45
1:A:167:HIS:CE1	1:A:169:ILE:HD12	2.52	0.45
1:E:58:GLU:O	1:E:58:GLU:HG2	2.17	0.45
1:E:68:MSE:HB3	1:E:72:HIS:HB2	1.98	0.45
1:E:343:ILE:HD12	1:E:348:ALA:HB2	1.99	0.45
1:C:196:LYS:HA	1:C:196:LYS:CE	2.37	0.45
1:C:261:GLN:O	1:C:262:GLN:C	2.60	0.45
1:D:358:LEU:C	1:D:360:ARG:H	2.24	0.45
1:F:102:ARG:C	1:F:104:SER:N	2.73	0.45
1:E:94:PHE:CE2	1:E:111:SER:OG	2.53	0.45
1:F:65:TYR:CD1	1:F:73:ARG:HD2	2.52	0.45
1:F:195:THR:HG22	1:F:196:LYS:N	2.30	0.45
1:F:358:LEU:C	1:F:360:ARG:N	2.73	0.45
1:E:54:ARG:O	1:E:56:THR:N	2.50	0.45
1:E:340:GLN:HB3	1:E:342:LEU:HD12	1.99	0.45
1:F:84:PHE:CE2	1:F:96:ALA:HB3	2.52	0.45
1:D:161:ASN:HA	1:D:184:SER:HG	1.82	0.44
1:D:271:PHE:HE2	1:E:252:ARG:NH1	2.15	0.44
1:E:22:ALA:O	1:E:27:ALA:HB3	2.16	0.44
1:E:142:THR:HG21	1:E:249:THR:OG1	2.17	0.44
1:E:259:LEU:CA	1:E:262:GLN:HB2	2.25	0.44
1:E:358:LEU:O	1:E:360:ARG:N	2.41	0.44
1:A:101:GLN:HE21	1:F:188:GLN:H	1.64	0.44
1:A:223:THR:O	1:A:224:VAL:C	2.57	0.44
1:B:52:PHE:O	1:B:53:PRO:C	2.59	0.44
1:B:149:LYS:NZ	2:B:375:SO4:O4	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:284:LYS:HG2	1:C:286:GLY:H	1.82	0.44
1:D:23:ILE:H	1:D:23:ILE:HG13	1.61	0.44
1:D:135:LYS:H	1:D:135:LYS:HD3	1.82	0.44
1:D:284:LYS:H	1:D:288:GLY:HA2	1.81	0.44
1:E:102:ARG:C	1:E:104:SER:H	2.25	0.44
1:F:167:HIS:CE1	1:F:169:ILE:HD12	2.51	0.44
1:A:86:PHE:CD2	1:A:86:PHE:N	2.85	0.44
1:A:307:ARG:CD	1:B:258:PRO:HB3	2.48	0.44
1:A:347:ASP:O	1:A:350:GLU:HB3	2.17	0.44
1:C:68:MSE:HE3	1:C:82:VAL:HG21	1.99	0.44
1:C:212:VAL:HG13	1:C:236:LEU:HB3	1.99	0.44
1:D:264:GLN:HA	1:D:267:ILE:HD12	2.00	0.44
1:F:312:GLN:CD	1:F:312:GLN:H	2.26	0.44
1:A:42:ILE:O	1:A:43:ASP:CB	2.59	0.44
1:B:102:ARG:C	1:B:104:SER:H	2.25	0.44
1:B:309:ASN:O	1:B:311:LEU:HG	2.17	0.44
1:A:129:LEU:HA	1:A:129:LEU:HD23	1.55	0.44
1:D:15:ILE:HG23	1:D:16:LEU:N	2.33	0.44
1:D:312:GLN:H	1:D:312:GLN:CD	2.25	0.44
1:A:54:ARG:O	1:A:56:THR:N	2.50	0.44
1:C:146:GLY:N	2:C:375:SO4:O1	2.35	0.44
1:D:68:MSE:HE3	1:D:82:VAL:HG21	1.99	0.44
1:D:142:THR:HG21	1:D:249:THR:OG1	2.18	0.44
1:E:170:THR:HB	1:E:214:PHE:HD2	1.83	0.44
1:E:271:PHE:CE2	1:F:350:GLU:CD	2.94	0.44
1:D:348:ALA:C	1:D:350:GLU:H	2.25	0.44
1:F:298:PRO:HB2	1:F:303:ARG:HH11	1.82	0.44
1:C:34:ALA:O	1:C:56:THR:O	2.36	0.44
1:E:135:LYS:H	1:E:135:LYS:HD3	1.83	0.44
1:C:229:ARG:NH1	1:D:144:PRO:HB2	2.33	0.44
1:D:165:SER:HB3	1:E:46:ILE:H	1.82	0.44
1:A:264:GLN:HA	1:A:267:ILE:HD12	2.00	0.43
1:B:158:ASP:O	1:B:161:ASN:HB3	2.18	0.43
1:B:175:ILE:H	1:B:175:ILE:HG13	1.56	0.43
1:F:207:ARG:C	1:F:209:ASP:H	2.25	0.43
1:C:167:HIS:ND1	1:C:210:PRO:HA	2.31	0.43
1:D:182:LYS:HB3	1:D:183:LYS:H	1.46	0.43
1:D:333:THR:HG22	1:D:333:THR:O	2.19	0.43
1:E:358:LEU:C	1:E:360:ARG:N	2.76	0.43
1:B:119:PHE:CE1	1:B:129:LEU:HG	2.53	0.43
1:C:71:LYS:NZ	1:C:196:LYS:HE2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:30:ILE:HD12	1:D:32:LEU:CD2	2.48	0.43
1:E:30:ILE:CD1	1:E:32:LEU:CD2	2.94	0.43
1:E:154:ALA:HB2	1:E:177:TYR:CD2	2.52	0.43
1:E:171:ILE:CD1	1:E:202:LEU:HA	2.48	0.43
1:C:195:THR:HG21	1:C:201:ALA:CB	2.48	0.43
1:D:284:LYS:HG2	1:D:286:GLY:H	1.83	0.43
1:F:86:PHE:N	1:F:86:PHE:CD2	2.86	0.43
1:F:171:ILE:CD1	1:F:202:LEU:HA	2.49	0.43
1:B:112:LEU:HA	1:B:113:PRO:HD3	1.84	0.43
1:B:261:GLN:O	1:B:262:GLN:C	2.61	0.43
1:E:291:LEU:HD12	1:E:291:LEU:C	2.43	0.43
1:F:175:ILE:H	1:F:175:ILE:HG13	1.66	0.43
1:F:259:LEU:CA	1:F:262:GLN:HB2	2.22	0.43
1:A:86:PHE:CE2	1:A:94:PHE:HB2	2.54	0.43
1:B:84:PHE:CE2	1:B:96:ALA:HB3	2.53	0.43
1:B:284:LYS:N	1:B:288:GLY:HA2	2.34	0.43
1:B:358:LEU:O	1:B:360:ARG:N	2.42	0.43
1:C:17:GLU:HA	1:C:20:LYS:HB2	2.00	0.43
1:C:269:LEU:HG	1:C:273:LEU:HD23	2.00	0.43
1:A:31:HIS:C	1:A:32:LEU:HD23	2.43	0.43
1:A:218:MSE:HE2	1:A:241:LEU:HD11	1.99	0.43
1:B:65:TYR:CD1	1:B:73:ARG:HD2	2.54	0.43
1:C:333:THR:HG22	1:C:333:THR:O	2.19	0.43
1:D:233:THR:CA	1:E:219:ARG:CD	2.97	0.43
1:F:30:ILE:CD1	1:F:32:LEU:HD21	2.48	0.43
1:F:343:ILE:HD12	1:F:348:ALA:HB2	2.00	0.43
1:C:173:ASP:HA	1:C:174:PRO:HA	1.86	0.43
1:F:42:ILE:O	1:F:43:ASP:CB	2.62	0.43
1:A:212:VAL:HG13	1:A:236:LEU:HB3	2.01	0.42
1:B:30:ILE:CD1	1:B:32:LEU:HD21	2.49	0.42
1:C:228:LEU:O	1:C:231:ALA:N	2.52	0.42
1:D:48:PHE:CD1	1:D:48:PHE:N	2.87	0.42
1:E:12:GLU:HB3	1:E:52:PHE:CZ	2.54	0.42
1:F:152:THR:O	1:F:153:ILE:C	2.61	0.42
1:A:22:ALA:O	1:A:27:ALA:HB3	2.19	0.42
1:B:344:THR:C	1:B:346:GLU:H	2.26	0.42
1:D:309:ASN:O	1:D:311:LEU:HG	2.18	0.42
1:E:344:THR:C	1:E:346:GLU:H	2.27	0.42
1:F:237:VAL:O	1:F:237:VAL:HG12	2.19	0.42
1:A:52:PHE:O	1:A:53:PRO:C	2.62	0.42
1:E:138:LEU:HD22	1:E:140:LEU:CD2	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:153:ILE:O	1:E:154:ALA:C	2.61	0.42
1:F:333:THR:HG22	1:F:333:THR:O	2.19	0.42
1:B:68:MSE:HE3	1:B:82:VAL:HG21	2.01	0.42
1:F:309:ASN:O	1:F:311:LEU:HG	2.20	0.42
1:A:15:ILE:HG23	1:A:16:LEU:H	1.84	0.42
1:A:30:ILE:HG13	1:A:109:LEU:HB2	2.01	0.42
1:A:333:THR:HG22	1:A:333:THR:O	2.19	0.42
1:B:195:THR:HG22	1:B:196:LYS:N	2.34	0.42
1:C:202:LEU:O	1:C:205:ALA:HB3	2.20	0.42
1:E:84:PHE:CE2	1:E:96:ALA:HB3	2.54	0.42
1:F:58:GLU:HG2	1:F:58:GLU:O	2.18	0.42
1:A:112:LEU:HA	1:A:113:PRO:HD2	1.74	0.42
1:A:195:THR:HG21	1:A:201:ALA:CB	2.46	0.42
1:D:254:VAL:HG12	1:D:262:GLN:HG2	2.01	0.42
1:A:102:ARG:C	1:A:104:SER:N	2.77	0.42
1:A:162:GLN:HG2	1:A:182:LYS:HG2	2.01	0.42
1:A:272:ILE:HD12	1:A:272:ILE:HA	1.91	0.42
1:B:282:LEU:HB3	1:B:283:PRO:HD2	2.02	0.42
1:C:254:VAL:HG12	1:C:262:GLN:HG2	2.02	0.42
1:C:358:LEU:C	1:C:360:ARG:N	2.77	0.42
1:D:61:GLN:O	1:D:65:TYR:HB2	2.20	0.42
1:D:102:ARG:C	1:D:104:SER:H	2.27	0.42
1:B:41:ARG:HD3	1:B:44:GLY:HA2	2.02	0.42
1:B:358:LEU:C	1:B:360:ARG:N	2.78	0.42
1:D:58:GLU:O	1:D:58:GLU:HG2	2.20	0.42
1:E:153:ILE:O	1:E:155:SER:N	2.53	0.42
1:A:210:PRO:HG2	1:A:213:ILE:HD11	2.01	0.42
1:C:175:ILE:H	1:C:175:ILE:HG13	1.53	0.42
1:D:291:LEU:HD12	1:D:292:ALA:N	2.35	0.42
1:F:130:GLU:HG2	1:F:134:ARG:HH21	1.85	0.42
1:D:270:SER:HB3	1:D:306:ILE:HB	2.01	0.42
1:E:229:ARG:CZ	1:E:229:ARG:HB3	2.49	0.42
1:F:15:ILE:HG23	1:F:16:LEU:H	1.85	0.42
1:B:197:SER:C	1:B:199:ALA:N	2.77	0.41
1:C:229:ARG:CZ	1:C:229:ARG:HB3	2.50	0.41
1:E:86:PHE:CE2	1:E:94:PHE:HB2	2.55	0.41
1:E:94:PHE:CE2	1:E:111:SER:CA	2.99	0.41
1:E:152:THR:O	1:E:155:SER:HB2	2.20	0.41
1:E:169:ILE:O	1:E:169:ILE:CG2	2.68	0.41
1:F:17:GLU:HA	1:F:20:LYS:HB2	2.02	0.41
1:F:129:LEU:HD23	1:F:129:LEU:HA	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:PHE:CE2	1:C:94:PHE:HB2	2.55	0.41
1:C:269:LEU:HD12	1:C:269:LEU:HA	1.96	0.41
1:C:284:LYS:N	1:C:288:GLY:HA2	2.32	0.41
1:D:207:ARG:C	1:D:209:ASP:H	2.28	0.41
1:F:214:PHE:O	1:F:214:PHE:CG	2.71	0.41
1:A:233:THR:HA	1:B:219:ARG:HE	1.85	0.41
1:B:152:THR:O	1:B:155:SER:HB2	2.20	0.41
1:C:49:LEU:O	1:C:51:ASP:N	2.53	0.41
1:F:49:LEU:O	1:F:51:ASP:N	2.53	0.41
1:D:187:ASN:HA	1:E:101:GLN:HE21	1.86	0.41
1:E:105:VAL:CG1	1:E:106:ALA:N	2.83	0.41
1:E:291:LEU:HD12	1:E:292:ALA:N	2.34	0.41
1:A:358:LEU:C	1:A:360:ARG:N	2.76	0.41
1:B:42:ILE:O	1:B:43:ASP:CB	2.59	0.41
1:B:71:LYS:HB3	1:B:71:LYS:HE2	1.81	0.41
1:B:149:LYS:NZ	2:B:375:SO4:O2	2.53	0.41
1:C:128:VAL:CG2	1:C:295:LEU:HD11	2.51	0.41
1:D:166:TYR:O	1:D:184:SER:HB2	2.21	0.41
1:F:226:THR:O	1:F:227:ALA:C	2.64	0.41
1:A:149:LYS:CD	1:A:149:LYS:N	2.59	0.41
1:D:125:PRO:HD3	1:D:293:TYR:OH	2.21	0.41
1:E:40:VAL:HG12	1:E:42:ILE:HG13	2.03	0.41
1:E:269:LEU:HD12	1:E:269:LEU:HA	1.82	0.41
1:E:298:PRO:HB2	1:E:303:ARG:HH11	1.86	0.41
1:D:153:ILE:O	1:D:155:SER:N	2.54	0.41
1:A:101:GLN:NE2	1:F:187:ASN:HA	2.35	0.41
1:A:188:GLN:H	1:B:101:GLN:NE2	2.13	0.41
1:A:298:PRO:HB2	1:A:303:ARG:HH11	1.86	0.41
1:B:233:THR:HG23	1:B:235:HIS:CE1	2.56	0.41
1:B:289:ARG:HA	1:B:289:ARG:HD3	1.68	0.41
1:B:312:GLN:H	1:B:312:GLN:CD	2.28	0.41
1:F:12:GLU:HB3	1:F:52:PHE:CZ	2.56	0.41
1:F:15:ILE:HG23	1:F:16:LEU:N	2.36	0.41
1:C:207:ARG:C	1:C:209:ASP:H	2.28	0.41
1:D:130:GLU:HG2	1:D:134:ARG:HH21	1.86	0.41
1:D:226:THR:HA	1:D:229:ARG:HB2	2.03	0.41
1:D:257:PHE:CE1	1:D:265:VAL:HG21	2.56	0.41
1:D:261:GLN:O	1:D:262:GLN:C	2.63	0.41
1:D:344:THR:C	1:D:346:GLU:H	2.28	0.41
1:E:112:LEU:HA	1:E:113:PRO:HD3	1.79	0.41
1:E:175:ILE:HD11	1:E:190:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:195:THR:HG22	1:E:196:LYS:N	2.36	0.41
1:F:36:ALA:HB1	1:F:37:PRO:CD	2.51	0.41
1:B:298:PRO:HB2	1:B:303:ARG:HH11	1.86	0.41
1:C:68:MSE:HB2	1:C:73:ARG:HG2	2.03	0.41
1:C:86:PHE:N	1:C:86:PHE:CD2	2.89	0.41
1:A:68:MSE:HE3	1:A:82:VAL:HG21	2.03	0.40
1:A:233:THR:HG23	1:A:235:HIS:CE1	2.55	0.40
1:C:205:ALA:O	1:C:210:PRO:HG3	2.21	0.40
1:D:230:ALA:HA	1:D:233:THR:HG22	2.03	0.40
1:E:185:ILE:HD11	1:F:33:THR:HB	2.02	0.40
1:F:48:PHE:CD1	1:F:48:PHE:N	2.89	0.40
1:B:257:PHE:CZ	1:B:265:VAL:HG21	2.56	0.40
1:E:318:MSE:C	1:E:319:GLN:HG3	2.46	0.40
1:F:41:ARG:HD3	1:F:44:GLY:HA2	2.03	0.40
1:F:95:ARG:CZ	1:F:174:PRO:HG3	2.52	0.40
1:F:261:GLN:O	1:F:262:GLN:C	2.63	0.40
1:F:318:MSE:O	1:F:319:GLN:HG3	2.19	0.40
1:F:347:ASP:O	1:F:350:GLU:HB3	2.21	0.40
1:A:128:VAL:CG2	1:A:295:LEU:HD11	2.51	0.40
1:D:228:LEU:O	1:D:232:GLU:HG2	2.20	0.40
1:F:131:LEU:C	1:F:133:HIS:H	2.29	0.40
1:A:95:ARG:HB2	1:A:112:LEU:HG	2.02	0.40
1:A:348:ALA:C	1:A:350:GLU:H	2.30	0.40
1:B:153:ILE:O	1:B:154:ALA:C	2.64	0.40
1:B:207:ARG:C	1:B:209:ASP:H	2.29	0.40
1:C:347:ASP:O	1:C:350:GLU:HB3	2.21	0.40
1:A:23:ILE:H	1:A:23:ILE:HG13	1.59	0.40
1:B:318:MSE:C	1:B:319:GLN:HG3	2.46	0.40
1:C:126:ASP:OD2	1:C:126:ASP:N	2.53	0.40
1:C:334:LEU:HD22	1:C:348:ALA:HB1	2.03	0.40
1:D:138:LEU:HD22	1:D:140:LEU:CD2	2.50	0.40
1:E:312:GLN:H	1:E:312:GLN:CD	2.30	0.40

All (5) 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)
1:B:310:LYS:NZ	1:D:319:GLN:OE1[4_555]	1.37	0.83
1:A:73:ARG:NH2	1:A:73:ARG:NH2[2_554]	1.77	0.43
1:B:310:LYS:NZ	1:D:319:GLN:CD[4_555]	2.06	0.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:GLU:OE1	1:B:61:GLN:NE2[2_554]	2.07	0.13
1:B:345:LEU:CD2	1:D:24:GLU:O[1_565]	2.12	0.08

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	339/363 (93%)	279 (82%)	52 (15%)	8 (2%)	4	28
1	B	339/363 (93%)	276 (81%)	54 (16%)	9 (3%)	4	26
1	C	339/363 (93%)	278 (82%)	51 (15%)	10 (3%)	3	24
1	D	339/363 (93%)	277 (82%)	54 (16%)	8 (2%)	4	28
1	E	339/363 (93%)	280 (83%)	51 (15%)	8 (2%)	4	28
1	F	339/363 (93%)	279 (82%)	49 (14%)	11 (3%)	3	22
All	All	2034/2178 (93%)	1669 (82%)	311 (15%)	54 (3%)	4	26

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	114	ALA
1	A	199	ALA
1	C	50	LYS
1	C	55	LEU
1	D	55	LEU
1	D	199	ALA
1	E	55	LEU
1	F	50	LYS
1	F	116	ILE
1	A	52	PHE
1	B	55	LEU
1	B	116	ILE
1	C	113	PRO

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Mol	Chain	Res	Type
1	C	199	ALA
1	D	153	ILE
1	E	52	PHE
1	E	199	ALA
1	F	55	LEU
1	F	199	ALA
1	A	55	LEU
1	A	113	PRO
1	A	300	THR
1	B	52	PHE
1	B	198	PHE
1	B	199	ALA
1	C	52	PHE
1	C	114	ALA
1	C	208	GLU
1	D	50	LYS
1	D	52	PHE
1	D	97	ASN
1	D	154	ALA
1	E	154	ALA
1	E	359	GLU
1	F	52	PHE
1	F	97	ASN
1	A	57	PRO
1	C	153	ILE
1	C	359	GLU
1	E	50	LYS
1	F	57	PRO
1	F	300	THR
1	F	359	GLU
1	A	50	LYS
1	B	208	GLU
1	C	57	PRO
1	B	153	ILE
1	D	57	PRO
1	F	113	PRO
1	E	57	PRO
1	E	153	ILE
1	B	57	PRO
1	A	210	PRO
1	F	153	ILE

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	297/303 (98%)	237 (80%)	60 (20%)	1	9
1	B	297/303 (98%)	233 (78%)	64 (22%)	1	6
1	C	297/303 (98%)	234 (79%)	63 (21%)	1	7
1	D	297/303 (98%)	237 (80%)	60 (20%)	1	9
1	E	297/303 (98%)	236 (80%)	61 (20%)	1	8
1	F	297/303 (98%)	236 (80%)	61 (20%)	1	8
All	All	1782/1818 (98%)	1413 (79%)	369 (21%)	1	7

All (369) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	15	ILE
1	A	23	ILE
1	A	29	ASP
1	A	30	ILE
1	A	42	ILE
1	A	49	LEU
1	A	54	ARG
1	A	56	THR
1	A	58	GLU
1	A	71	LYS
1	A	74	GLN
1	A	75	LYS
1	A	79	ASN
1	A	82	VAL
1	A	85	SER
1	A	86	PHE
1	A	89	ARG
1	A	95	ARG
1	A	104	SER
1	A	111	SER
1	A	112	LEU

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Mol	Chain	Res	Type
1	A	118	GLU
1	A	126	ASP
1	A	129	LEU
1	A	135	LYS
1	A	149	LYS
1	A	150	SER
1	A	169	ILE
1	A	175	ILE
1	A	183	LYS
1	A	185	ILE
1	A	196	LYS
1	A	200	ASP
1	A	202	LEU
1	A	206	LEU
1	A	219	ARG
1	A	221	LEU
1	A	226	THR
1	A	229	ARG
1	A	240	THR
1	A	244	ASN
1	A	251	HIS
1	A	261	GLN
1	A	263	GLU
1	A	272	ILE
1	A	273	LEU
1	A	289	ARG
1	A	290	VAL
1	A	291	LEU
1	A	295	LEU
1	A	300	THR
1	A	312	GLN
1	A	313	GLN
1	A	317	LEU
1	A	319	GLN
1	A	327	MSE
1	A	329	THR
1	A	330	MSE
1	A	359	GLU
1	B	12	GLU
1	B	15	ILE
1	B	19	ILE
1	B	23	ILE

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Mol	Chain	Res	Type
1	B	29	ASP
1	B	30	ILE
1	B	38	PRO
1	B	40	VAL
1	B	42	ILE
1	B	48	PHE
1	B	49	LEU
1	B	54	ARG
1	B	56	THR
1	B	58	GLU
1	B	71	LYS
1	B	74	GLN
1	B	75	LYS
1	B	79	ASN
1	B	82	VAL
1	B	85	SER
1	B	89	ARG
1	B	95	ARG
1	B	104	SER
1	B	115	GLU
1	B	118	GLU
1	B	126	ASP
1	B	129	LEU
1	B	135	LYS
1	B	149	LYS
1	B	169	ILE
1	B	175	ILE
1	B	182	LYS
1	B	183	LYS
1	B	185	ILE
1	B	196	LYS
1	B	200	ASP
1	B	202	LEU
1	B	206	LEU
1	B	217	GLU
1	B	219	ARG
1	B	221	LEU
1	B	226	THR
1	B	228	LEU
1	B	229	ARG
1	B	240	THR
1	B	244	ASN

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Mol	Chain	Res	Type
1	B	251	HIS
1	B	261	GLN
1	B	263	GLU
1	B	272	ILE
1	B	273	LEU
1	B	289	ARG
1	B	290	VAL
1	B	291	LEU
1	B	295	LEU
1	B	300	THR
1	B	312	GLN
1	B	313	GLN
1	B	317	LEU
1	B	319	GLN
1	B	327	MSE
1	B	329	THR
1	B	330	MSE
1	B	359	GLU
1	C	12	GLU
1	C	15	ILE
1	C	23	ILE
1	C	29	ASP
1	C	30	ILE
1	C	40	VAL
1	C	42	ILE
1	C	48	PHE
1	C	49	LEU
1	C	54	ARG
1	C	56	THR
1	C	58	GLU
1	C	71	LYS
1	C	74	GLN
1	C	75	LYS
1	C	82	VAL
1	C	85	SER
1	C	89	ARG
1	C	95	ARG
1	C	104	SER
1	C	118	GLU
1	C	124	LEU
1	C	126	ASP
1	C	129	LEU

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Mol	Chain	Res	Type
1	C	135	LYS
1	C	149	LYS
1	C	150	SER
1	C	169	ILE
1	C	175	ILE
1	C	182	LYS
1	C	183	LYS
1	C	185	ILE
1	C	196	LYS
1	C	200	ASP
1	C	202	LEU
1	C	206	LEU
1	C	217	GLU
1	C	219	ARG
1	C	221	LEU
1	C	226	THR
1	C	228	LEU
1	C	229	ARG
1	C	240	THR
1	C	244	ASN
1	C	251	HIS
1	C	252	ARG
1	C	259	LEU
1	C	261	GLN
1	C	263	GLU
1	C	272	ILE
1	C	273	LEU
1	C	290	VAL
1	C	291	LEU
1	C	295	LEU
1	C	300	THR
1	C	312	GLN
1	C	313	GLN
1	C	317	LEU
1	C	319	GLN
1	C	327	MSE
1	C	329	THR
1	C	330	MSE
1	C	359	GLU
1	D	12	GLU
1	D	15	ILE
1	D	19	ILE

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Mol	Chain	Res	Type
1	D	23	ILE
1	D	29	ASP
1	D	30	ILE
1	D	32	LEU
1	D	42	ILE
1	D	48	PHE
1	D	49	LEU
1	D	54	ARG
1	D	56	THR
1	D	58	GLU
1	D	71	LYS
1	D	74	GLN
1	D	75	LYS
1	D	82	VAL
1	D	85	SER
1	D	89	ARG
1	D	95	ARG
1	D	104	SER
1	D	124	LEU
1	D	126	ASP
1	D	129	LEU
1	D	135	LYS
1	D	149	LYS
1	D	150	SER
1	D	169	ILE
1	D	175	ILE
1	D	182	LYS
1	D	183	LYS
1	D	185	ILE
1	D	196	LYS
1	D	200	ASP
1	D	202	LEU
1	D	206	LEU
1	D	219	ARG
1	D	221	LEU
1	D	226	THR
1	D	228	LEU
1	D	229	ARG
1	D	240	THR
1	D	244	ASN
1	D	251	HIS
1	D	261	GLN

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Mol	Chain	Res	Type
1	D	263	GLU
1	D	273	LEU
1	D	289	ARG
1	D	290	VAL
1	D	291	LEU
1	D	295	LEU
1	D	300	THR
1	D	312	GLN
1	D	313	GLN
1	D	317	LEU
1	D	319	GLN
1	D	327	MSE
1	D	329	THR
1	D	330	MSE
1	D	359	GLU
1	E	12	GLU
1	E	15	ILE
1	E	19	ILE
1	E	23	ILE
1	E	29	ASP
1	E	30	ILE
1	E	40	VAL
1	E	42	ILE
1	E	43	ASP
1	E	48	PHE
1	E	49	LEU
1	E	54	ARG
1	E	56	THR
1	E	58	GLU
1	E	71	LYS
1	E	74	GLN
1	E	75	LYS
1	E	79	ASN
1	E	82	VAL
1	E	85	SER
1	E	95	ARG
1	E	104	SER
1	E	115	GLU
1	E	126	ASP
1	E	129	LEU
1	E	135	LYS
1	E	149	LYS

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Mol	Chain	Res	Type
1	E	150	SER
1	E	169	ILE
1	E	175	ILE
1	E	182	LYS
1	E	183	LYS
1	E	185	ILE
1	E	191	VAL
1	E	196	LYS
1	E	200	ASP
1	E	202	LEU
1	E	215	VAL
1	E	219	ARG
1	E	221	LEU
1	E	226	THR
1	E	229	ARG
1	E	240	THR
1	E	244	ASN
1	E	251	HIS
1	E	261	GLN
1	E	263	GLU
1	E	272	ILE
1	E	273	LEU
1	E	289	ARG
1	E	290	VAL
1	E	291	LEU
1	E	295	LEU
1	E	300	THR
1	E	312	GLN
1	E	313	GLN
1	E	319	GLN
1	E	327	MSE
1	E	329	THR
1	E	330	MSE
1	E	359	GLU
1	F	12	GLU
1	F	15	ILE
1	F	23	ILE
1	F	29	ASP
1	F	30	ILE
1	F	42	ILE
1	F	49	LEU
1	F	54	ARG

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Mol	Chain	Res	Type
1	F	56	THR
1	F	58	GLU
1	F	71	LYS
1	F	74	GLN
1	F	75	LYS
1	F	79	ASN
1	F	82	VAL
1	F	85	SER
1	F	89	ARG
1	F	95	ARG
1	F	104	SER
1	F	115	GLU
1	F	116	ILE
1	F	118	GLU
1	F	126	ASP
1	F	129	LEU
1	F	135	LYS
1	F	149	LYS
1	F	150	SER
1	F	169	ILE
1	F	175	ILE
1	F	182	LYS
1	F	183	LYS
1	F	185	ILE
1	F	196	LYS
1	F	200	ASP
1	F	202	LEU
1	F	206	LEU
1	F	217	GLU
1	F	219	ARG
1	F	221	LEU
1	F	226	THR
1	F	228	LEU
1	F	229	ARG
1	F	240	THR
1	F	244	ASN
1	F	251	HIS
1	F	261	GLN
1	F	263	GLU
1	F	272	ILE
1	F	273	LEU
1	F	289	ARG

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Mol	Chain	Res	Type
1	F	290	VAL
1	F	291	LEU
1	F	295	LEU
1	F	300	THR
1	F	312	GLN
1	F	313	GLN
1	F	317	LEU
1	F	319	GLN
1	F	329	THR
1	F	330	MSE
1	F	359	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (58) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	HIS
1	A	74	GLN
1	A	133	HIS
1	A	187	ASN
1	A	261	GLN
1	A	312	GLN
1	A	313	GLN
1	A	331	ASN
1	B	72	HIS
1	B	74	GLN
1	B	101	GLN
1	B	133	HIS
1	B	161	ASN
1	B	187	ASN
1	B	260	ASN
1	B	261	GLN
1	B	304	ASN
1	B	312	GLN
1	B	313	GLN
1	B	331	ASN
1	C	74	GLN
1	C	133	HIS
1	C	161	ASN
1	C	187	ASN
1	C	260	ASN
1	C	261	GLN
1	C	264	GLN

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Mol	Chain	Res	Type
1	C	304	ASN
1	C	312	GLN
1	C	313	GLN
1	D	161	ASN
1	D	251	HIS
1	D	260	ASN
1	D	261	GLN
1	D	312	GLN
1	E	72	HIS
1	E	74	GLN
1	E	187	ASN
1	E	242	HIS
1	E	260	ASN
1	E	261	GLN
1	E	304	ASN
1	E	309	ASN
1	E	312	GLN
1	E	313	GLN
1	E	331	ASN
1	F	72	HIS
1	F	74	GLN
1	F	133	HIS
1	F	181	HIS
1	F	187	ASN
1	F	251	HIS
1	F	260	ASN
1	F	261	GLN
1	F	304	ASN
1	F	312	GLN
1	F	313	GLN
1	F	331	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are 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	ADP	F	500	-	28,29,29	2.04	7 (25%)	43,45,45	2.10	10 (23%)
2	SO4	C	375	-	4,4,4	0.35	0	6,6,6	0.52	0
2	SO4	B	375	-	4,4,4	1.55	1 (25%)	6,6,6	1.47	1 (16%)
2	SO4	E	375	-	4,4,4	2.24	1 (25%)	6,6,6	0.64	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
3	ADP	F	500	-	-	2/16/32/32	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	500	ADP	C5-C4	6.15	1.50	1.39
3	F	500	ADP	PA-O3A	5.22	1.65	1.59
2	E	375	SO4	O2-S	3.92	1.68	1.44
3	F	500	ADP	C5-C6	3.58	1.51	1.41
3	F	500	ADP	C8-N7	2.75	1.37	1.31
2	B	375	SO4	O2-S	2.46	1.59	1.44
3	F	500	ADP	C1'-N9	2.33	1.52	1.46
3	F	500	ADP	C4-N3	2.28	1.38	1.34
3	F	500	ADP	O4'-C1'	2.20	1.47	1.42

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	500	ADP	C5-C4-N3	-6.77	117.40	126.72
3	F	500	ADP	N3-C4-N9	5.30	136.19	127.17
3	F	500	ADP	C2-N3-C4	4.24	122.18	111.83
3	F	500	ADP	N3-C2-N1	-3.76	122.89	128.58
3	F	500	ADP	O4'-C1'-N9	3.71	115.22	108.09
3	F	500	ADP	C4-C5-N7	-3.65	106.41	110.58
3	F	500	ADP	O3B-PB-O3A	2.67	113.59	104.64
2	B	375	SO4	O4-S-O2	2.63	123.31	109.56
3	F	500	ADP	C5-N7-C8	2.60	107.54	103.45
3	F	500	ADP	C2-N1-C6	2.38	122.64	118.73
3	F	500	ADP	O3A-PB-O1B	-2.17	99.64	111.04

There are no chirality outliers.

All (2) torsion outliers are listed below:

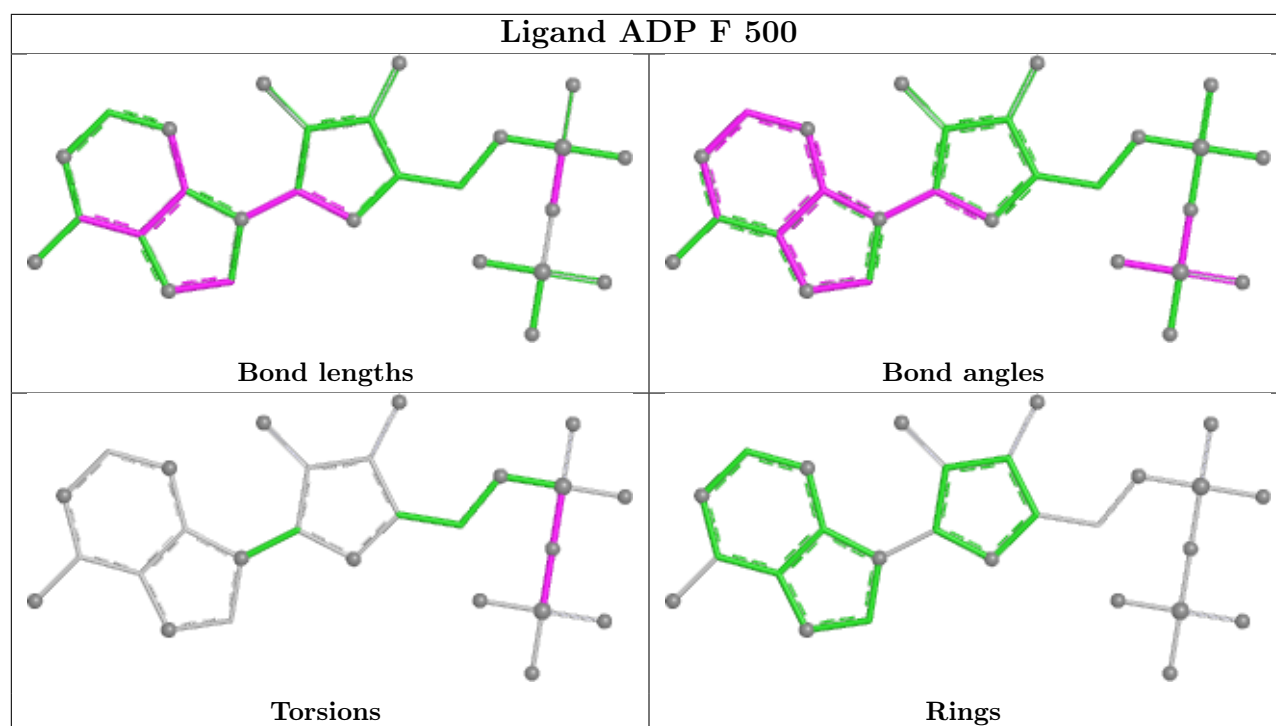
Mol	Chain	Res	Type	Atoms
3	F	500	ADP	PA-O3A-PB-O1B
3	F	500	ADP	PB-O3A-PA-O2A

There are no ring outliers.

4 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	500	ADP	7	0
2	C	375	SO4	4	0
2	B	375	SO4	6	0
2	E	375	SO4	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	A	334/363 (92%)	0.19	7 (2%) 63 49	82, 118, 160, 176	0
1	B	334/363 (92%)	0.05	1 (0%) 90 80	82, 118, 160, 176	0
1	C	334/363 (92%)	-0.04	2 (0%) 85 72	82, 118, 160, 176	0
1	D	334/363 (92%)	-0.04	0 100 100	82, 118, 160, 176	0
1	E	334/363 (92%)	0.02	3 (0%) 81 66	82, 118, 160, 176	0
1	F	334/363 (92%)	0.07	2 (0%) 85 72	82, 118, 160, 176	0
All	All	2004/2178 (92%)	0.04	15 (0%) 84 70	82, 118, 160, 176	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	316	SER	4.0
1	A	250	ILE	3.2
1	C	90	GLY	3.1
1	E	27	ALA	2.8
1	A	348	ALA	2.6
1	A	340	GLN	2.4
1	A	82	VAL	2.4
1	E	28	SER	2.4
1	C	91	VAL	2.4
1	A	265	VAL	2.2
1	A	247	ILE	2.2
1	F	317	LEU	2.2
1	E	306	ILE	2.1
1	B	292	ALA	2.1
1	A	339	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

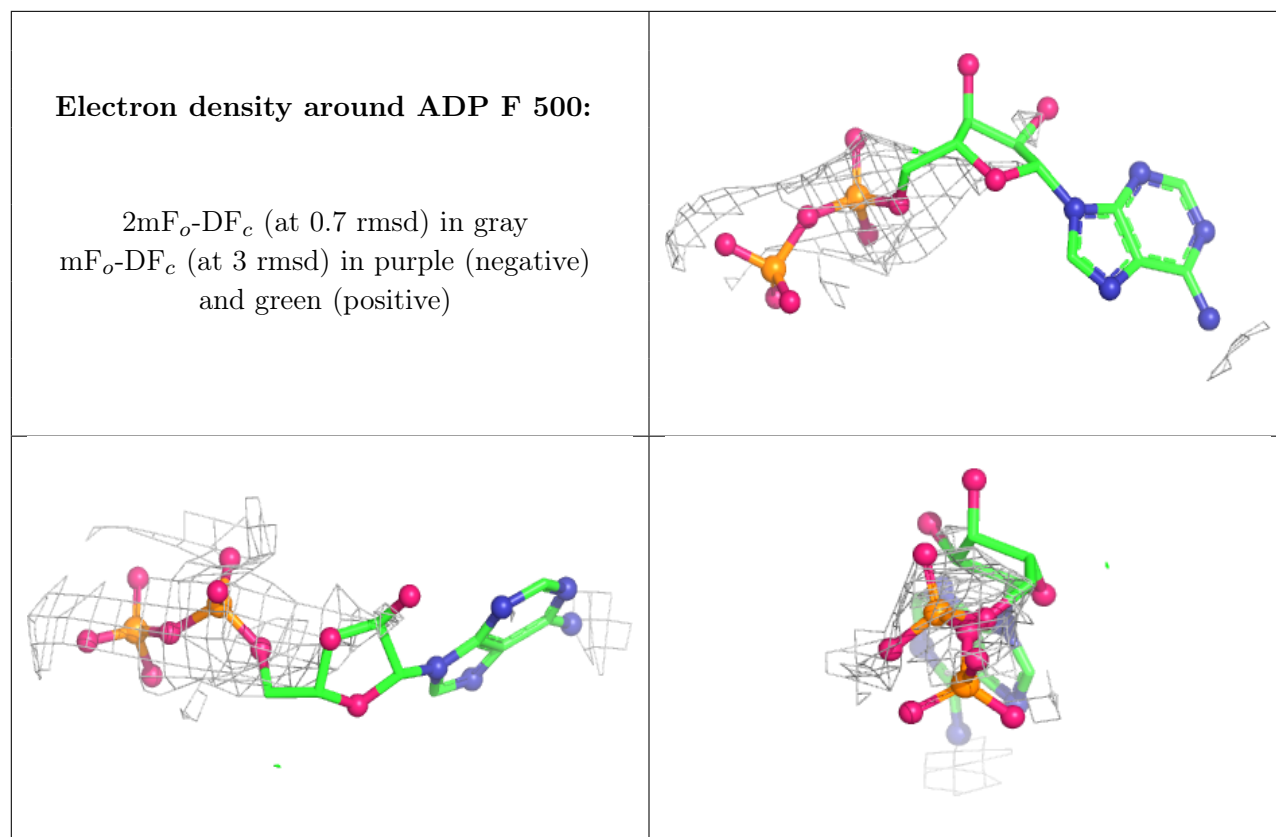
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ADP	F	500	27/27	0.68	0.12	153,177,179,179	0
2	SO4	E	375	5/5	0.81	0.08	148,148,148,149	0
2	SO4	B	375	5/5	0.85	0.12	88,88,89,90	0
2	SO4	C	375	5/5	0.92	0.06	112,113,114,115	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.