



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2023 – 03:10 AM EDT

PDB ID : 2HOI
Title : Crystal structure of the tetrameric pre-cleavage synaptic complex in the cre-loxp site-specific recombination
Authors : Ghosh, K.; Van Duyne, G.D.
Deposited on : 2006-07-14
Resolution : 2.60 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

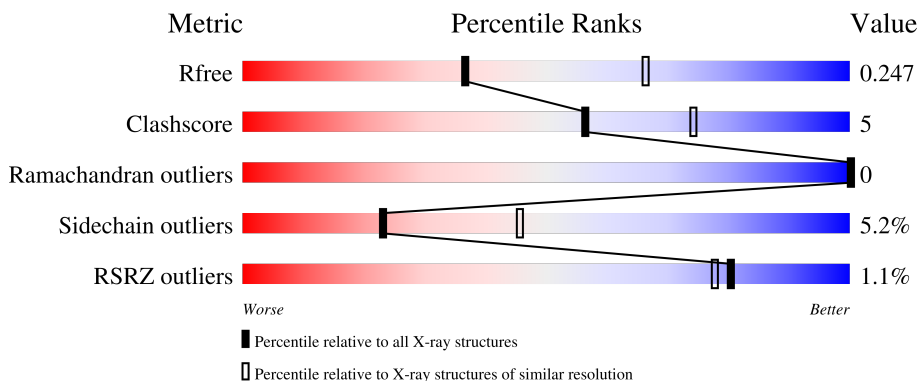
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	C	35	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 57%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 43%; height: 10px; background-color: orange; margin-right: 5px;"></div> </div>
1	E	35	<div style="display: flex; align-items: center;"> <div style="width: 66%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 31%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 3%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div>
2	D	35	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 77%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 20%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 3%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div>
2	F	35	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 71%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 3%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div>
3	A	343	<div style="display: flex; align-items: center;"> <div style="width: 80%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 3%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div>

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Mol	Chain	Length	Quality of chain
3	B	343	 83% 11% 6%
3	G	343	%  80% 12% • 6%
3	H	343	%  82% 10% • 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13811 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 DNA chain called LoxP DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	C	35	Total	C	N	O	P	0	0	0
			710	344	124	208	34			
1	E	34	Total	C	N	O	P	0	0	0
			693	334	122	203	34			

- Molecule 2 is a DNA chain called LoxP DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	D	34	Total	C	N	O	P	0	0	0
			701	337	125	205	34			
2	F	34	Total	C	N	O	P	0	0	0
			701	337	125	205	34			

- Molecule 3 is a protein called Recombinase Cre.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	322	Total	C	N	O	S	0	0	0
			2546	1581	485	465	15			
3	B	322	Total	C	N	O	S	0	0	0
			2546	1581	485	465	15			
3	G	322	Total	C	N	O	S	0	0	0
			2546	1581	485	465	15			
3	H	322	Total	C	N	O	S	0	0	0
			2546	1581	485	465	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	ALA	LYS	engineered mutation	UNP P06956
B	201	ALA	LYS	engineered mutation	UNP P06956
G	201	ALA	LYS	engineered mutation	UNP P06956
H	201	ALA	LYS	engineered mutation	UNP P06956

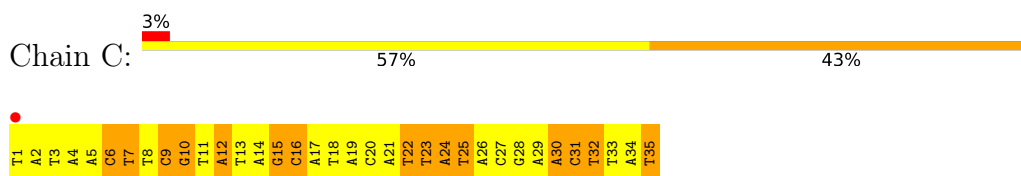
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	50	Total O 50 50	0	0
4	D	42	Total O 42 42	0	0
4	E	36	Total O 36 36	0	0
4	F	50	Total O 50 50	0	0
4	A	168	Total O 168 168	0	0
4	B	177	Total O 177 177	0	0
4	G	144	Total O 144 144	0	0
4	H	155	Total O 155 155	0	0

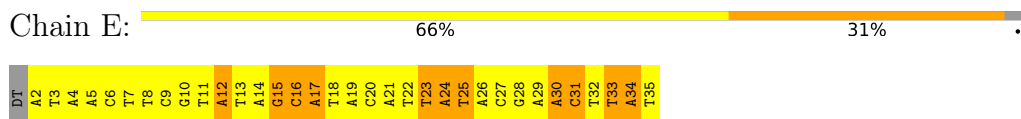
3 Residue-property plots [i](#)

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

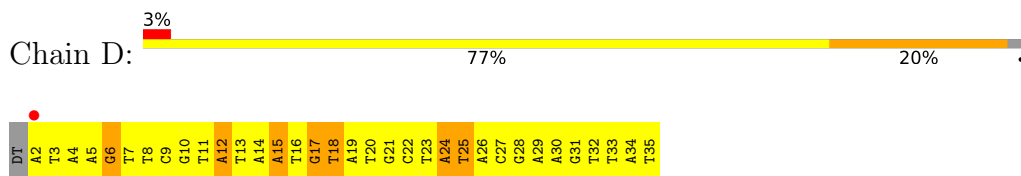
- Molecule 1: LoxP DNA



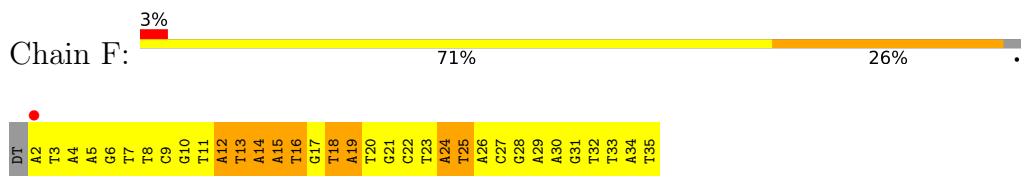
- Molecule 1: LoxP DNA



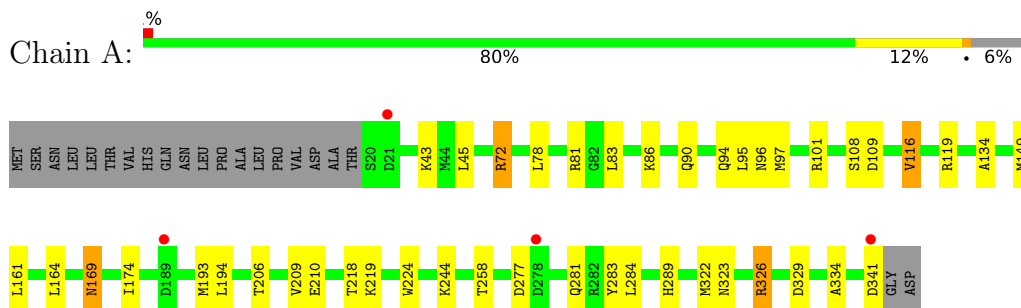
- Molecule 2: LoxP DNA




- Molecule 2: LoxP DNA

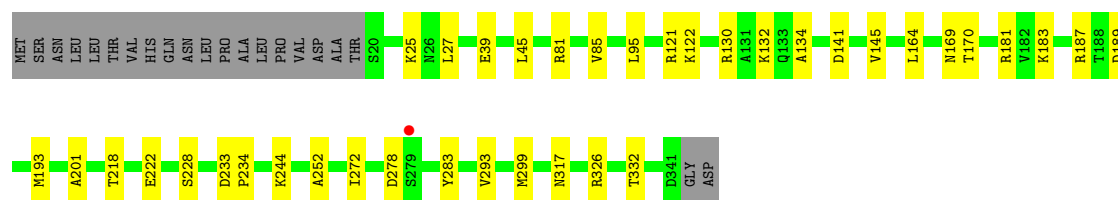


- Molecule 3: Recombinase Cre




- Molecule 3: Recombinase Cre

Chain B:  83% 11% 6%




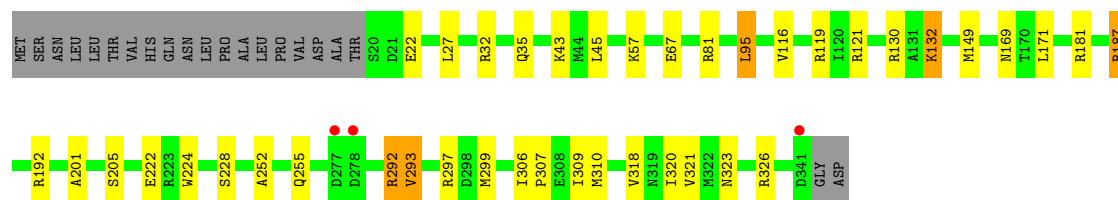
- Molecule 3: Recombinase Cre

Chain G:  80% 12% 6%



- Molecule 3: Recombinase Cre

Chain H:  82% 10% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	136.78Å 136.78Å 218.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.92 – 2.60 19.92 – 2.60	Depositor EDS
% Data completeness (in resolution range)	81.5 (19.92-2.60) 81.5 (19.92-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.02 (at 2.59Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.184 , 0.246 0.187 , 0.247	Depositor DCC
R_{free} test set	3007 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13811	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% 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

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	C	1.07	3/795 (0.4%)	1.93	60/1224 (4.9%)
1	E	1.09	4/776 (0.5%)	1.83	55/1194 (4.6%)
2	D	1.04	2/786 (0.3%)	1.90	51/1212 (4.2%)
2	F	1.01	1/786 (0.1%)	1.91	57/1212 (4.7%)
3	A	0.38	0/2587	0.58	1/3489 (0.0%)
3	B	0.36	0/2587	0.58	0/3489
3	G	0.35	0/2587	0.57	0/3489
3	H	0.37	0/2587	0.61	0/3489
All	All	0.60	10/13491 (0.1%)	1.09	224/18798 (1.2%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1	DT	C5-C7	8.11	1.54	1.50
2	D	22	DC	N1-C2	-7.00	1.33	1.40
1	E	27	DC	N1-C2	-6.54	1.33	1.40
2	D	27	DC	N1-C2	-5.88	1.34	1.40
2	F	22	DC	N1-C2	-5.78	1.34	1.40
1	E	16	DC	N1-C2	-5.61	1.34	1.40
1	C	6	DC	N1-C2	-5.27	1.34	1.40
1	C	16	DC	N1-C2	-5.23	1.34	1.40
1	E	20	DC	N1-C2	-5.16	1.34	1.40
1	E	9	DC	N1-C2	-5.11	1.35	1.40

All (224) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	20	DC	O4'-C1'-N1	10.33	115.23	108.00
2	F	17	DG	O4'-C4'-C3'	-9.91	100.05	106.00
2	D	17	DG	O4'-C4'-C3'	-8.54	100.88	106.00
2	D	26	DA	O4'-C4'-C3'	-8.44	100.94	106.00
2	F	6	DG	O4'-C4'-C3'	-7.72	101.37	106.00
1	E	6	DC	O4'-C4'-C3'	-7.62	101.43	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	16	DT	O4'-C1'-N1	7.57	113.30	108.00
1	C	33	DT	OP1-P-OP2	-7.10	108.94	119.60
2	F	2	DA	OP1-P-OP2	-7.06	109.01	119.60
1	C	31	DC	O4'-C4'-C3'	-7.05	101.68	104.50
2	D	11	DT	OP1-P-OP2	-7.00	109.10	119.60
1	E	28	DG	OP1-P-OP2	-6.97	109.14	119.60
2	D	22	DC	N3-C4-C5	-6.95	119.12	121.90
1	C	11	DT	OP1-P-OP2	-6.88	109.29	119.60
2	D	9	DC	OP1-P-OP2	-6.86	109.32	119.60
1	E	31	DC	O4'-C1'-N1	6.84	112.79	108.00
2	D	6	DG	OP1-P-OP2	-6.84	109.34	119.60
1	E	3	DT	OP1-P-OP2	-6.84	109.34	119.60
2	F	12	DA	OP1-P-OP2	-6.83	109.35	119.60
1	C	2	DA	OP1-P-OP2	-6.83	109.36	119.60
2	F	28	DG	OP1-P-OP2	-6.82	109.36	119.60
1	E	6	DC	OP1-P-OP2	-6.80	109.40	119.60
2	F	8	DT	OP1-P-OP2	-6.78	109.43	119.60
2	F	16	DT	OP1-P-OP2	-6.76	109.45	119.60
1	E	30	DA	OP1-P-OP2	-6.74	109.48	119.60
2	D	31	DG	OP1-P-OP2	-6.74	109.50	119.60
1	E	9	DC	OP1-P-OP2	-6.74	109.50	119.60
2	D	22	DC	OP1-P-OP2	-6.73	109.51	119.60
2	F	18	DT	O4'-C1'-N1	6.73	112.71	108.00
1	E	7	DT	OP1-P-OP2	-6.72	109.52	119.60
2	D	23	DT	OP1-P-OP2	-6.72	109.52	119.60
1	E	2	DA	OP1-P-OP2	-6.71	109.53	119.60
2	D	30	DA	OP1-P-OP2	-6.71	109.53	119.60
1	E	25	DT	OP1-P-OP2	-6.67	109.59	119.60
1	C	16	DC	OP1-P-OP2	-6.67	109.60	119.60
2	D	32	DT	OP1-P-OP2	-6.66	109.61	119.60
1	C	32	DT	OP1-P-OP2	-6.66	109.61	119.60
2	F	18	DT	OP1-P-OP2	-6.66	109.62	119.60
1	E	13	DT	O4'-C1'-N1	6.65	112.66	108.00
1	C	35	DT	OP1-P-OP2	-6.65	109.62	119.60
2	F	9	DC	OP1-P-OP2	-6.65	109.63	119.60
1	C	31	DC	C6-N1-C2	6.65	122.96	120.30
2	F	10	DG	OP1-P-OP2	-6.64	109.63	119.60
1	E	26	DA	OP1-P-OP2	-6.62	109.67	119.60
2	D	19	DA	OP1-P-OP2	-6.60	109.70	119.60
2	D	25	DT	OP1-P-OP2	-6.59	109.71	119.60
2	D	2	DA	OP1-P-OP2	-6.58	109.73	119.60
1	E	31	DC	OP1-P-OP2	-6.58	109.73	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	23	DT	OP1-P-OP2	-6.56	109.76	119.60
1	C	20	DC	OP1-P-OP2	-6.56	109.76	119.60
1	C	26	DA	OP1-P-OP2	-6.56	109.77	119.60
1	C	6	DC	OP1-P-OP2	-6.55	109.77	119.60
1	E	10	DG	OP1-P-OP2	-6.54	109.78	119.60
1	C	3	DT	OP1-P-OP2	-6.54	109.80	119.60
2	D	27	DC	OP1-P-OP2	-6.53	109.81	119.60
2	D	20	DT	OP1-P-OP2	-6.53	109.81	119.60
2	D	3	DT	OP1-P-OP2	-6.52	109.82	119.60
1	C	28	DG	OP1-P-OP2	-6.51	109.83	119.60
2	D	15	DA	OP1-P-OP2	-6.51	109.84	119.60
2	F	21	DG	OP1-P-OP2	-6.50	109.86	119.60
1	E	16	DC	OP1-P-OP2	-6.50	109.86	119.60
1	C	25	DT	OP1-P-OP2	-6.49	109.86	119.60
1	E	7	DT	C4-C5-C7	6.48	122.89	119.00
1	C	13	DT	OP1-P-OP2	-6.47	109.89	119.60
1	C	34	DA	OP1-P-OP2	-6.47	109.89	119.60
1	C	8	DT	OP1-P-OP2	-6.47	109.89	119.60
1	C	18	DT	C4-C5-C7	6.45	122.87	119.00
2	F	16	DT	O4'-C1'-N1	6.45	112.52	108.00
2	F	4	DA	OP1-P-OP2	-6.45	109.93	119.60
1	E	20	DC	OP1-P-OP2	-6.44	109.93	119.60
2	D	13	DT	OP1-P-OP2	-6.44	109.94	119.60
2	D	21	DG	OP1-P-OP2	-6.44	109.94	119.60
2	F	34	DA	OP1-P-OP2	-6.43	109.95	119.60
2	D	35	DT	OP1-P-OP2	-6.43	109.96	119.60
2	D	17	DG	OP1-P-OP2	-6.42	109.97	119.60
2	D	4	DA	OP1-P-OP2	-6.42	109.97	119.60
1	E	12	DA	OP1-P-OP2	-6.40	110.00	119.60
2	F	25	DT	C4-C5-C7	6.40	122.84	119.00
1	C	14	DA	OP1-P-OP2	-6.39	110.01	119.60
2	F	27	DC	OP1-P-OP2	-6.39	110.01	119.60
2	F	11	DT	OP1-P-OP2	-6.39	110.02	119.60
1	C	5	DA	O4'-C1'-N9	6.38	112.47	108.00
2	F	15	DA	OP1-P-OP2	-6.37	110.04	119.60
1	C	24	DA	OP1-P-OP2	-6.37	110.04	119.60
1	C	12	DA	OP1-P-OP2	-6.36	110.07	119.60
1	E	19	DA	OP1-P-OP2	-6.36	110.07	119.60
2	D	18	DT	OP1-P-OP2	-6.35	110.07	119.60
1	C	19	DA	OP1-P-OP2	-6.34	110.09	119.60
2	D	28	DG	OP1-P-OP2	-6.34	110.09	119.60
2	F	32	DT	OP1-P-OP2	-6.33	110.10	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	6	DG	OP1-P-OP2	-6.33	110.11	119.60
1	E	22	DT	OP1-P-OP2	-6.32	110.11	119.60
1	C	31	DC	OP1-P-OP2	-6.32	110.12	119.60
1	C	22	DT	OP1-P-OP2	-6.31	110.13	119.60
2	D	12	DA	OP1-P-OP2	-6.31	110.14	119.60
2	F	5	DA	OP1-P-OP2	-6.30	110.15	119.60
1	C	17	DA	OP1-P-OP2	-6.30	110.15	119.60
1	E	29	DA	OP1-P-OP2	-6.29	110.16	119.60
1	E	33	DT	OP1-P-OP2	-6.29	110.16	119.60
1	E	34	DA	OP1-P-OP2	-6.29	110.16	119.60
1	E	8	DT	OP1-P-OP2	-6.29	110.17	119.60
1	C	15	DG	OP1-P-OP2	-6.29	110.17	119.60
2	F	19	DA	OP1-P-OP2	-6.29	110.17	119.60
1	C	21	DA	OP1-P-OP2	-6.28	110.18	119.60
2	F	35	DT	C4-C5-C7	6.28	122.77	119.00
1	C	18	DT	C6-C5-C7	-6.27	119.14	122.90
1	E	7	DT	C6-C5-C7	-6.26	119.14	122.90
2	F	13	DT	OP1-P-OP2	-6.26	110.21	119.60
2	F	20	DT	OP1-P-OP2	-6.26	110.21	119.60
1	E	14	DA	OP1-P-OP2	-6.26	110.21	119.60
1	C	23	DT	OP1-P-OP2	-6.26	110.22	119.60
1	E	17	DA	OP1-P-OP2	-6.25	110.23	119.60
2	F	29	DA	OP1-P-OP2	-6.25	110.23	119.60
2	F	22	DC	N3-C4-C5	-6.24	119.40	121.90
2	F	25	DT	OP1-P-OP2	-6.24	110.24	119.60
1	E	35	DT	OP1-P-OP2	-6.23	110.25	119.60
1	E	13	DT	C6-C5-C7	-6.23	119.16	122.90
2	D	8	DT	OP1-P-OP2	-6.22	110.27	119.60
2	F	26	DA	OP1-P-OP2	-6.21	110.28	119.60
1	E	13	DT	OP1-P-OP2	-6.20	110.30	119.60
1	E	32	DT	OP1-P-OP2	-6.20	110.30	119.60
2	F	35	DT	OP1-P-OP2	-6.20	110.31	119.60
2	D	10	DG	OP1-P-OP2	-6.19	110.31	119.60
2	D	7	DT	OP1-P-OP2	-6.18	110.32	119.60
1	E	23	DT	OP1-P-OP2	-6.18	110.33	119.60
1	C	30	DA	OP1-P-OP2	-6.18	110.33	119.60
1	E	18	DT	OP1-P-OP2	-6.16	110.36	119.60
1	C	4	DA	OP1-P-OP2	-6.16	110.37	119.60
1	C	5	DA	OP1-P-OP2	-6.15	110.37	119.60
2	F	24	DA	OP1-P-OP2	-6.15	110.38	119.60
2	D	34	DA	OP1-P-OP2	-6.13	110.40	119.60
1	C	7	DT	OP1-P-OP2	-6.13	110.40	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	10	DG	O4'-C1'-N9	6.13	112.29	108.00
1	E	21	DA	OP1-P-OP2	-6.12	110.42	119.60
2	D	29	DA	OP1-P-OP2	-6.12	110.42	119.60
2	F	3	DT	OP1-P-OP2	-6.12	110.43	119.60
2	D	33	DT	OP1-P-OP2	-6.11	110.44	119.60
2	D	5	DA	OP1-P-OP2	-6.10	110.45	119.60
2	D	16	DT	OP1-P-OP2	-6.10	110.45	119.60
2	D	26	DA	OP1-P-OP2	-6.10	110.45	119.60
1	C	29	DA	OP1-P-OP2	-6.07	110.50	119.60
1	E	24	DA	OP1-P-OP2	-6.07	110.49	119.60
1	C	18	DT	OP1-P-OP2	-6.06	110.51	119.60
1	C	33	DT	C4-C5-C7	6.05	122.63	119.00
1	E	27	DC	OP1-P-OP2	-6.05	110.52	119.60
1	C	8	DT	C4-C5-C7	6.05	122.63	119.00
2	F	31	DG	OP1-P-OP2	-6.05	110.52	119.60
2	F	14	DA	OP1-P-OP2	-6.04	110.54	119.60
2	D	14	DA	OP1-P-OP2	-6.04	110.54	119.60
1	E	5	DA	OP1-P-OP2	-6.03	110.55	119.60
1	E	4	DA	OP1-P-OP2	-6.03	110.56	119.60
2	F	7	DT	OP1-P-OP2	-6.02	110.56	119.60
1	C	9	DC	O4'-C1'-N1	6.01	112.21	108.00
2	F	33	DT	OP1-P-OP2	-6.01	110.59	119.60
2	D	24	DA	OP1-P-OP2	-5.99	110.61	119.60
1	C	27	DC	OP1-P-OP2	-5.97	110.64	119.60
1	E	13	DT	C4-C5-C7	5.96	122.58	119.00
1	C	22	DT	C4-C5-C7	5.96	122.58	119.00
2	D	25	DT	C6-C5-C7	-5.95	119.33	122.90
2	D	18	DT	O4'-C1'-N1	5.94	112.16	108.00
1	E	15	DG	OP1-P-OP2	-5.94	110.69	119.60
2	D	8	DT	C4-C5-C7	5.93	122.56	119.00
2	F	26	DA	O4'-C1'-N9	-5.91	103.86	108.00
1	E	23	DT	C4-C5-C7	5.90	122.54	119.00
1	E	35	DT	C4-C5-C7	5.87	122.52	119.00
1	C	25	DT	C4-C5-C7	5.86	122.52	119.00
1	C	8	DT	C6-C5-C7	-5.83	119.40	122.90
1	E	35	DT	C6-C5-C7	-5.80	119.42	122.90
2	F	25	DT	C6-C5-C7	-5.78	119.43	122.90
1	E	18	DT	C4-C5-C7	5.67	122.40	119.00
2	F	35	DT	C6-C5-C7	-5.66	119.50	122.90
2	F	22	DC	OP1-P-OP2	-5.66	111.11	119.60
2	F	3	DT	C6-C5-C7	-5.66	119.51	122.90
1	C	13	DT	O4'-C1'-N1	5.65	111.95	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	8	DT	C6-C5-C7	-5.63	119.52	122.90
1	C	9	DC	OP1-P-OP2	-5.62	111.16	119.60
1	C	3	DT	O4'-C1'-N1	5.62	111.94	108.00
1	C	10	DG	OP1-P-OP2	-5.62	111.17	119.60
1	C	11	DT	C4-C5-C7	5.61	122.37	119.00
2	F	17	DG	OP1-P-OP2	-5.61	111.18	119.60
2	D	20	DT	C4-C5-C7	5.61	122.36	119.00
2	D	35	DT	C4-C5-C7	5.60	122.36	119.00
1	E	23	DT	C6-C5-C7	-5.59	119.54	122.90
2	F	30	DA	OP1-P-OP2	-5.59	111.21	119.60
2	F	3	DT	C4-C5-C7	5.58	122.35	119.00
1	E	33	DT	C4-C5-C7	5.58	122.35	119.00
1	C	33	DT	C6-C5-C7	-5.57	119.56	122.90
3	A	72	ARG	CD-NE-CZ	5.56	131.38	123.60
1	C	7	DT	C4-C5-C7	5.55	122.33	119.00
1	C	22	DT	C6-C5-C7	-5.55	119.57	122.90
2	D	22	DC	C2-N3-C4	5.54	122.67	119.90
2	D	20	DT	C6-C5-C7	-5.54	119.57	122.90
1	E	11	DT	OP1-P-OP2	-5.50	111.35	119.60
1	E	33	DT	C6-C5-C7	-5.46	119.62	122.90
2	F	33	DT	C3'-C2'-C1'	-5.44	95.97	102.50
1	C	5	DA	C3'-C2'-C1'	-5.44	95.98	102.50
2	D	5	DA	O4'-C1'-N9	5.39	111.77	108.00
2	F	11	DT	O4'-C1'-N1	5.38	111.77	108.00
2	F	3	DT	O4'-C1'-N1	5.38	111.77	108.00
1	E	5	DA	O4'-C1'-N9	5.37	111.76	108.00
1	C	13	DT	C4-C5-C7	5.33	122.20	119.00
2	D	25	DT	C4-C5-C7	5.32	122.19	119.00
1	C	1	DT	O4'-C4'-C3'	-5.28	102.39	104.50
1	E	22	DT	C4-C5-C7	5.27	122.16	119.00
2	F	18	DT	C6-C5-C7	-5.27	119.74	122.90
2	F	5	DA	O4'-C1'-N9	5.24	111.67	108.00
1	E	2	DA	O4'-C4'-C3'	-5.23	102.41	104.50
2	F	7	DT	C4-C5-C7	5.22	122.13	119.00
1	E	18	DT	C6-C5-C7	-5.21	119.77	122.90
1	E	32	DT	C4-C5-C7	5.20	122.12	119.00
2	D	11	DT	C4-C5-C7	5.20	122.12	119.00
2	F	18	DT	C4-C5-C7	5.18	122.11	119.00
1	C	12	DA	O4'-C1'-N9	5.17	111.62	108.00
2	F	32	DT	C6-C5-C7	-5.15	119.81	122.90
2	D	35	DT	C6-C5-C7	-5.15	119.81	122.90
1	C	35	DT	C4-C5-C7	5.14	122.08	119.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	14	DA	O4'-C4'-C3'	-5.13	102.45	104.50
1	C	13	DT	C6-C5-C7	-5.09	119.84	122.90
1	C	20	DC	C3'-C2'-C1'	-5.09	96.39	102.50
1	E	25	DT	O4'-C4'-C3'	-5.07	102.47	104.50
1	C	2	DA	P-O3'-C3'	5.06	125.78	119.70
2	F	22	DC	C2-N3-C4	5.05	122.43	119.90
2	F	23	DT	O4'-C1'-N1	5.04	111.53	108.00
2	F	13	DT	C3'-C2'-C1'	-5.03	96.47	102.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	710	0	400	11	0
1	E	693	0	387	11	0
2	D	701	0	388	6	0
2	F	701	0	388	8	0
3	A	2546	0	2563	37	0
3	B	2546	0	2563	22	0
3	G	2546	0	2563	29	0
3	H	2546	0	2563	25	0
4	A	168	0	0	4	0
4	B	177	0	0	4	0
4	C	50	0	0	3	0
4	D	42	0	0	0	0
4	E	36	0	0	2	0
4	F	50	0	0	4	0
4	G	144	0	0	2	0
4	H	155	0	0	3	0
All	All	13811	0	11815	124	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 5.

All (124) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:428:HOH:O	3:H:121:ARG:HD2	1.69	0.92
1:C:22:DT:H72	4:A:430:HOH:O	1.70	0.91
3:A:72:ARG:HG3	3:A:116:VAL:HG11	1.56	0.86
3:A:72:ARG:HG3	3:A:116:VAL:CG1	2.05	0.85
4:C:60:HOH:O	3:A:97:MET:SD	2.36	0.82
3:A:72:ARG:HD2	3:A:116:VAL:HB	1.64	0.80
2:F:12:DA:OP1	3:G:81:ARG:NH1	2.13	0.79
3:A:72:ARG:CD	3:A:116:VAL:HB	2.14	0.77
1:E:30:DA:H2''	1:E:31:DC:H5''	1.68	0.76
3:A:72:ARG:HG3	3:A:116:VAL:CB	2.19	0.73
3:G:146:ARG:O	3:G:150:GLU:HB2	1.89	0.72
2:D:6:DG:OP2	3:A:156:GLN:NE2	2.26	0.68
2:F:24:DA:H5'	3:H:201:ALA:HB2	1.77	0.67
3:A:72:ARG:CG	3:A:116:VAL:HB	2.26	0.65
3:A:72:ARG:HG2	3:A:116:VAL:HG21	1.77	0.65
3:B:193:MET:HG3	3:B:218:THR:HG23	1.78	0.65
3:A:72:ARG:HG3	3:A:116:VAL:HB	1.78	0.65
3:G:174:ILE:HD12	3:G:258:THR:HB	1.79	0.64
2:F:16:DT:OP2	4:F:133:HOH:O	2.14	0.64
1:C:12:DA:OP1	3:B:81:ARG:NH2	2.27	0.64
3:A:96:ASN:HD21	3:A:108:SER:H	1.46	0.64
3:A:164:LEU:HA	4:A:451:HOH:O	1.98	0.62
3:A:72:ARG:CG	3:A:116:VAL:CB	2.78	0.62
1:E:16:DC:H2''	1:E:17:DA:C8	2.36	0.61
1:C:31:DC:H2'	1:C:32:DT:H71	1.82	0.61
3:A:119:ARG:HG3	3:H:35:GLN:HB2	1.83	0.61
1:E:33:DT:H2''	1:E:34:DA:C8	2.38	0.59
3:H:181:ARG:NH2	3:H:252:ALA:O	2.38	0.57
3:G:307:PRO:HG3	3:H:306:ILE:HD11	1.85	0.57
2:D:24:DA:H5'	3:B:201:ALA:HB2	1.86	0.56
3:B:299:MET:CE	3:G:334:ALA:HB3	2.36	0.56
3:G:187:ARG:NH2	3:G:222:GLU:OE2	2.40	0.55
1:C:23:DT:OP1	3:B:122:LYS:NZ	2.35	0.55
3:G:133:GLN:HE22	3:G:323:ASN:HB3	1.69	0.55
3:A:193:MET:HG3	3:A:218:THR:HG23	1.89	0.54
3:H:293:VAL:O	3:H:297:ARG:HG3	2.07	0.53
1:C:24:DA:H2'	1:C:25:DT:H72	1.90	0.53
3:A:72:ARG:NH2	3:H:32:ARG:HD2	2.23	0.53
1:C:6:DC:H2'	1:C:7:DT:C6	2.44	0.53
3:B:145:VAL:HG22	3:B:272:ILE:HD11	1.90	0.53
3:B:187:ARG:NH2	3:B:222:GLU:OE2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:181:ARG:HD3	3:B:183:LYS:HE2	1.91	0.52
3:A:169:ASN:C	3:A:169:ASN:HD22	2.12	0.52
1:C:15:DG:OP2	3:B:326:ARG:NH2	2.42	0.52
3:A:334:ALA:HB3	3:H:299:MET:HE3	1.92	0.52
3:A:209:VAL:HG23	3:A:210:GLU:HG3	1.91	0.51
4:F:109:HOH:O	3:G:86:LYS:HD2	2.11	0.51
3:H:171:LEU:HD21	4:H:435:HOH:O	2.10	0.51
3:B:134:ALA:HA	3:B:283:TYR:CD2	2.45	0.50
1:C:15:DG:H4'	1:C:16:DC:OP1	2.11	0.50
4:F:685:HOH:O	3:G:43:LYS:HD3	2.12	0.50
3:A:322:MET:O	3:A:326:ARG:HB3	2.12	0.50
3:G:72:ARG:HG3	3:G:116:VAL:HG11	1.93	0.49
3:A:72:ARG:CG	3:A:116:VAL:HG11	2.35	0.49
3:B:141:ASP:O	3:B:145:VAL:HG23	2.13	0.49
3:G:305:SER:HB3	3:G:307:PRO:HD2	1.94	0.49
3:A:72:ARG:CG	3:A:116:VAL:HG21	2.43	0.48
3:A:109:ASP:HB2	4:A:471:HOH:O	2.12	0.48
3:A:159:ARG:HB2	3:A:224:TRP:CZ3	2.48	0.48
3:B:332:THR:O	3:B:332:THR:HG22	2.11	0.48
2:D:24:DA:H2'	2:D:25:DT:C6	2.49	0.48
2:F:24:DA:H2'	2:F:25:DT:C6	2.49	0.48
3:G:159:ARG:HB2	3:G:224:TRP:CZ3	2.49	0.48
3:A:72:ARG:HD2	3:A:116:VAL:CB	2.39	0.48
1:C:35:DT:H1'	3:A:244:LYS:HD2	1.96	0.47
3:B:164:LEU:HA	4:B:519:HOH:O	2.14	0.47
1:C:9:DC:H2''	1:C:10:DG:C8	2.50	0.47
1:C:30:DA:H2''	1:C:31:DC:H5''	1.97	0.47
3:H:292:ARG:NH1	4:H:473:HOH:O	2.47	0.47
3:G:134:ALA:HA	3:G:283:TYR:CD2	2.49	0.47
4:E:742:HOH:O	3:H:43:LYS:HD2	2.15	0.46
3:A:281:GLN:HE21	3:A:284:LEU:HD21	1.81	0.46
1:E:24:DA:H2'	1:E:25:DT:C6	2.51	0.46
3:G:112:ALA:O	3:G:116:VAL:HG22	2.15	0.46
3:G:23:VAL:HB	4:G:378:HOH:O	2.15	0.45
2:F:18:DT:H2''	2:F:19:DA:C8	2.51	0.45
3:B:299:MET:HE2	3:G:334:ALA:HB3	1.97	0.45
1:E:24:DA:C2	2:F:14:DA:C2	3.05	0.45
3:B:228:SER:HB2	4:B:509:HOH:O	2.16	0.45
3:G:132:LYS:HB3	4:G:389:HOH:O	2.16	0.45
3:H:310:MET:SD	3:H:318:VAL:HG12	2.57	0.45
3:G:33:ASP:OD1	3:H:119:ARG:NH1	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:DG:OP2	3:H:326:ARG:NH2	2.49	0.44
3:G:239:PHE:HB3	3:G:256:LEU:HD12	1.99	0.44
3:H:255:GLN:NE2	4:H:350:HOH:O	2.43	0.44
1:E:15:DG:H4'	1:E:16:DC:OP1	2.17	0.44
2:F:15:DA:H62	3:G:86:LYS:NZ	2.15	0.44
3:H:224:TRP:CZ3	3:H:228:SER:HB3	2.53	0.44
3:B:181:ARG:NH2	3:B:252:ALA:O	2.51	0.43
3:H:320:ILE:HD12	3:H:321:VAL:N	2.33	0.43
4:C:76:HOH:O	3:B:244:LYS:HD3	2.19	0.43
3:B:132:LYS:HD3	4:B:422:HOH:O	2.17	0.43
1:E:23:DT:O4	3:G:90:GLN:NE2	2.48	0.43
4:E:173:HOH:O	3:G:40:HIS:HE1	2.01	0.43
3:G:179:ARG:HG2	3:G:255:GLN:NE2	2.33	0.43
1:E:30:DA:C2'	1:E:31:DC:H5''	2.42	0.43
3:B:85:VAL:HG11	3:B:121:ARG:HG3	2.01	0.43
3:G:133:GLN:NE2	3:G:323:ASN:HB3	2.33	0.43
3:G:209:VAL:HG23	3:G:210:GLU:HG3	2.00	0.43
3:G:169:ASN:HD22	3:G:169:ASN:C	2.23	0.42
3:H:299:MET:HE2	3:H:309:ILE:HA	2.01	0.42
3:A:326:ARG:HD3	4:A:377:HOH:O	2.20	0.42
3:H:132:LYS:HA	3:H:132:LYS:HD2	1.83	0.42
2:D:15:DA:H62	3:A:86:LYS:NZ	2.18	0.42
3:A:323:ASN:HA	3:A:326:ARG:HD2	2.02	0.42
3:H:95:LEU:HD12	3:H:95:LEU:HA	1.89	0.42
3:H:187:ARG:NH2	3:H:222:GLU:OE2	2.53	0.42
1:E:16:DC:H5''	3:H:320:ILE:HG21	2.00	0.42
3:A:329:ASP:HB3	3:H:192:ARG:HH21	1.84	0.42
4:C:51:HOH:O	3:B:317:ASN:HB3	2.19	0.42
3:A:78:LEU:HD22	3:A:83:LEU:HD12	2.02	0.42
3:B:233:ASP:HA	3:B:234:PRO:HD2	1.92	0.42
3:A:134:ALA:HA	3:A:283:TYR:CD2	2.55	0.41
2:D:17:DG:H2''	2:D:18:DT:H5'	2.01	0.41
3:G:237:TYR:CZ	3:G:255:GLN:HG2	2.55	0.41
2:D:12:DA:OP1	3:A:81:ARG:NH1	2.54	0.41
3:A:72:ARG:CG	3:A:116:VAL:CG2	2.99	0.41
3:A:174:ILE:HD12	3:A:258:THR:HB	2.03	0.41
3:B:170:THR:HG22	4:B:458:HOH:O	2.19	0.41
3:G:179:ARG:HG2	3:G:255:GLN:HE22	1.85	0.41
3:H:306:ILE:HB	3:H:307:PRO:HD3	2.03	0.41
3:A:90:GLN:HE22	3:A:94:GLN:HE21	1.68	0.41
2:F:13:DT:H71	3:G:87:THR:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:12:DA:OP1	3:H:81:ARG:NH2	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	320/343 (93%)	318 (99%)	2 (1%)	0	100	100
3	B	320/343 (93%)	319 (100%)	1 (0%)	0	100	100
3	G	320/343 (93%)	314 (98%)	6 (2%)	0	100	100
3	H	320/343 (93%)	317 (99%)	3 (1%)	0	100	100
All	All	1280/1372 (93%)	1268 (99%)	12 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	268/286 (94%)	253 (94%)	15 (6%)	21	42
3	B	268/286 (94%)	258 (96%)	10 (4%)	34	60
3	G	268/286 (94%)	253 (94%)	15 (6%)	21	42
3	H	268/286 (94%)	252 (94%)	16 (6%)	19	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1072/1144 (94%)	1016 (95%)	56 (5%)	23 46

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	43	LYS
3	A	45	LEU
3	A	95	LEU
3	A	101	ARG
3	A	116	VAL
3	A	149	MET
3	A	161	LEU
3	A	169	ASN
3	A	194	LEU
3	A	206	THR
3	A	219	LYS
3	A	277	ASP
3	A	289	HIS
3	A	326	ARG
3	A	341	ASP
3	B	25	LYS
3	B	27	LEU
3	B	39	GLU
3	B	45	LEU
3	B	95	LEU
3	B	130	ARG
3	B	169	ASN
3	B	189	ASP
3	B	278	ASP
3	B	293	VAL
3	G	86	LYS
3	G	92	LEU
3	G	95	LEU
3	G	116	VAL
3	G	122	LYS
3	G	146	ARG
3	G	161	LEU
3	G	169	ASN
3	G	189	ASP
3	G	219	LYS
3	G	227	VAL
3	G	238	LEU

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Mol	Chain	Res	Type
3	G	271	LEU
3	G	289	HIS
3	G	341	ASP
3	H	22	GLU
3	H	27	LEU
3	H	45	LEU
3	H	57	LYS
3	H	67	GLU
3	H	95	LEU
3	H	116	VAL
3	H	130	ARG
3	H	132	LYS
3	H	149	MET
3	H	169	ASN
3	H	187	ARG
3	H	205	SER
3	H	292	ARG
3	H	293	VAL
3	H	323	ASN

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

Mol	Chain	Res	Type
3	A	40	HIS
3	A	90	GLN
3	A	96	ASN
3	A	133	GLN
3	A	151	ASN
3	A	281	GLN
3	A	289	HIS
3	A	311	GLN
3	A	323	ASN
3	B	35	GLN
3	B	60	ASN
3	B	319	ASN
3	G	40	HIS
3	G	144	GLN
3	G	281	GLN
3	G	323	ASN
3	H	255	GLN
3	H	311	GLN
3	H	323	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	C	35/35 (100%)	-0.23	1 (2%) 51 45	16, 30, 60, 77	0
1	E	34/35 (97%)	-0.44	0 100 100	15, 31, 57, 62	0
2	D	34/35 (97%)	-0.55	1 (2%) 51 45	17, 31, 48, 74	0
2	F	34/35 (97%)	-0.56	1 (2%) 51 45	16, 33, 55, 79	0
3	A	322/343 (93%)	-0.49	4 (1%) 79 76	18, 28, 39, 50	0
3	B	322/343 (93%)	-0.54	1 (0%) 94 93	19, 28, 38, 42	0
3	G	322/343 (93%)	-0.42	4 (1%) 79 76	17, 32, 49, 54	0
3	H	322/343 (93%)	-0.55	3 (0%) 84 82	16, 26, 38, 46	0
All	All	1425/1512 (94%)	-0.49	15 (1%) 80 78	15, 29, 43, 79	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	DT	5.5
3	H	341	ASP	5.0
3	B	279	SER	3.0
3	A	21	ASP	2.7
2	D	2	DA	2.6
3	A	341	ASP	2.6
3	G	278	ASP	2.5
3	A	189	ASP	2.5
3	G	341	ASP	2.4
3	A	278	ASP	2.3
3	H	277	ASP	2.1
3	H	278	ASP	2.1
3	G	189	ASP	2.1
3	G	277	ASP	2.0
2	F	2	DA	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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.