



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 02:33 AM UTC

PDB ID : 5H9E / pdb_00005h9e
Title : Crystal structure of E. coli Cascade bound to a PAM-containing dsDNA target (32-nt spacer) at 3.20 angstrom resolution.
Authors : Hayes, R.P.; Xiao, Y.; Ding, F.; van Erp, P.B.G.; Rajashankar, K.; Bailey, S.; Wiedenheft, B.; Ke, A.
Deposited on : 2015-12-28
Resolution : 3.21 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

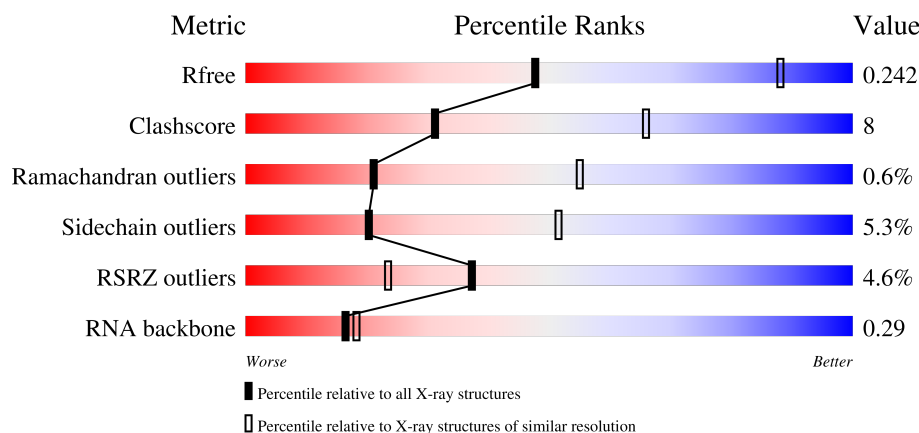
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.21 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	1768 (3.24-3.20)
Clashscore	190562	1879 (3.24-3.20)
Ramachandran outliers	187476	1844 (3.24-3.20)
Sidechain outliers	187428	1843 (3.24-3.20)
RSRZ outliers	180081	1768 (3.24-3.20)
RNA backbone	3983	1055 (3.50-2.94)

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	502	
2	B	182	
2	C	182	
3	D	363	

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Mol	Chain	Length	Quality of chain
3	E	363	
3	F	363	
3	G	363	
3	H	363	
3	I	363	
4	J	224	
5	L	61	
6	M	47	
7	N	47	
8	K	199	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 27217 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 CRISPR system Cascade subunit CasA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	S	0	0	0
			3728	2379	656	674	19			

- Molecule 2 is a protein called CRISPR system Cascade subunit CasB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	151	Total	C	N	O	S	0	0	0
			1216	765	234	210	7			
2	C	150	Total	C	N	O	S	0	0	0
			1219	767	230	215	7			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-21	MET	-	expression tag	UNP P76632
B	-20	ALA	-	expression tag	UNP P76632
B	-19	SER	-	expression tag	UNP P76632
B	-18	HIS	-	expression tag	UNP P76632
B	-17	HIS	-	expression tag	UNP P76632
B	-16	HIS	-	expression tag	UNP P76632
B	-15	HIS	-	expression tag	UNP P76632
B	-14	HIS	-	expression tag	UNP P76632
B	-13	HIS	-	expression tag	UNP P76632
B	-12	GLY	-	expression tag	UNP P76632
B	-11	ALA	-	expression tag	UNP P76632
B	-10	LEU	-	expression tag	UNP P76632
B	-9	GLU	-	expression tag	UNP P76632
B	-8	VAL	-	expression tag	UNP P76632
B	-7	LEU	-	expression tag	UNP P76632
B	-6	PHE	-	expression tag	UNP P76632
B	-5	GLN	-	expression tag	UNP P76632
B	-4	GLY	-	expression tag	UNP P76632

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PRO	-	expression tag	UNP P76632
B	-2	GLY	-	expression tag	UNP P76632
B	-1	TYR	-	expression tag	UNP P76632
B	0	GLN	-	expression tag	UNP P76632
C	-21	MET	-	expression tag	UNP P76632
C	-20	ALA	-	expression tag	UNP P76632
C	-19	SER	-	expression tag	UNP P76632
C	-18	HIS	-	expression tag	UNP P76632
C	-17	HIS	-	expression tag	UNP P76632
C	-16	HIS	-	expression tag	UNP P76632
C	-15	HIS	-	expression tag	UNP P76632
C	-14	HIS	-	expression tag	UNP P76632
C	-13	HIS	-	expression tag	UNP P76632
C	-12	GLY	-	expression tag	UNP P76632
C	-11	ALA	-	expression tag	UNP P76632
C	-10	LEU	-	expression tag	UNP P76632
C	-9	GLU	-	expression tag	UNP P76632
C	-8	VAL	-	expression tag	UNP P76632
C	-7	LEU	-	expression tag	UNP P76632
C	-6	PHE	-	expression tag	UNP P76632
C	-5	GLN	-	expression tag	UNP P76632
C	-4	GLY	-	expression tag	UNP P76632
C	-3	PRO	-	expression tag	UNP P76632
C	-2	GLY	-	expression tag	UNP P76632
C	-1	TYR	-	expression tag	UNP P76632
C	0	GLN	-	expression tag	UNP P76632

- Molecule 3 is a protein called CRISPR system Cascade subunit CasC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	318	Total	C	N	O	S	0	0	0
			2356	1476	427	439	14			
3	E	354	Total	C	N	O	S	0	0	0
			2694	1685	479	515	15			
3	F	361	Total	C	N	O	S	0	0	0
			2755	1721	490	529	15			
3	G	354	Total	C	N	O	S	0	0	0
			2713	1698	484	516	15			
3	H	352	Total	C	N	O	S	0	0	0
			2691	1681	479	516	15			
3	I	351	Total	C	N	O	S	0	0	0
			2671	1669	474	513	15			

- Molecule 4 is a protein called CRISPR system Cascade subunit CasD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	219	Total	C	N	O	S	0	0	0
			1731	1097	308	317	9			

- Molecule 5 is a RNA chain called crRNA (61-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	L	61	Total	C	N	O	P	0	0	0
			1300	580	233	426	61			

- Molecule 6 is a DNA chain called DNA (47-MER) Non-target.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	M	19	Total	C	N	O	P	0	0	0
			387	188	58	122	19			

- Molecule 7 is a DNA chain called DNA (47-MER) Target.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	N	40	Total	C	N	O	P	0	0	0
			820	389	154	237	40			

- Molecule 8 is a protein called CRISPR system Cascade subunit CasE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	K	139	Total	C	N	O	S	0	0	0
			935	597	156	176	6			

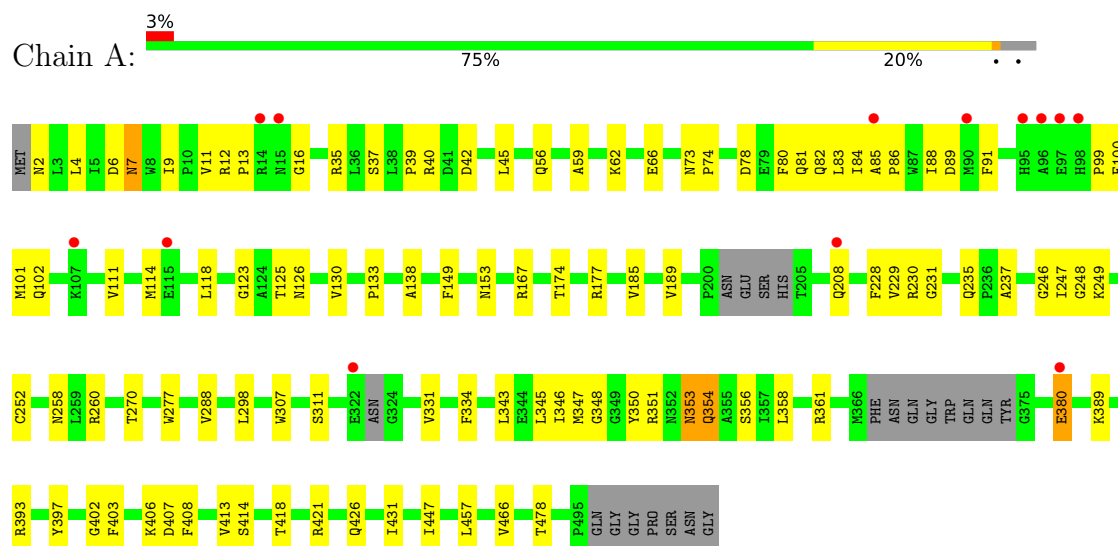
- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Zn	0	0
			1	1		

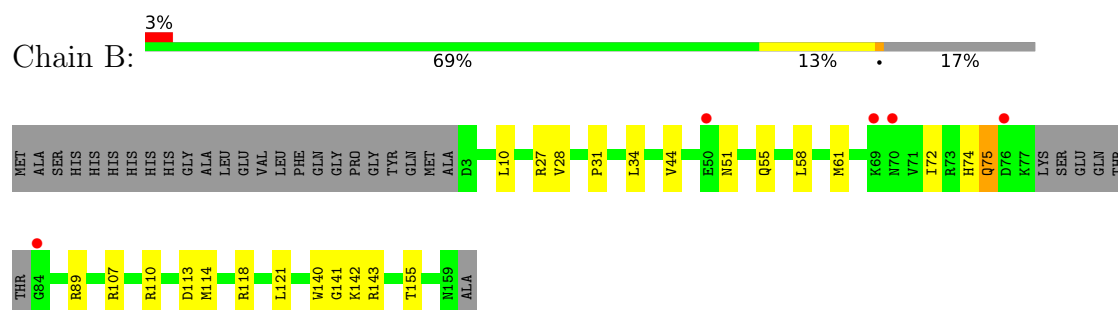
3 Residue-property plots [i](#)

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

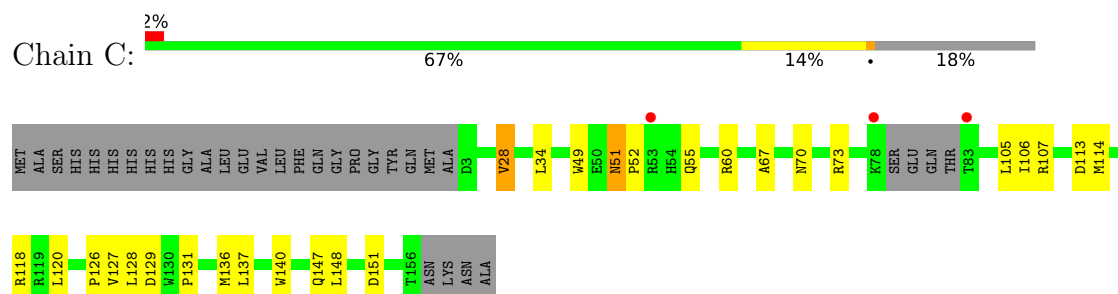
• Molecule 1: CRISPR system Cascade subunit CasA



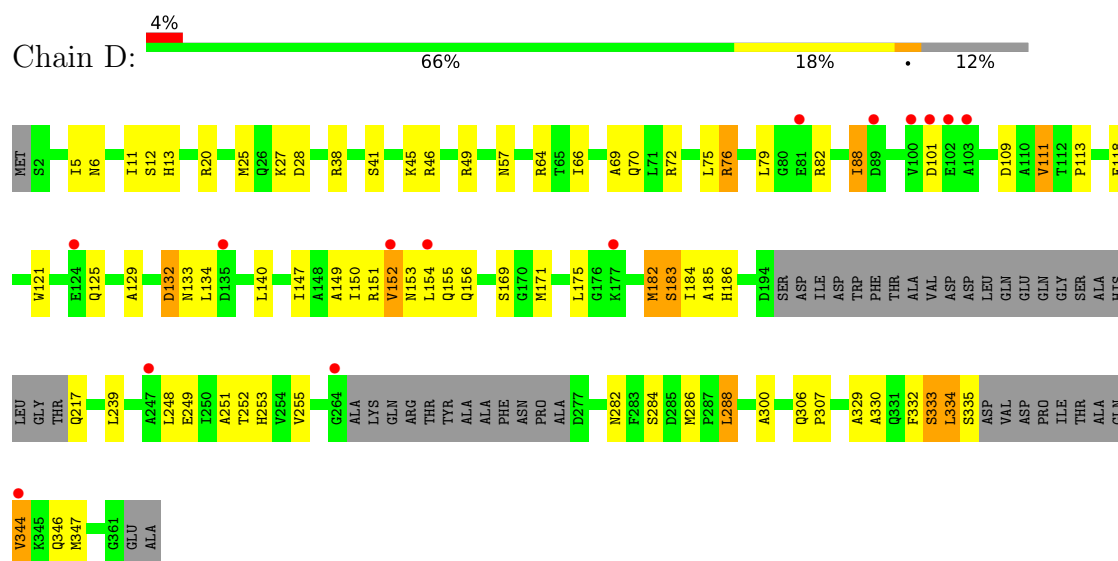
• Molecule 2: CRISPR system Cascade subunit CasB



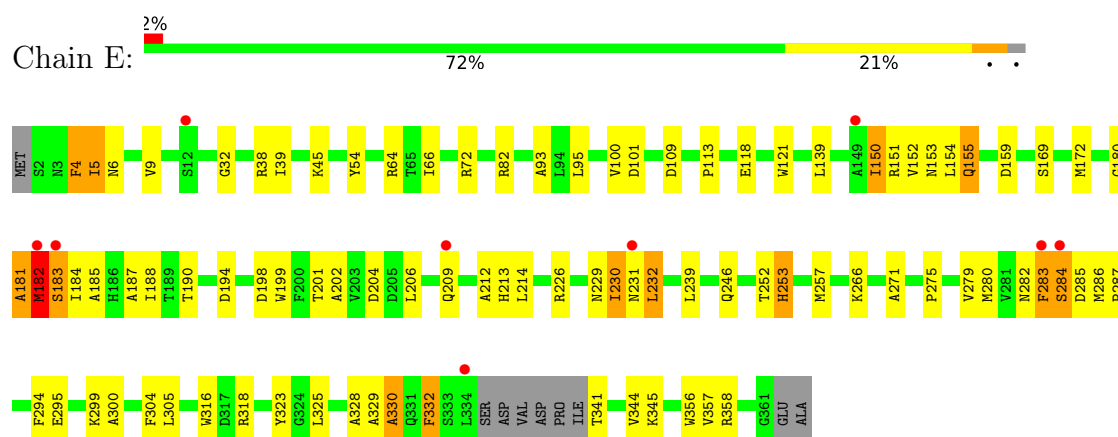
• Molecule 2: CRISPR system Cascade subunit CasB



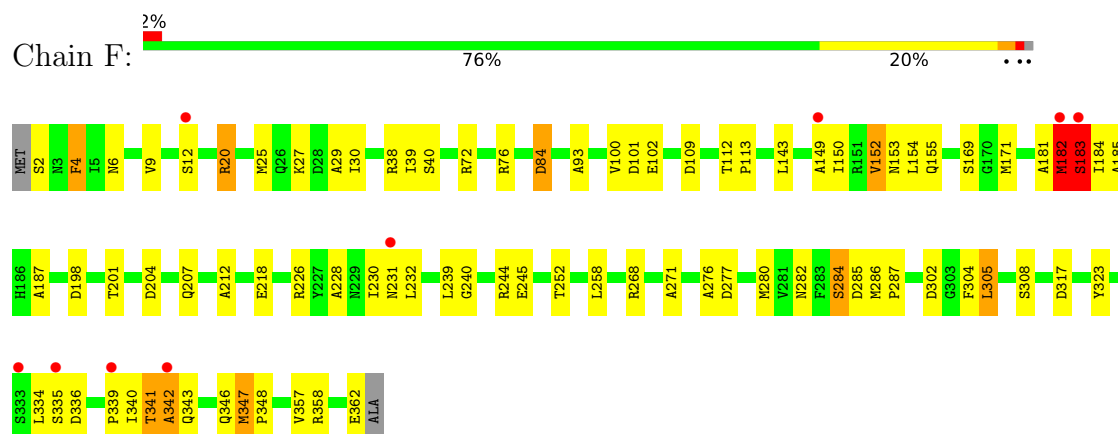
• Molecule 3: CRISPR system Cascade subunit CasC



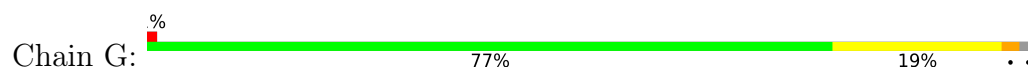
• Molecule 3: CRISPR system Cascade subunit CasC

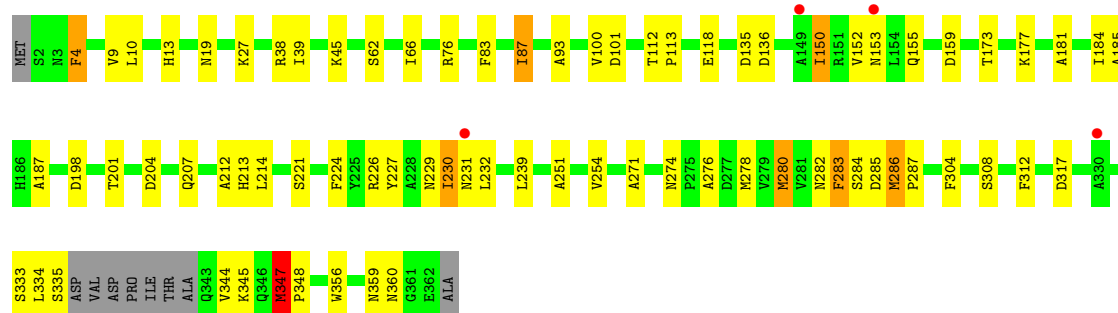


• Molecule 3: CRISPR system Cascade subunit CasC

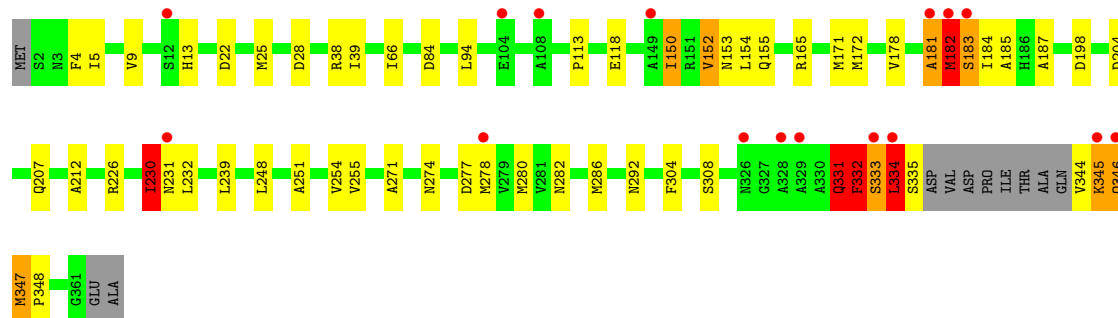
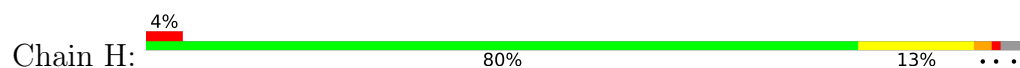


• Molecule 3: CRISPR system Cascade subunit CasC

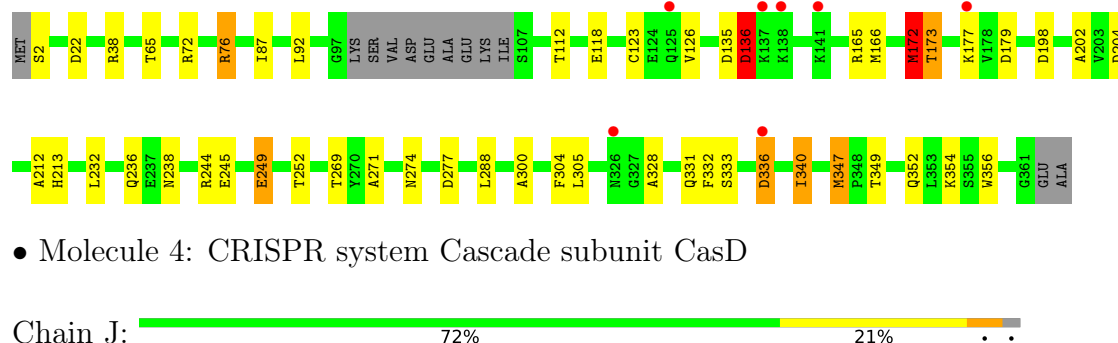
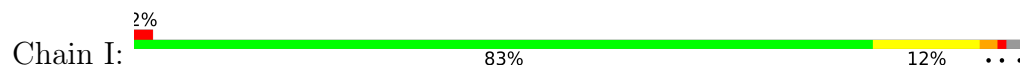




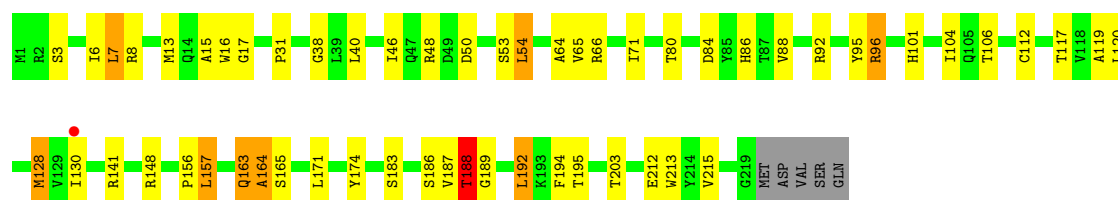
• Molecule 3: CRISPR system Cascade subunit CasC



• Molecule 3: CRISPR system Cascade subunit CasC



• Molecule 4: CRISPR system Cascade subunit CasD

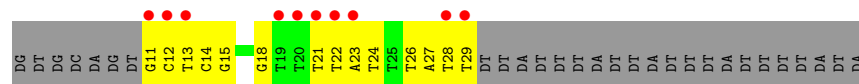


• Molecule 5: crRNA (61-MER)

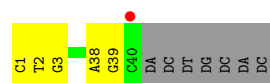
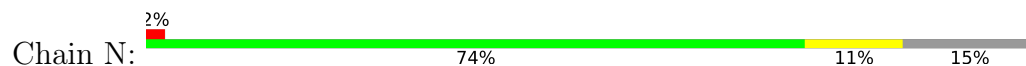




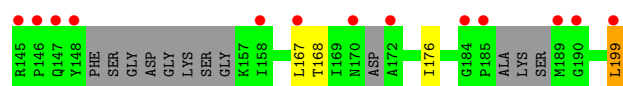
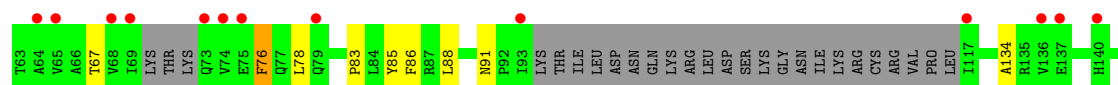
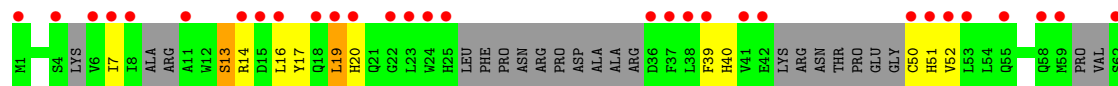
• Molecule 6: DNA (47-MER) Non-target



• Molecule 7: DNA (47-MER) Target



• Molecule 8: CRISPR system Cascade subunit CasE



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	92.81Å 149.82Å 404.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.09 – 3.21 50.09 – 3.21	Depositor EDS
% Data completeness (in resolution range)	97.2 (50.09-3.21) 91.1 (50.09-3.21)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.209 , 0.247 0.211 , 0.242	Depositor DCC
R_{free} test set	2000 reflections (2.22%)	wwPDB-VP
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.599	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	27217	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 23G

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	0.37	0/3811	0.79	5/5177 (0.1%)
2	B	0.41	0/1240	0.79	2/1679 (0.1%)
2	C	0.40	0/1243	0.78	2/1682 (0.1%)
3	D	0.34	0/2390	0.74	1/3235 (0.0%)
3	E	0.44	2/2737 (0.1%)	0.84	14/3702 (0.4%)
3	F	0.44	1/2800 (0.0%)	0.93	11/3790 (0.3%)
3	G	0.45	0/2756	0.78	6/3721 (0.2%)
3	H	0.60	6/2734 (0.2%)	1.08	29/3697 (0.8%)
3	I	0.40	0/2715	0.76	6/3676 (0.2%)
4	J	0.47	0/1773	0.82	3/2407 (0.1%)
5	L	0.21	0/1423	0.45	0/2216
6	M	0.46	1/430 (0.2%)	0.60	0/662
7	N	0.25	0/920	0.40	0/1417
8	K	0.30	0/940	0.83	0/1278
All	All	0.42	10/27912 (0.0%)	0.81	79/38339 (0.2%)

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
3	E	0	1
3	H	0	2
All	All	0	3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	345	LYS	C-O	9.22	1.35	1.23
3	H	333	SER	C-O	7.53	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	346	GLN	N-CA	-7.36	1.37	1.46
3	F	182	MET	CA-C	6.18	1.61	1.52
3	E	182	MET	CA-C	6.08	1.60	1.52
3	E	253	HIS	CG-CD2	5.76	1.42	1.35
3	H	334	LEU	N-CA	5.65	1.53	1.45
3	H	182	MET	CA-C	5.48	1.60	1.52
6	M	26	DT	O3'-P	-5.31	1.53	1.61
3	H	181	ALA	C-O	-5.25	1.19	1.23

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	347	MET	CA-C-N	16.89	136.53	118.97
3	F	347	MET	C-N-CA	16.89	136.53	118.97
3	H	346	GLN	CA-C-N	-13.40	105.89	122.64
3	H	346	GLN	C-N-CA	-13.40	105.89	122.64
3	H	332	PHE	CA-C-N	-11.31	103.10	122.67
3	H	332	PHE	C-N-CA	-11.31	103.10	122.67
3	H	333	SER	O-C-N	10.71	135.26	122.84
3	H	334	LEU	CA-CB-CG	10.13	151.76	116.30
3	H	345	LYS	CA-C-O	9.71	132.82	121.46
3	H	333	SER	CA-C-N	8.87	136.17	122.24
3	H	333	SER	C-N-CA	8.87	136.17	122.24
3	H	345	LYS	CA-C-N	-8.47	111.19	123.05
3	H	345	LYS	C-N-CA	-8.47	111.19	123.05
2	C	51	ASN	CA-C-N	8.04	129.89	119.84
2	C	51	ASN	C-N-CA	8.04	129.89	119.84
3	H	331	GLN	CA-C-O	-7.76	112.48	120.71
3	H	331	GLN	N-CA-C	-7.74	97.13	109.59
3	E	4	PHE	CA-C-N	-7.36	113.55	123.12
3	E	4	PHE	C-N-CA	-7.36	113.55	123.12
3	H	346	GLN	CB-CA-C	7.32	122.19	110.19
3	I	177	LYS	N-CA-C	-6.87	93.54	107.41
3	F	342	ALA	N-CA-C	-6.86	101.98	110.41
3	F	182	MET	CA-CB-CG	6.67	127.44	114.10
4	J	17	GLY	N-CA-C	6.64	121.04	112.54
3	F	4	PHE	CA-C-N	-6.50	114.58	122.90
3	F	4	PHE	C-N-CA	-6.50	114.58	122.90
1	A	353	ASN	N-CA-C	-6.43	102.24	110.53
1	A	431	ILE	N-CA-C	6.42	120.06	112.35
3	F	184	ILE	N-CA-C	6.33	117.24	108.12
3	H	348	PRO	N-CA-C	-6.25	105.02	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	184	ILE	N-CA-C	6.20	116.79	108.11
3	E	284	SER	N-CA-C	6.10	116.29	108.24
3	H	347	MET	CB-CA-C	6.09	120.66	110.55
3	I	347	MET	CA-C-N	6.03	127.38	119.84
3	I	347	MET	C-N-CA	6.03	127.38	119.84
3	H	345	LYS	N-CA-C	5.94	119.23	109.85
3	H	346	GLN	N-CA-C	-5.90	98.90	108.52
3	E	180	GLY	N-CA-C	5.82	118.17	111.36
4	J	188	THR	N-CA-C	5.77	123.09	110.80
3	F	182	MET	CA-C-N	5.71	132.44	121.54
3	F	182	MET	C-N-CA	5.71	132.44	121.54
3	H	184	ILE	N-CA-C	5.67	115.83	108.35
3	G	347	MET	CA-C-N	5.63	124.98	118.85
3	G	347	MET	C-N-CA	5.63	124.98	118.85
3	E	182	MET	N-CA-C	5.61	122.75	110.80
3	H	333	SER	N-CA-C	5.54	118.67	110.46
3	H	344	VAL	CA-C-N	-5.54	113.50	122.81
3	H	344	VAL	C-N-CA	-5.54	113.50	122.81
3	E	230	ILE	CA-C-N	-5.50	113.56	121.42
3	E	230	ILE	C-N-CA	-5.50	113.56	121.42
3	H	334	LEU	CB-CA-C	-5.44	99.88	109.02
3	F	335	SER	N-CA-C	5.41	115.42	108.34
3	H	66	ILE	N-CA-C	-5.36	108.06	113.47
3	E	66	ILE	N-CA-C	-5.33	108.65	113.71
3	F	341	THR	N-CA-C	5.32	117.63	109.07
3	G	4	PHE	CA-C-N	-5.23	116.08	122.93
3	G	4	PHE	C-N-CA	-5.23	116.08	122.93
3	I	136	ASP	CB-CA-C	-5.19	109.04	115.89
1	A	431	ILE	CB-CA-C	-5.18	107.21	114.00
3	D	66	ILE	N-CA-C	-5.18	108.79	113.71
2	B	51	ASN	CA-C-N	5.18	126.31	119.84
2	B	51	ASN	C-N-CA	5.18	126.31	119.84
1	A	237	ALA	CA-C-N	-5.17	114.80	122.41
1	A	237	ALA	C-N-CA	-5.17	114.80	122.41
4	J	164	ALA	N-CA-C	5.17	116.05	107.73
3	E	155	GLN	CA-C-N	-5.15	114.11	122.65
3	E	155	GLN	C-N-CA	-5.15	114.11	122.65
3	H	4	PHE	CA-C-N	-5.13	116.20	122.93
3	H	4	PHE	C-N-CA	-5.13	116.20	122.93
3	H	230	ILE	CA-C-N	-5.13	114.08	121.42
3	H	230	ILE	C-N-CA	-5.13	114.08	121.42
3	G	66	ILE	N-CA-C	-5.12	108.29	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	333	SER	N-CA-C	5.11	117.02	108.99
3	E	182	MET	CA-C-N	5.11	131.29	121.54
3	E	182	MET	C-N-CA	5.11	131.29	121.54
3	H	347	MET	N-CA-C	-5.06	97.80	108.73
3	I	172	MET	N-CA-C	5.03	121.83	113.89
3	E	232	LEU	CA-CB-CG	5.01	133.82	116.30
3	G	333	SER	N-CA-C	5.00	116.84	108.99

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	181	ALA	Peptide
3	H	331	GLN	Peptide
3	H	332	PHE	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	3728	0	3704	58	0
2	B	1216	0	1194	10	0
2	C	1219	0	1203	17	0
3	D	2356	0	2270	45	0
3	E	2694	0	2629	58	0
3	F	2755	0	2692	61	0
3	G	2713	0	2674	44	0
3	H	2691	0	2627	44	0
3	I	2671	0	2595	41	0
4	J	1731	0	1723	43	0
5	L	1300	0	659	28	0
6	M	387	0	221	19	0
7	N	820	0	449	4	0
8	K	935	0	832	13	0
9	A	1	0	0	0	0
All	All	27217	0	25472	431	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 8.

All (431) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:172:MET:CE	4:J:96:ARG:HB3	1.60	1.32
8:K:13:SER:HG	8:K:50:CYS:N	1.34	1.25
3:H:182:MET:HA	3:H:230:ILE:HA	1.29	1.14
5:L:52:G:N7	5:L:55:A:N6	2.00	1.09
3:I:172:MET:HE1	4:J:96:ARG:CB	1.83	1.07
3:F:20:ARG:NH1	5:L:29:G:OP2	1.90	1.05
3:D:72:ARG:NH1	3:D:101:ASP:O	1.94	1.00
3:F:182:MET:HA	3:F:230:ILE:HA	1.42	0.98
3:E:182:MET:HA	3:E:230:ILE:HA	1.46	0.97
5:L:52:G:C8	5:L:55:A:N6	2.32	0.97
3:I:172:MET:HE1	4:J:96:ARG:HB3	0.96	0.95
3:H:332:PHE:HA	3:H:347:MET:HB2	1.49	0.94
3:D:333:SER:C	3:D:334:LEU:HD23	1.93	0.93
4:J:48:ARG:NH1	5:L:2:U:OP2	2.01	0.93
5:L:60:G:H3'	5:L:61:23G:H5'	1.49	0.91
4:J:192:LEU:HB3	4:J:215:VAL:HB	1.52	0.88
1:A:249:LYS:NZ	4:J:203:THR:O	2.06	0.88
3:E:72:ARG:NH1	3:E:101:ASP:O	2.08	0.87
3:G:204:ASP:HB2	3:G:212:ALA:HB2	1.57	0.85
3:I:118:GLU:OE2	3:I:173:THR:OG1	1.94	0.84
4:J:92:ARG:NH1	5:L:6:C:O2	2.11	0.83
3:I:204:ASP:HB2	3:I:212:ALA:HB2	1.62	0.82
3:F:204:ASP:HB2	3:F:212:ALA:HB2	1.61	0.81
3:H:333:SER:OG	3:H:334:LEU:N	2.12	0.80
6:M:27:DA:H2''	6:M:28:DT:H5'	1.63	0.80
3:F:341:THR:HG22	3:F:342:ALA:O	1.82	0.80
3:I:38:ARG:HD2	4:J:13:MET:HE1	1.65	0.79
1:A:246:GLY:O	1:A:260:ARG:NH1	2.16	0.79
3:G:181:ALA:HB1	3:G:231:ASN:O	1.83	0.78
5:L:52:G:HO2'	5:L:53:C:H5	1.28	0.78
5:L:46:C:N3	5:L:61:23G:O6	2.17	0.78
3:D:27:LYS:NZ	5:L:39:A:OP1	2.17	0.77
3:E:299:LYS:NZ	3:F:302:ASP:OD2	2.19	0.76
8:K:13:SER:OG	8:K:50:CYS:N	2.17	0.76
3:D:329:ALA:HB1	3:D:344:VAL:HG13	1.66	0.75
3:F:182:MET:HG3	3:F:183:SER:H	1.52	0.74
3:G:204:ASP:HB3	3:G:207:GLN:HB3	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:13:DT:O2	7:N:39:DG:N2	2.21	0.74
3:G:93:ALA:HB2	3:G:100:VAL:HG22	1.69	0.74
3:I:172:MET:HE3	4:J:96:ARG:HB3	1.66	0.73
3:E:182:MET:HG2	3:E:183:SER:H	1.52	0.73
3:D:334:LEU:HD23	3:D:334:LEU:N	2.03	0.73
3:H:182:MET:HG2	3:H:183:SER:H	1.54	0.73
6:M:28:DT:H1'	6:M:29:DT:C7	2.18	0.72
3:H:28:ASP:O	3:H:38:ARG:NH1	2.22	0.72
3:E:204:ASP:HB2	3:E:212:ALA:HB2	1.72	0.71
3:G:231:ASN:OD1	3:G:232:LEU:N	2.24	0.70
3:F:182:MET:CA	3:F:230:ILE:HA	2.21	0.70
5:L:60:G:C3'	5:L:61:23G:H5'	2.22	0.69
3:D:38:ARG:NH2	3:E:198:ASP:OD1	2.25	0.69
3:D:329:ALA:CB	3:D:344:VAL:HG13	2.23	0.69
3:E:93:ALA:HB2	3:E:100:VAL:HG22	1.75	0.69
3:F:204:ASP:HB3	3:F:207:GLN:HG2	1.74	0.68
1:A:380:GLU:HG2	1:A:447:ILE:HD13	1.76	0.68
6:M:28:DT:O3'	6:M:29:DT:H73	1.93	0.68
3:H:204:ASP:HB2	3:H:212:ALA:HB2	1.75	0.68
1:A:101:MET:HE2	1:A:235:GLN:HG2	1.76	0.68
3:E:318:ARG:NH2	3:F:336:ASP:OD1	2.26	0.68
3:E:5:ILE:HG23	3:E:230:ILE:HB	1.75	0.68
3:I:172:MET:HE2	4:J:96:ARG:HD2	1.76	0.68
3:I:172:MET:CE	4:J:96:ARG:HD2	2.24	0.67
6:M:29:DT:H6	6:M:29:DT:O5'	1.78	0.67
3:H:181:ALA:O	3:H:231:ASN:HB3	1.94	0.67
3:F:93:ALA:HB2	3:F:100:VAL:HG22	1.76	0.67
3:E:39:ILE:HB	3:E:187:ALA:HB3	1.76	0.67
3:D:109:ASP:OD2	3:D:169:SER:OG	2.14	0.66
5:L:49:C:H2'	5:L:50:G:C8	2.31	0.66
3:E:152:VAL:O	3:E:155:GLN:N	2.28	0.65
3:F:76:ARG:NH2	3:F:102:GLU:OE1	2.29	0.65
1:A:208:GLN:O	1:A:230:ARG:NH1	2.27	0.65
1:A:177:ARG:HB2	1:A:346:ILE:HG13	1.78	0.65
2:C:70:ASN:O	2:C:73:ARG:NH1	2.30	0.64
3:H:332:PHE:HD1	3:H:347:MET:O	1.80	0.64
4:J:186:SER:O	4:J:187:VAL:HG23	1.99	0.63
3:H:332:PHE:CA	3:H:347:MET:HB2	2.27	0.63
3:D:140:LEU:HD13	3:D:171:MET:HG3	1.80	0.62
5:L:50:G:O2'	5:L:51:C:H5'	1.99	0.62
1:A:99:PRO:HB2	1:A:102:GLN:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:27:LYS:NZ	5:L:21:A:OP1	2.33	0.61
3:D:69:ALA:O	3:D:72:ARG:HG3	2.00	0.61
3:H:331:GLN:H	3:H:345:LYS:H	1.48	0.61
3:H:204:ASP:HB3	3:H:207:GLN:HB3	1.82	0.61
3:E:284:SER:OG	3:E:285:ASP:N	2.33	0.61
7:N:38:DA:H2'	7:N:39:DG:C8	2.36	0.61
3:F:317:ASP:OD1	3:F:341:THR:OG1	2.19	0.60
3:I:112:THR:HG23	3:I:238:ASN:HA	1.82	0.60
3:E:323:TYR:OH	3:F:276:ALA:O	2.19	0.60
3:G:10:LEU:HD12	3:G:278:MET:HE3	1.83	0.60
3:F:182:MET:O	3:F:183:SER:OG	2.18	0.60
3:H:185:ALA:HB2	3:I:271:ALA:HB3	1.82	0.59
3:D:129:ALA:O	3:D:133:ASN:N	2.34	0.59
3:I:135:ASP:CG	3:I:136:ASP:H	2.10	0.59
3:F:342:ALA:O	3:F:343:GLN:HB2	2.02	0.59
3:E:253:HIS:O	3:E:257:MET:HG3	2.03	0.58
3:F:182:MET:HA	3:F:230:ILE:CA	2.26	0.58
3:H:230:ILE:HD11	3:H:254:VAL:HG21	1.85	0.58
3:H:231:ASN:OD1	3:H:232:LEU:N	2.37	0.58
3:H:38:ARG:NH2	3:I:198:ASP:OD1	2.36	0.58
3:I:179:ASP:OD1	4:J:48:ARG:NH2	2.36	0.58
3:E:32:GLY:HA2	3:E:295:GLU:OE2	2.02	0.58
3:E:252:THR:HG22	3:E:357:VAL:HB	1.86	0.58
3:D:45:LYS:HE3	5:L:37:A:OP1	2.03	0.58
3:E:329:ALA:HB3	3:E:344:VAL:HA	1.85	0.57
3:F:182:MET:HG3	3:F:183:SER:N	2.19	0.57
3:D:28:ASP:O	3:D:38:ARG:NH1	2.36	0.57
3:G:286:MET:HG3	3:G:287:PRO:HD2	1.87	0.57
1:A:2:ASN:ND2	1:A:91:PHE:O	2.38	0.57
3:E:252:THR:HG21	3:E:358:ARG:HG3	1.85	0.57
2:B:141:GLY:O	2:B:143:ARG:N	2.38	0.57
3:E:182:MET:HG3	3:E:230:ILE:HD13	1.87	0.57
3:G:38:ARG:NH2	3:H:198:ASP:OD1	2.38	0.57
4:J:163:GLN:O	4:J:164:ALA:HB2	2.05	0.57
4:J:188:THR:OG1	4:J:189:GLY:N	2.35	0.57
5:L:50:G:C6	5:L:51:C:N4	2.73	0.57
3:I:38:ARG:NH2	4:J:84:ASP:OD1	2.37	0.57
4:J:8:ARG:NH2	4:J:117:THR:OG1	2.38	0.57
3:D:249:GLU:O	3:D:252:THR:OG1	2.19	0.56
3:D:72:ARG:HD3	3:D:76:ARG:HH11	1.70	0.56
3:G:185:ALA:HB2	3:H:271:ALA:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:135:ASP:OD1	3:I:136:ASP:N	2.36	0.56
3:E:101:ASP:OD1	3:E:101:ASP:N	2.38	0.56
3:I:331:GLN:NE2	3:I:340:ILE:HD11	2.20	0.56
6:M:28:DT:H1'	6:M:29:DT:H72	1.87	0.56
5:L:51:C:H2'	5:L:52:G:O4'	2.05	0.56
3:E:95:LEU:HD22	3:E:172:MET:HE2	1.88	0.56
4:J:40:LEU:HD11	4:J:120:LEU:HD11	1.88	0.56
3:F:252:THR:HG22	3:F:357:VAL:HB	1.88	0.56
3:F:284:SER:OG	3:F:285:ASP:N	2.39	0.56
3:F:84:ASP:OD1	3:F:84:ASP:N	2.39	0.55
3:I:172:MET:CE	4:J:96:ARG:CB	2.56	0.55
3:D:72:ARG:CD	3:D:76:ARG:HH11	2.20	0.55
3:G:152:VAL:O	3:G:155:GLN:HB2	2.06	0.55
4:J:46:ILE:HG21	4:J:54:LEU:HD13	1.88	0.55
3:E:185:ALA:HB2	3:F:271:ALA:HB3	1.89	0.55
2:C:52:PRO:O	2:C:55:GLN:HB2	2.06	0.55
3:F:30:ILE:O	3:G:221:SER:OG	2.24	0.55
3:G:230:ILE:HD12	3:G:251:ALA:HA	1.89	0.55
1:A:126:ASN:HA	4:J:104:ILE:HD12	1.89	0.54
2:C:60:ARG:NH1	2:C:137:LEU:O	2.39	0.54
3:F:185:ALA:HB2	3:G:271:ALA:HB3	1.89	0.54
3:D:11:ILE:HG12	3:D:12:SER:H	1.71	0.54
3:H:152:VAL:O	3:H:155:GLN:HB2	2.07	0.54
3:H:346:GLN:HA	3:H:346:GLN:OE1	2.08	0.54
3:E:109:ASP:OD2	3:E:169:SER:OG	2.14	0.54
3:F:286:MET:HG3	3:F:287:PRO:HD2	1.90	0.54
3:F:304:PHE:O	3:F:308:SER:OG	2.17	0.54
1:A:42:ASP:OD2	1:A:350:TYR:OH	2.22	0.54
3:G:181:ALA:O	3:G:231:ASN:N	2.40	0.54
1:A:353:ASN:H	1:A:358:LEU:HG	1.72	0.54
3:F:182:MET:CG	3:F:183:SER:H	2.14	0.54
3:G:230:ILE:HD11	3:G:254:VAL:HG21	1.89	0.54
3:I:252:THR:HG23	3:I:354:LYS:HB3	1.89	0.54
5:L:45:U:O4	8:K:91:ASN:ND2	2.33	0.54
3:E:199:TRP:CZ2	3:E:214:LEU:HD23	2.44	0.53
4:J:3:SER:HB3	4:J:130:ILE:HD13	1.89	0.53
4:J:7:LEU:HG	4:J:157:LEU:HD22	1.91	0.53
3:D:132:ASP:OD1	3:D:132:ASP:N	2.39	0.53
3:E:38:ARG:NH2	3:F:198:ASP:OD1	2.41	0.53
3:D:288:LEU:HD21	3:E:275:PRO:HG3	1.90	0.53
2:C:136:MET:HE1	2:C:148:LEU:HD23	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:ARG:HB2	3:F:25:MET:HE1	1.90	0.53
3:I:332:PHE:HA	3:I:347:MET:O	2.09	0.53
3:F:323:TYR:OH	3:G:276:ALA:O	2.23	0.53
3:D:149:ALA:O	3:D:152:VAL:HG12	2.09	0.52
1:A:4:LEU:HB3	1:A:88:ILE:HD13	1.91	0.52
1:A:331:VAL:HG13	1:A:343:LEU:HD21	1.91	0.52
3:F:231:ASN:OD1	3:F:232:LEU:N	2.42	0.52
3:H:94:LEU:HB3	3:H:171:MET:HE2	1.91	0.52
3:H:154:LEU:HD11	3:H:178:VAL:HG21	1.92	0.52
5:L:52:G:O2'	5:L:53:C:H5	1.90	0.52
5:L:53:C:H5''	5:L:54:C:H5	1.74	0.52
3:H:230:ILE:HD12	3:H:251:ALA:HA	1.90	0.52
1:A:85:ALA:O	1:A:88:ILE:HB	2.10	0.52
1:A:125:THR:HB	4:J:101:HIS:CD2	2.45	0.52
5:L:50:G:H2'	5:L:51:C:C6	2.45	0.52
4:J:6:ILE:HG13	4:J:174:TYR:CE1	2.45	0.51
1:A:149:PHE:O	1:A:153:ASN:ND2	2.35	0.51
3:H:304:PHE:O	3:H:308:SER:OG	2.25	0.51
6:M:22:DT:H4'	6:M:23:DA:OP1	2.10	0.51
3:G:155:GLN:HA	3:G:239:LEU:HD22	1.92	0.51
3:F:181:ALA:O	3:F:231:ASN:HB3	2.10	0.51
1:A:2:ASN:N	1:A:6:ASP:OD2	2.43	0.51
3:D:332:PHE:CE1	3:D:334:LEU:HD21	2.46	0.51
3:E:181:ALA:O	3:E:231:ASN:HB3	2.10	0.51
3:E:183:SER:HB2	3:E:229:ASN:OD1	2.09	0.51
3:E:330:ALA:HA	3:E:345:LYS:O	2.11	0.51
3:D:155:GLN:HA	3:D:239:LEU:HD22	1.92	0.51
3:E:6:ASN:ND2	3:E:284:SER:HB3	2.26	0.51
3:D:151:ARG:NH2	3:D:175:LEU:O	2.44	0.51
3:E:316:TRP:HZ3	3:E:341:THR:HG21	1.73	0.51
3:F:72:ARG:NH1	3:F:101:ASP:O	2.43	0.51
1:A:45:LEU:HD22	1:A:348:GLY:HA3	1.93	0.50
3:H:39:ILE:HB	3:H:187:ALA:HB3	1.94	0.50
1:A:247:ILE:HG13	1:A:258:ASN:HA	1.92	0.50
6:M:21:DT:H2''	6:M:22:DT:OP2	2.10	0.50
3:F:152:VAL:O	3:F:155:GLN:HB2	2.12	0.50
3:F:252:THR:HG21	3:F:358:ARG:HG3	1.92	0.50
3:G:360:ASN:O	3:G:360:ASN:ND2	2.44	0.50
3:E:279:VAL:HB	3:E:332:PHE:HD2	1.76	0.50
1:A:12:ARG:HG2	1:A:37:SER:HB2	1.94	0.50
1:A:138:ALA:HB1	1:A:260:ARG:HE	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:150:ILE:HA	3:E:153:ASN:HD22	1.76	0.50
3:E:64:ARG:NH2	3:E:159:ASP:OD2	2.43	0.49
1:A:270:THR:HG21	6:M:18:DG:OP1	2.12	0.49
3:H:331:GLN:O	3:H:345:LYS:O	2.30	0.49
3:H:331:GLN:O	3:H:345:LYS:C	2.55	0.49
3:I:288:LEU:HD11	4:J:156:PRO:HG3	1.95	0.49
2:C:105:LEU:HD22	2:C:120:LEU:HD12	1.94	0.49
4:J:38:GLY:HA3	5:L:2:U:O4'	2.11	0.49
2:C:147:GLN:NE2	2:C:151:ASP:OD1	2.44	0.49
1:A:13:PRO:HG2	1:A:16:GLY:HA3	1.93	0.49
3:E:121:TRP:CD1	3:E:153:ASN:HD21	2.31	0.49
3:G:62:SER:N	3:G:159:ASP:OD1	2.43	0.49
6:M:14:DC:H2''	6:M:15:DG:H5'	1.95	0.49
3:D:300:ALA:HB2	3:D:307:PRO:HG2	1.95	0.49
1:A:123:GLY:O	1:A:356:SER:OG	2.30	0.49
2:B:113:ASP:OD1	2:B:114:MET:N	2.45	0.48
5:L:47:C:H42	5:L:60:G:H1	1.59	0.48
5:L:54:C:H4'	5:L:55:A:O5'	2.13	0.48
3:H:9:VAL:HB	3:H:226:ARG:HB2	1.94	0.48
3:D:41:SER:HB2	3:D:184:ILE:HG23	1.96	0.48
3:E:64:ARG:HG2	3:E:113:PRO:HB3	1.94	0.48
2:C:107:ARG:HB3	3:H:25:MET:HE1	1.96	0.48
8:K:85:TYR:CE2	8:K:199:LEU:HB3	2.48	0.48
1:A:393:ARG:NH1	6:M:23:DA:H2''	2.29	0.48
6:M:12:DC:H2''	6:M:13:DT:OP1	2.14	0.48
3:E:155:GLN:HA	3:E:239:LEU:HD22	1.96	0.48
8:K:16:LEU:HA	8:K:19:LEU:HD13	1.96	0.48
2:B:27:ARG:NH2	7:N:3:DG:N7	2.52	0.47
3:G:347:MET:HA	3:G:348:PRO:HD3	1.76	0.47
3:H:155:GLN:HA	3:H:239:LEU:HD22	1.96	0.47
3:G:19:ASN:OD1	3:G:27:LYS:HD2	2.14	0.47
2:C:151:ASP:OD1	6:M:27:DA:H2	1.97	0.47
6:M:27:DA:C2'	6:M:28:DT:H5'	2.39	0.47
8:K:76:PHE:HB2	8:K:78:LEU:HD13	1.97	0.47
1:A:84:ILE:O	1:A:88:ILE:HG12	2.14	0.47
1:A:406:LYS:HB3	1:A:408:PHE:HD2	1.80	0.47
2:C:113:ASP:OD1	2:C:114:MET:N	2.48	0.47
3:D:182:MET:HB3	3:D:183:SER:H	1.51	0.47
3:G:9:VAL:HB	3:G:226:ARG:HB2	1.96	0.47
4:J:48:ARG:NH1	5:L:2:U:P	2.88	0.47
1:A:84:ILE:HD12	1:A:88:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:10:LEU:HB2	3:G:278:MET:HB3	1.97	0.47
4:J:128:MET:H	4:J:128:MET:HG2	1.53	0.47
4:J:195:THR:HG22	4:J:212:GLU:HG2	1.96	0.47
3:F:2:SER:HB3	3:F:284:SER:O	2.15	0.46
3:F:152:VAL:HG12	3:F:240:GLY:HA3	1.98	0.46
5:L:61:23G:OC1	5:L:61:23G:H1'	2.15	0.46
3:F:182:MET:CB	3:F:230:ILE:HG12	2.46	0.46
3:I:165:ARG:HH11	4:J:92:ARG:NH1	2.14	0.46
1:A:59:ALA:HB2	1:A:83:LEU:HD13	1.96	0.46
1:A:133:PRO:HB3	4:J:95:TYR:CD1	2.50	0.46
3:D:64:ARG:HG2	3:D:113:PRO:HB3	1.96	0.46
2:B:89:ARG:HG2	2:B:155:THR:OG1	2.16	0.46
3:I:245:GLU:OE2	3:I:245:GLU:N	2.48	0.46
2:C:28:VAL:HG21	2:C:34:LEU:HD23	1.98	0.46
3:E:152:VAL:O	3:E:155:GLN:HB2	2.16	0.46
3:G:118:GLU:HA	3:G:153:ASN:HB3	1.98	0.46
1:A:228:PHE:HA	1:A:277:TRP:HZ2	1.80	0.45
6:M:11:DG:H2''	6:M:12:DC:H5''	1.97	0.45
1:A:56:GLN:HA	1:A:189:VAL:HG13	1.97	0.45
8:K:16:LEU:O	8:K:19:LEU:HB2	2.17	0.45
3:G:280:MET:HE3	3:G:312:PHE:HE2	1.81	0.45
4:J:80:THR:OG1	4:J:112:CYS:HB2	2.15	0.45
4:J:64:ALA:HB3	4:J:119:ALA:HB3	1.98	0.45
3:E:9:VAL:HB	3:E:226:ARG:HB2	1.97	0.45
1:A:174:THR:HG23	1:A:345:LEU:HD13	1.98	0.45
3:G:13:HIS:HA	3:G:274:ASN:OD1	2.17	0.45
3:G:45:LYS:HD2	3:G:184:ILE:HG21	1.99	0.45
4:J:50:ASP:OD2	4:J:53:SER:OG	2.27	0.45
2:C:67:ALA:HB2	2:C:118:ARG:HG3	1.99	0.45
3:F:4:PHE:CE1	3:F:287:PRO:HG3	2.51	0.45
3:F:6:ASN:HD22	3:F:284:SER:HB3	1.82	0.45
3:I:123:CYS:HA	3:I:126:VAL:HG12	1.99	0.45
3:D:72:ARG:HD3	3:D:76:ARG:NH1	2.32	0.45
3:D:79:LEU:HD12	3:D:88:ILE:HD11	1.97	0.45
3:D:248:LEU:O	3:D:252:THR:HG23	2.17	0.45
1:A:231:GLY:HA3	1:A:277:TRP:CZ2	2.51	0.45
3:E:4:PHE:CD2	3:E:287:PRO:HD3	2.51	0.45
3:H:22:ASP:OD1	3:H:22:ASP:N	2.50	0.44
3:I:135:ASP:C	3:I:136:ASP:OD1	2.61	0.44
3:I:252:THR:HG23	3:I:354:LYS:HD2	1.98	0.44
2:C:49:TRP:C	2:C:51:ASN:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:2:SER:O	3:I:244:ARG:NH1	2.44	0.44
3:E:328:ALA:HB1	3:E:356:TRP:CZ2	2.52	0.44
3:G:177:LYS:HB2	3:G:177:LYS:NZ	2.32	0.44
3:H:118:GLU:HA	3:H:153:ASN:HB3	1.99	0.44
2:B:10:LEU:HD23	2:B:61:MET:HE2	1.99	0.44
3:D:185:ALA:HB2	3:E:271:ALA:HB3	1.98	0.44
3:F:27:LYS:NZ	3:G:198:ASP:OD1	2.46	0.44
3:F:155:GLN:HA	3:F:239:LEU:HD22	1.99	0.44
1:A:9:ILE:HG22	1:A:11:VAL:HG13	2.00	0.44
3:F:29:ALA:HB2	3:F:38:ARG:HD3	1.99	0.44
6:M:14:DC:H2'	6:M:15:DG:C8	2.52	0.44
1:A:85:ALA:HB3	1:A:86:PRO:HD3	1.99	0.44
1:A:81:GLN:HA	1:A:84:ILE:HG12	2.00	0.44
3:F:6:ASN:ND2	3:F:284:SER:HB3	2.32	0.44
4:J:88:VAL:HB	4:J:104:ILE:HG12	1.98	0.44
3:E:328:ALA:HB1	3:E:356:TRP:HZ2	1.83	0.44
3:G:39:ILE:HB	3:G:187:ALA:HB3	2.00	0.44
8:K:78:LEU:HD22	8:K:176:ILE:HD11	1.99	0.44
3:F:39:ILE:HB	3:F:187:ALA:HB3	2.00	0.43
3:F:182:MET:HA	3:F:231:ASN:N	2.33	0.43
3:F:182:MET:HB2	3:F:230:ILE:HG12	2.00	0.43
3:H:13:HIS:HA	3:H:274:ASN:OD1	2.18	0.43
3:D:251:ALA:O	3:D:255:VAL:HG23	2.17	0.43
3:E:190:THR:HG23	3:E:294:PHE:CG	2.53	0.43
7:N:1:DC:H2'	7:N:2:DT:C6	2.53	0.43
2:B:44:VAL:HB	2:B:58:LEU:HD13	2.00	0.43
3:D:6:ASN:ND2	3:D:284:SER:OG	2.52	0.43
3:G:227:TYR:OH	3:G:229:ASN:HB3	2.18	0.43
3:E:202:ALA:HB3	3:E:213:HIS:HB3	2.00	0.43
3:F:149:ALA:O	3:F:152:VAL:HG22	2.19	0.43
3:I:202:ALA:HB3	3:I:213:HIS:HB3	1.99	0.43
3:D:111:VAL:HG21	3:E:202:ALA:HB1	2.01	0.43
3:I:22:ASP:OD1	3:I:22:ASP:N	2.48	0.43
4:J:15:ALA:HB3	4:J:148:ARG:HG3	1.99	0.43
3:D:46:ARG:HA	3:D:49:ARG:HG2	2.01	0.43
3:F:150:ILE:O	3:F:153:ASN:HB2	2.19	0.43
3:H:84:ASP:OD1	3:H:84:ASP:N	2.43	0.43
3:H:181:ALA:O	3:H:231:ASN:CB	2.64	0.43
3:F:109:ASP:OD2	3:F:169:SER:OG	2.22	0.43
4:J:86:HIS:O	4:J:106:THR:OG1	2.29	0.43
4:J:128:MET:HE2	4:J:128:MET:HB3	1.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:194:PHE:HB3	4:J:213:TRP:HB2	2.01	0.43
3:D:41:SER:H	3:D:186:HIS:CD2	2.37	0.43
1:A:361:ARG:HA	1:A:361:ARG:HD3	1.88	0.43
1:A:418:THR:HG22	1:A:421:ARG:NH1	2.34	0.43
3:F:27:LYS:HD3	3:F:38:ARG:NH2	2.34	0.43
1:A:80:PHE:CE2	1:A:84:ILE:HD13	2.54	0.42
1:A:307:TRP:O	1:A:311:SER:OG	2.31	0.42
2:C:151:ASP:OD2	6:M:28:DT:N3	2.43	0.42
3:F:112:THR:HA	3:F:113:PRO:HD3	1.89	0.42
3:F:228:ALA:HB3	3:F:258:LEU:HD11	2.01	0.42
1:A:126:ASN:O	1:A:130:VAL:HG22	2.18	0.42
3:D:118:GLU:OE2	3:D:150:ILE:HG22	2.20	0.42
3:D:346:GLN:O	3:D:347:MET:SD	2.77	0.42
1:A:12:ARG:HD2	1:A:35:ARG:NH2	2.35	0.42
1:A:397:TYR:CD2	6:M:24:DT:H5"	2.54	0.42
3:I:118:GLU:CD	3:I:172:MET:H	2.26	0.42
3:E:286:MET:HG3	3:E:287:PRO:HD2	2.01	0.42
3:F:182:MET:HA	3:F:231:ASN:H	1.84	0.42
3:I:87:ILE:HG23	3:I:126:VAL:HG13	2.01	0.42
8:K:17:TYR:HA	8:K:20:HIS:CD2	2.54	0.42
2:B:74:HIS:CE1	2:B:75:GLN:O	2.72	0.42
3:D:155:GLN:HG3	3:D:239:LEU:HB3	2.01	0.42
3:H:331:GLN:HG2	3:H:345:LYS:O	2.19	0.42
1:A:7:ASN:OD1	1:A:7:ASN:N	2.51	0.42
3:E:231:ASN:OD1	3:E:232:LEU:N	2.53	0.42
3:E:300:ALA:HB2	3:E:304:PHE:CE1	2.55	0.42
3:F:154:LEU:HD23	3:F:154:LEU:HA	1.76	0.42
2:C:73:ARG:HB2	2:C:127:VAL:HG22	2.00	0.42
3:E:45:LYS:NZ	5:L:31:U:OP1	2.50	0.42
3:E:118:GLU:HA	3:E:153:ASN:HB3	2.02	0.42
3:G:283:PHE:HD2	3:G:356:TRP:CZ3	2.38	0.42
2:C:126:PRO:HB2	2:C:128:LEU:HD23	2.02	0.42
3:E:54:TYR:HB2	3:E:257:MET:HE1	2.00	0.42
3:F:40:SER:OG	5:L:27:U:OP1	2.37	0.42
3:D:171:MET:HG2	3:D:175:LEU:HD12	2.01	0.42
3:D:306:GLN:HB2	3:D:307:PRO:HD3	2.00	0.42
3:H:25:MET:HE3	3:H:25:MET:HB2	1.76	0.42
4:J:66:ARG:NH1	4:J:171:LEU:O	2.53	0.42
8:K:83:PRO:HG2	8:K:199:LEU:HD11	2.01	0.42
8:K:134:ALA:HB1	8:K:168:THR:O	2.20	0.42
2:B:31:PRO:O	2:B:34:LEU:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:57:ASN:HB3	3:D:253:HIS:CE1	2.54	0.42
3:F:339:PRO:HB3	3:F:346:GLN:NE2	2.35	0.42
3:H:332:PHE:CD1	3:H:347:MET:O	2.67	0.42
3:I:166:MET:HE3	3:I:166:MET:HB2	1.92	0.42
3:I:336:ASP:OD1	3:I:336:ASP:N	2.53	0.42
1:A:39:PRO:HG2	1:A:252:CYS:O	2.19	0.41
2:C:129:ASP:OD1	2:C:131:PRO:HD2	2.19	0.41
1:A:40:ARG:NH2	1:A:118:LEU:O	2.52	0.41
3:G:150:ILE:HA	3:G:153:ASN:HD22	1.85	0.41
3:E:6:ASN:HD22	3:E:284:SER:HB3	1.85	0.41
3:F:245:GLU:CD	3:F:245:GLU:H	2.28	0.41
3:H:150:ILE:O	3:H:153:ASN:HB2	2.19	0.41
3:I:277:ASP:CG	3:I:305:LEU:HD21	2.45	0.41
1:A:73:ASN:HA	1:A:74:PRO:HD3	1.85	0.41
3:F:347:MET:HA	3:F:348:PRO:HD3	1.54	0.41
3:E:283:PHE:HB3	3:E:328:ALA:HB3	2.01	0.41
3:G:13:HIS:HD2	3:G:224:PHE:CD1	2.39	0.41
3:H:251:ALA:O	3:H:255:VAL:HG23	2.20	0.41
3:I:249:GLU:O	3:I:252:THR:HB	2.20	0.41
1:A:62:LYS:HG2	1:A:66:GLU:OE1	2.20	0.41
3:G:4:PHE:CE1	3:G:287:PRO:HG3	2.55	0.41
3:G:304:PHE:O	3:G:308:SER:OG	2.31	0.41
3:I:72:ARG:O	3:I:76:ARG:HB2	2.20	0.41
2:C:136:MET:HE2	2:C:140:TRP:CZ3	2.56	0.41
3:G:135:ASP:OD1	3:G:136:ASP:N	2.54	0.41
1:A:334:PHE:CD2	1:A:343:LEU:HD13	2.56	0.41
2:B:72:ILE:HD11	2:B:121:LEU:HD13	2.01	0.41
3:E:151:ARG:HA	3:E:154:LEU:HB2	2.02	0.41
3:E:199:TRP:HZ2	3:E:214:LEU:HD23	1.83	0.41
3:I:300:ALA:HB2	3:I:304:PHE:CE1	2.56	0.41
6:M:28:DT:C1'	6:M:29:DT:H72	2.50	0.41
1:A:100:PHE:O	1:A:102:GLN:HG3	2.20	0.41
1:A:248:GLY:N	1:A:260:ARG:NH1	2.69	0.41
3:D:121:TRP:CG	3:D:153:ASN:HD21	2.39	0.41
3:F:143:LEU:HD12	3:F:171:MET:HE1	2.03	0.41
3:G:83:PHE:HB3	3:G:87:ILE:HD11	2.03	0.41
3:G:201:THR:HG22	3:G:214:LEU:HD22	2.02	0.41
3:G:213:HIS:O	3:G:214:LEU:HD23	2.20	0.41
3:H:172:MET:HA	3:H:172:MET:HE2	2.03	0.41
3:H:292:ASN:ND2	3:I:274:ASN:HB3	2.35	0.41
4:J:16:TRP:CG	4:J:31:PRO:HA	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:31:PRO:HD2	4:J:65:VAL:HG11	2.01	0.41
1:A:185:VAL:O	1:A:189:VAL:HG23	2.21	0.41
3:F:12:SER:HB2	3:F:305:LEU:HG	2.03	0.41
3:G:83:PHE:CD1	3:G:87:ILE:HD11	2.56	0.41
3:G:173:THR:O	3:G:177:LYS:HE3	2.21	0.41
3:H:5:ILE:HD11	3:H:248:LEU:HD23	2.03	0.41
3:H:113:PRO:HG2	3:H:165:ARG:HD3	2.03	0.41
8:K:83:PRO:HB2	8:K:199:LEU:HD21	2.02	0.41
3:D:118:GLU:HA	3:D:153:ASN:HB3	2.02	0.40
1:A:153:ASN:HB3	1:A:167:ARG:NH2	2.37	0.40
3:F:9:VAL:HB	3:F:226:ARG:HB2	2.03	0.40
8:K:86:PHE:CD1	8:K:167:LEU:HG	2.55	0.40
3:I:328:ALA:HB1	3:I:356:TRP:CZ2	2.56	0.40
3:I:349:THR:OG1	3:I:352:GLN:HG3	2.21	0.40
5:L:53:C:H5'	5:L:54:C:C5	2.53	0.40
1:A:389:LYS:HE3	1:A:389:LYS:HB3	1.88	0.40
1:A:402:GLY:HA3	1:A:478:THR:HG23	2.04	0.40
3:G:112:THR:HA	3:G:113:PRO:HD3	1.88	0.40
3:H:182:MET:HG2	3:H:183:SER:N	2.29	0.40
3:I:232:LEU:O	3:I:236:GLN:HG3	2.21	0.40
1:A:403:PHE:CZ	1:A:408:PHE:HB3	2.56	0.40
1:A:426:GLN:HB2	1:A:457:LEU:HD21	2.04	0.40
3:D:20:ARG:HA	3:D:25:MET:O	2.21	0.40
3:E:213:HIS:C	3:E:214:LEU:HD12	2.46	0.40
3:E:280:MET:HE3	3:E:282:ASN:HB2	2.03	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	473/502 (94%)	446 (94%)	26 (6%)	1 (0%)	43 73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	147/182 (81%)	137 (93%)	8 (5%)	2 (1%)	9	37
2	C	146/182 (80%)	141 (97%)	5 (3%)	0	100	100
3	D	310/363 (85%)	286 (92%)	21 (7%)	3 (1%)	12	44
3	E	350/363 (96%)	324 (93%)	21 (6%)	5 (1%)	9	37
3	F	359/363 (99%)	340 (95%)	17 (5%)	2 (1%)	21	55
3	G	350/363 (96%)	334 (95%)	16 (5%)	0	100	100
3	H	348/363 (96%)	332 (95%)	14 (4%)	2 (1%)	21	55
3	I	347/363 (96%)	334 (96%)	13 (4%)	0	100	100
4	J	217/224 (97%)	207 (95%)	9 (4%)	1 (0%)	24	58
8	K	117/199 (59%)	107 (92%)	7 (6%)	3 (3%)	4	25
All	All	3164/3467 (91%)	2988 (94%)	157 (5%)	19 (1%)	21	55

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	GLN
2	B	142	LYS
3	D	182	MET
3	D	183	SER
3	D	330	ALA
3	E	182	MET
3	E	183	SER
3	E	332	PHE
3	F	182	MET
3	F	183	SER
3	H	182	MET
3	H	183	SER
3	E	209	GLN
4	J	188	THR
8	K	39	PHE
8	K	40	HIS
3	E	330	ALA
8	K	14	ARG
2	B	140	TRP

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	399/426 (94%)	382 (96%)	17 (4%)	26	57
2	B	123/155 (79%)	118 (96%)	5 (4%)	27	58
2	C	126/155 (81%)	124 (98%)	2 (2%)	55	73
3	D	234/298 (78%)	211 (90%)	23 (10%)	7	30
3	E	278/298 (93%)	265 (95%)	13 (5%)	23	55
3	F	287/298 (96%)	271 (94%)	16 (6%)	19	50
3	G	283/298 (95%)	265 (94%)	18 (6%)	16	46
3	H	280/298 (94%)	269 (96%)	11 (4%)	28	60
3	I	277/298 (93%)	267 (96%)	10 (4%)	31	61
4	J	186/192 (97%)	175 (94%)	11 (6%)	18	48
8	K	82/170 (48%)	73 (89%)	9 (11%)	6	25
All	All	2555/2886 (88%)	2420 (95%)	135 (5%)	20	51

All (135) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	78	ASP
1	A	82	GLN
1	A	89	ASP
1	A	111	VAL
1	A	114	MET
1	A	229	VAL
1	A	288	VAL
1	A	298	LEU
1	A	347	MET
1	A	351	ARG
1	A	354	GLN
1	A	380	GLU
1	A	407	ASP
1	A	413	VAL

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Mol	Chain	Res	Type
1	A	414	SER
1	A	466	VAL
2	B	28	VAL
2	B	55	GLN
2	B	75	GLN
2	B	110	ARG
2	B	118	ARG
2	C	28	VAL
2	C	106	ILE
3	D	5	ILE
3	D	13	HIS
3	D	70	GLN
3	D	75	LEU
3	D	76	ARG
3	D	82	ARG
3	D	88	ILE
3	D	111	VAL
3	D	125	GLN
3	D	132	ASP
3	D	134	LEU
3	D	147	ILE
3	D	152	VAL
3	D	154	LEU
3	D	156	GLN
3	D	217	GLN
3	D	282	ASN
3	D	286	MET
3	D	288	LEU
3	D	333	SER
3	D	334	LEU
3	D	335	SER
3	D	344	VAL
3	E	5	ILE
3	E	82	ARG
3	E	139	LEU
3	E	150	ILE
3	E	188	ILE
3	E	194	ASP
3	E	201	THR
3	E	206	LEU
3	E	246	GLN
3	E	266	LYS

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Mol	Chain	Res	Type
3	E	283	PHE
3	E	305	LEU
3	E	325	LEU
3	F	20	ARG
3	F	84	ASP
3	F	152	VAL
3	F	183	SER
3	F	201	THR
3	F	218	GLU
3	F	244	ARG
3	F	268	ARG
3	F	277	ASP
3	F	280	MET
3	F	282	ASN
3	F	284	SER
3	F	305	LEU
3	F	334	LEU
3	F	340	ILE
3	F	362	GLU
3	G	76	ARG
3	G	87	ILE
3	G	101	ASP
3	G	150	ILE
3	G	230	ILE
3	G	280	MET
3	G	282	ASN
3	G	283	PHE
3	G	284	SER
3	G	285	ASP
3	G	286	MET
3	G	317	ASP
3	G	334	LEU
3	G	335	SER
3	G	344	VAL
3	G	345	LYS
3	G	347	MET
3	G	359	ASN
3	H	150	ILE
3	H	152	VAL
3	H	230	ILE
3	H	277	ASP
3	H	278	MET

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Mol	Chain	Res	Type
3	H	280	MET
3	H	282	ASN
3	H	286	MET
3	H	331	GLN
3	H	334	LEU
3	H	335	SER
3	I	65	THR
3	I	76	ARG
3	I	92	LEU
3	I	136	ASP
3	I	172	MET
3	I	173	THR
3	I	249	GLU
3	I	269	THR
3	I	336	ASP
3	I	340	ILE
4	J	7	LEU
4	J	54	LEU
4	J	71	ILE
4	J	96	ARG
4	J	128	MET
4	J	141	ARG
4	J	157	LEU
4	J	163	GLN
4	J	165	SER
4	J	183	SER
4	J	192	LEU
8	K	7	ILE
8	K	13	SER
8	K	19	LEU
8	K	51	HIS
8	K	52	VAL
8	K	67	THR
8	K	76	PHE
8	K	88	LEU
8	K	199	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	281	HIS
1	A	320	GLN

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Mol	Chain	Res	Type
1	A	422	HIS
2	B	159	ASN
3	D	8	HIS
3	D	125	GLN
3	D	217	GLN
3	D	236	GLN
3	E	85	GLN
3	E	153	ASN
3	E	274	ASN
3	F	57	ASN
3	F	246	GLN
3	F	256	HIS
3	F	306	GLN
3	F	352	GLN
3	F	360	ASN
3	G	13	HIS
3	G	85	GLN
3	G	282	ASN
3	H	57	ASN
3	H	213	HIS
3	H	282	ASN
3	H	314	GLN
3	H	352	GLN
3	I	77	GLN
3	I	234	GLN
3	I	292	ASN
3	I	331	GLN
3	I	346	GLN
4	J	47	GLN
4	J	62	GLN
4	J	105	GLN
8	K	21	GLN
8	K	91	ASN
8	K	170	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	L	60/61 (98%)	20 (33%)	1 (1%)

All (20) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	L	8	G
5	L	9	A
5	L	15	U
5	L	21	A
5	L	22	G
5	L	27	U
5	L	28	G
5	L	33	G
5	L	34	C
5	L	38	C
5	L	39	A
5	L	43	G
5	L	44	U
5	L	47	C
5	L	52	G
5	L	53	C
5	L	54	C
5	L	55	A
5	L	56	G
5	L	59	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	L	54	C

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

1 non-standard protein/DNA/RNA residue 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
5	23G	L	61	5	24,29,30	1.42	4 (16%)	34,45,48	2.25	11 (32%)

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
5	23G	L	61	5	-	0/7/35/36	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	61	23G	C6-N1	-3.10	1.33	1.38
5	L	61	23G	C4-N9	-2.80	1.30	1.38
5	L	61	23G	C5-C4	2.70	1.46	1.38
5	L	61	23G	C5-N7	-2.34	1.34	1.39

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	61	23G	C5-C4-N3	-5.14	120.20	128.39
5	L	61	23G	C6-C5-N7	4.47	138.42	130.29
5	L	61	23G	C2-N3-C4	4.34	119.77	112.30
5	L	61	23G	O4'-C1'-N9	4.19	117.84	108.36
5	L	61	23G	C4-C5-N7	-3.89	104.51	110.67
5	L	61	23G	OC1-PC-OC2	3.32	120.61	109.89
5	L	61	23G	O3'-PC-OC2	-2.39	109.46	115.76
5	L	61	23G	N9-C4-N3	2.38	130.71	125.95
5	L	61	23G	N2-C2-N3	-2.34	115.11	119.67
5	L	61	23G	C8-N7-C5	2.16	108.12	104.26
5	L	61	23G	C3'-C2'-C1'	-2.01	98.75	103.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	61	23G	4	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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 ⓘ

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	481/502 (95%)	0.23	13 (2%) 56 37	30, 53, 87, 112	0
2	B	151/182 (82%)	0.31	5 (3%) 49 31	39, 70, 102, 128	0
2	C	150/182 (82%)	-0.04	3 (2%) 65 45	26, 43, 65, 94	0
3	D	318/363 (87%)	0.70	14 (4%) 39 24	66, 86, 118, 142	0
3	E	354/363 (97%)	0.32	9 (2%) 58 39	41, 61, 88, 110	0
3	F	361/363 (99%)	0.22	9 (2%) 58 39	35, 56, 84, 108	0
3	G	354/363 (97%)	-0.01	4 (1%) 78 60	30, 45, 67, 86	0
3	H	352/363 (96%)	0.18	16 (4%) 38 24	27, 46, 86, 109	0
3	I	351/363 (96%)	0.11	7 (1%) 65 45	24, 44, 86, 114	0
4	J	219/224 (97%)	-0.03	1 (0%) 87 76	27, 44, 72, 103	0
5	L	60/61 (98%)	0.45	5 (8%) 17 11	30, 51, 179, 191	0
6	M	19/47 (40%)	1.82	10 (52%) 0 1	59, 113, 169, 185	0
7	N	40/47 (85%)	0.13	1 (2%) 58 39	33, 43, 160, 202	0
8	K	139/199 (69%)	1.79	56 (40%) 0 1	82, 117, 153, 166	0
All	All	3349/3622 (92%)	0.29	153 (4%) 37 23	24, 55, 110, 202	0

All (153) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	K	185	PRO	5.9
8	K	4	SER	5.9
3	H	333	SER	5.1
8	K	25	HIS	4.8
8	K	69	ILE	4.8
6	M	19	DT	4.6
8	K	50	CYS	4.4
3	H	345	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
8	K	93	ILE	4.3
1	A	95	HIS	4.1
6	M	21	DT	4.0
8	K	64	ALA	4.0
8	K	148	TYR	3.8
3	I	137	LYS	3.7
8	K	41	VAL	3.7
3	G	231	ASN	3.6
3	D	264	GLY	3.6
3	D	101	ASP	3.6
5	L	43	G	3.5
8	K	8	ILE	3.5
8	K	14	ARG	3.5
8	K	172	ALA	3.5
3	H	329	ALA	3.4
3	F	12	SER	3.4
3	F	149	ALA	3.3
8	K	65	VAL	3.3
8	K	140	HIS	3.3
8	K	6	VAL	3.3
3	D	344	VAL	3.3
7	N	40	DC	3.3
8	K	158	ILE	3.3
3	D	103	ALA	3.2
8	K	23	LEU	3.2
6	M	23	DA	3.1
8	K	39	PHE	3.1
8	K	24	TRP	3.1
3	D	81	GLU	3.1
2	B	76	ASP	3.1
2	B	70	ASN	3.1
8	K	59	MET	3.0
8	K	147	GLN	2.9
6	M	12	DC	2.9
8	K	74	VAL	2.9
8	K	53	LEU	2.9
8	K	199	LEU	2.9
3	E	284	SER	2.8
3	E	334	LEU	2.8
8	K	117	ILE	2.8
3	D	89	ASP	2.8
3	E	231	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
8	K	20	HIS	2.8
3	E	12	SER	2.8
3	F	183	SER	2.7
3	G	149	ALA	2.7
8	K	137	GLU	2.7
2	C	53	ARG	2.7
3	H	326	ASN	2.7
8	K	79	GLN	2.7
3	I	336	ASP	2.7
6	M	22	DT	2.6
3	D	102	GLU	2.6
8	K	190	GLY	2.6
3	D	154	LEU	2.6
8	K	51	HIS	2.6
8	K	36	ASP	2.6
1	A	90	MET	2.6
1	A	107	LYS	2.6
8	K	189	MET	2.6
1	A	380	GLU	2.6
8	K	62	SER	2.6
8	K	146	PRO	2.5
1	A	115	GLU	2.5
8	K	68	VAL	2.5
3	H	183	SER	2.5
8	K	55	GLN	2.5
3	D	100	VAL	2.5
8	K	7	ILE	2.5
8	K	73	GLN	2.5
3	D	135	ASP	2.5
8	K	18	GLN	2.5
8	K	136	VAL	2.5
3	D	247	ALA	2.5
1	A	322	GLU	2.5
8	K	22	GLY	2.5
3	F	342	ALA	2.4
3	H	231	ASN	2.4
8	K	15	ASP	2.4
3	F	335	SER	2.4
8	K	75	GLU	2.4
3	I	138	LYS	2.4
3	D	152	VAL	2.4
6	M	28	DT	2.4

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Mol	Chain	Res	Type	RSRZ
8	K	1	MET	2.4
3	H	104	GLU	2.4
3	F	231	ASN	2.4
8	K	184	GLY	2.4
4	J	130	ILE	2.4
8	K	11	ALA	2.4
3	E	209	GLN	2.4
8	K	37	PHE	2.4
3	E	149	ALA	2.4
1	A	97	GLU	2.4
6	M	13	DT	2.4
3	F	182	MET	2.3
2	B	84	GLY	2.3
3	G	330	ALA	2.3
6	M	29	DT	2.3
3	F	333	SER	2.3
6	M	20	DT	2.3
1	A	96	ALA	2.3
3	H	149	ALA	2.3
3	H	328	ALA	2.3
3	E	183	SER	2.3
8	K	52	VAL	2.3
3	E	182	MET	2.2
2	C	78	LYS	2.2
3	H	12	SER	2.2
3	G	153	ASN	2.2
8	K	170	ASN	2.2
3	F	339	PRO	2.2
3	H	182	MET	2.2
3	D	124	GLU	2.2
8	K	167	LEU	2.2
1	A	85	ALA	2.2
8	K	145	ARG	2.2
8	K	19	LEU	2.2
2	B	50	GLU	2.2
3	D	177	LYS	2.2
5	L	44	U	2.2
5	L	57	C	2.1
3	H	108	ALA	2.1
1	A	15	ASN	2.1
2	B	69	LYS	2.1
3	H	278	MET	2.1

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Mol	Chain	Res	Type	RSRZ
8	K	42	GLU	2.1
1	A	98	HIS	2.1
3	H	181	ALA	2.1
3	I	125	GLN	2.1
3	E	283	PHE	2.1
5	L	59	G	2.1
1	A	208	GLN	2.1
3	I	177	LYS	2.1
1	A	14	ARG	2.1
3	H	334	LEU	2.1
3	I	326	ASN	2.0
3	H	346	GLN	2.0
8	K	58	GLN	2.0
6	M	11	DG	2.0
8	K	38	LEU	2.0
2	C	83	THR	2.0
3	I	141	LYS	2.0
8	K	16	LEU	2.0
5	L	53	C	2.0

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

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
5	23G	L	61	26/27	0.62	0.18	86,134,211,233	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
9	ZN	A	601	1/1	1.00	0.03	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.