



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 09:48 PM EDT

PDB ID : 2O7D / pdb_00002o7d
Title : Tyrosine ammonia-lyase from Rhodobacter sphaeroides, complexed with caffeine
Authors : Louie, G.V.; Bowman, M.E.; Moffitt, M.C.; Baiga, T.J.; Moore, B.S.; Noel, J.P.
Deposited on : 2006-12-10
Resolution : 1.90 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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.48.1

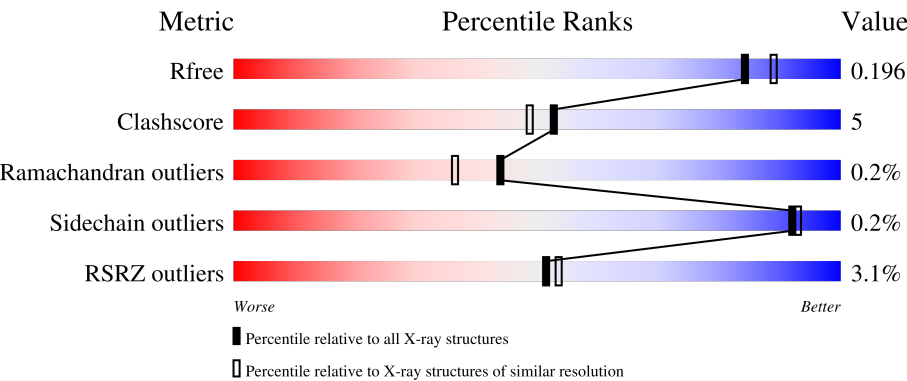
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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	521	<div><div>4%</div><div>88%</div><div>10%</div><div>..</div></div>
1	B	521	<div><div>2%</div><div>84%</div><div>14%</div><div>..</div></div>
1	C	521	<div><div>2%</div><div>87%</div><div>11%</div><div>..</div></div>
1	D	521	<div><div>5%</div><div>85%</div><div>13%</div><div>..</div></div>
1	E	521	<div><div>3%</div><div>89%</div><div>9%</div><div>..</div></div>

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Mol	Chain	Length	Quality of chain
1	F	521	<div><div>%</div><div><div></div><div>88%</div><div>10%<div>••</div></div></div></div>
1	G	521	<div><div>%</div><div><div></div><div>88%</div><div>10%<div>•</div></div></div></div>
1	H	521	<div><div>6%</div><div><div></div><div>86%</div><div>12%<div>••</div></div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 33789 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 Putative histidine ammonia-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	0	0
			3813	2363	731	705	14			
1	B	515	Total	C	N	O	S	0	0	0
			3813	2363	731	705	14			
1	C	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	D	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	E	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	F	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	G	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			
1	H	514	Total	C	N	O	S	0	0	0
			3806	2358	730	704	14			

There are 24 discrepancies between the modelled and reference sequences:

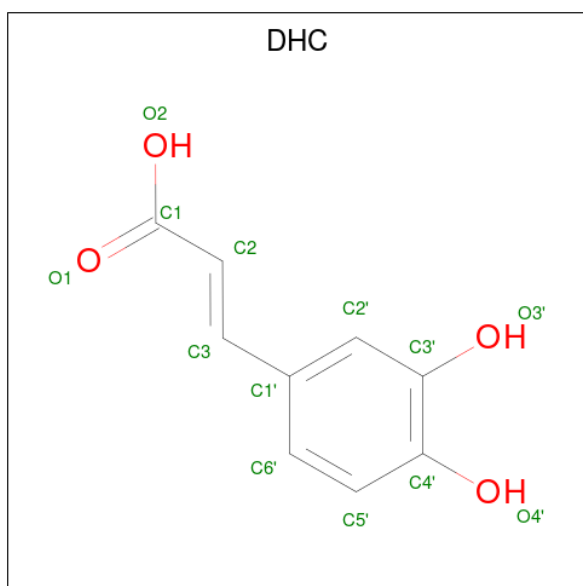
Chain	Residue	Modelled	Actual	Comment	Reference
A	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
A	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
A	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
B	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
B	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
B	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
C	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
C	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
C	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
D	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
D	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
D	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
E	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
E	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
F	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
F	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
F	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
G	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
G	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
G	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0
H	149	MDO	ALA	SEE REMARK 999	UNP Q3IWB0
H	149	MDO	SER	SEE REMARK 999	UNP Q3IWB0
H	149	MDO	GLY	SEE REMARK 999	UNP Q3IWB0

- Molecule 2 is CAFFEIC ACID (CCD ID: DHC) (formula: $C_9H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	9	4		
2	B	1	Total	C	O	0	0
			13	9	4		
2	C	1	Total	C	O	0	0
			13	9	4		
2	D	1	Total	C	O	0	0
			13	9	4		
2	E	1	Total	C	O	0	0
			13	9	4		
2	F	1	Total	C	O	0	0
			13	9	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	G	1	Total	C	O	0	0
			13	9	4		
2	H	1	Total	C	O	0	0
			13	9	4		

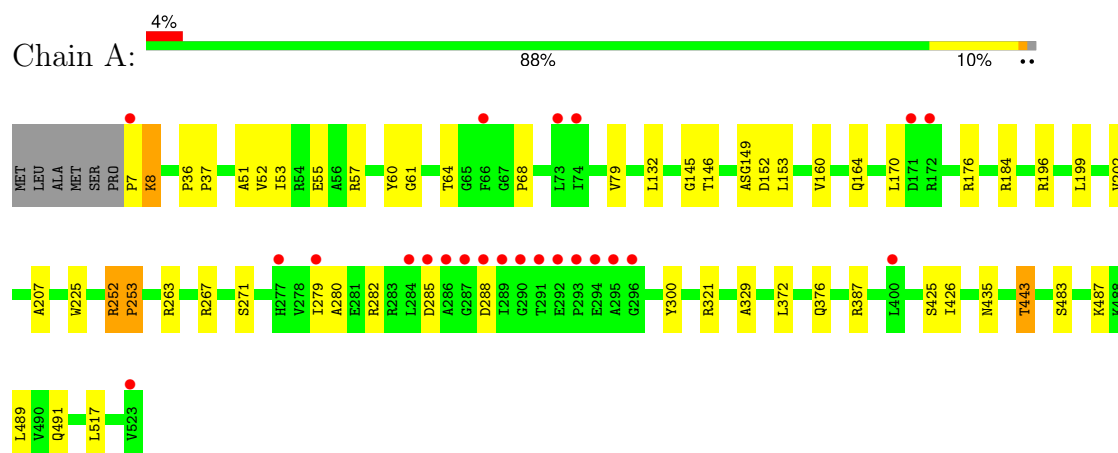
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	360	Total	O	0	0
			360	360		
3	B	369	Total	O	0	0
			369	369		
3	C	407	Total	O	0	0
			407	407		
3	D	404	Total	O	0	0
			404	404		
3	E	382	Total	O	0	0
			382	382		
3	F	491	Total	O	0	0
			491	491		
3	G	431	Total	O	0	0
			431	431		
3	H	379	Total	O	0	0
			379	379		

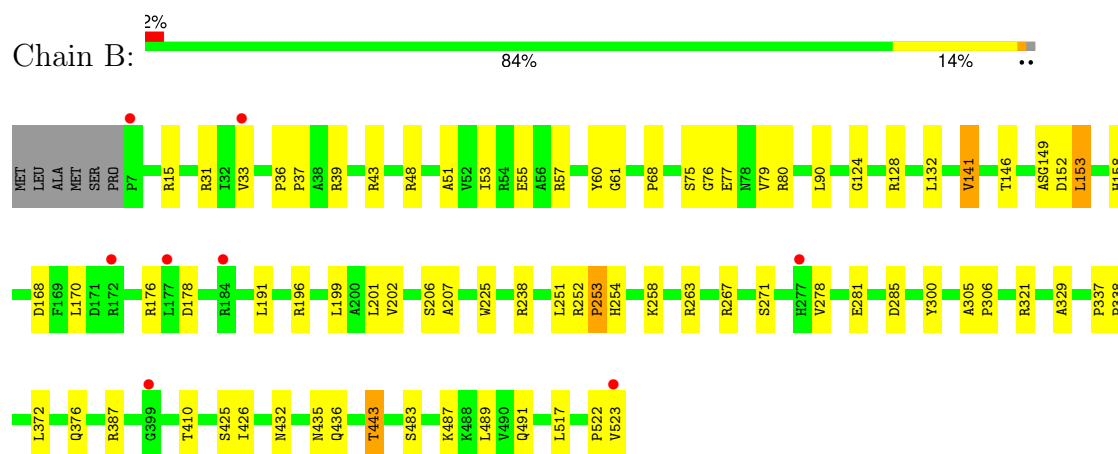
3 Residue-property plots

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.

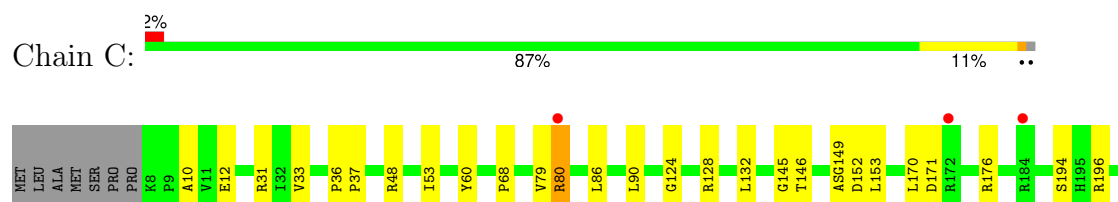
• Molecule 1: Putative histidine ammonia-lyase

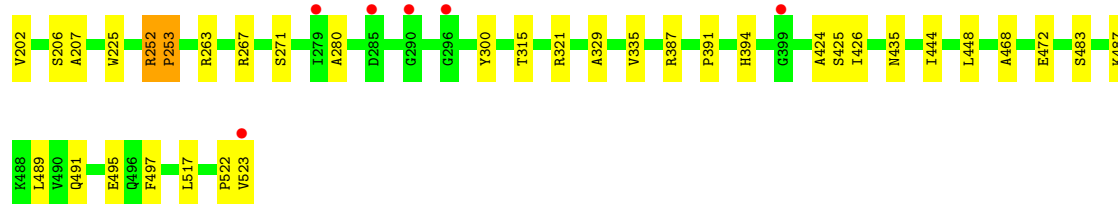


• Molecule 1: Putative histidine ammonia-lyase

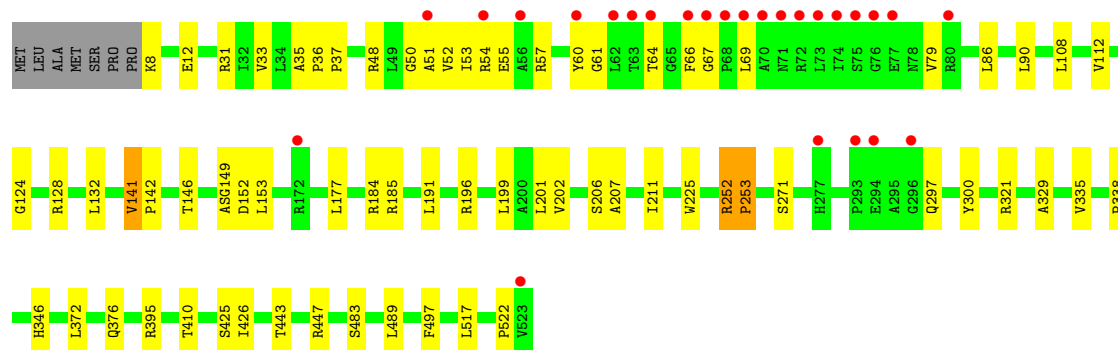
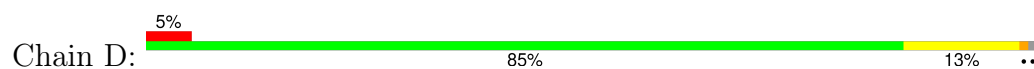


• Molecule 1: Putative histidine ammonia-lyase

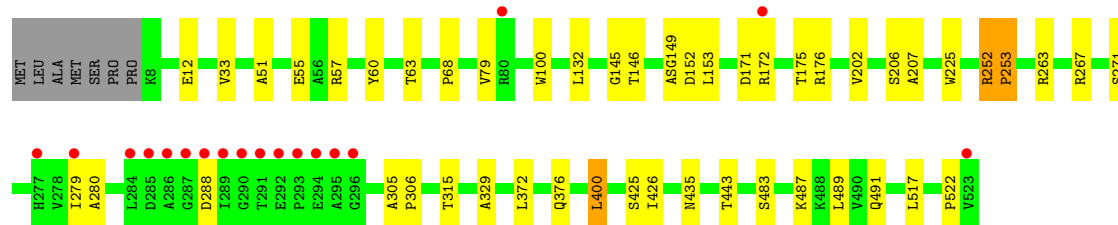
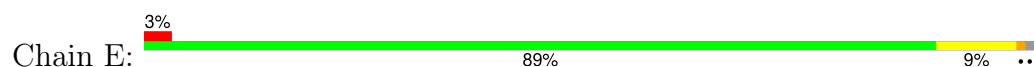




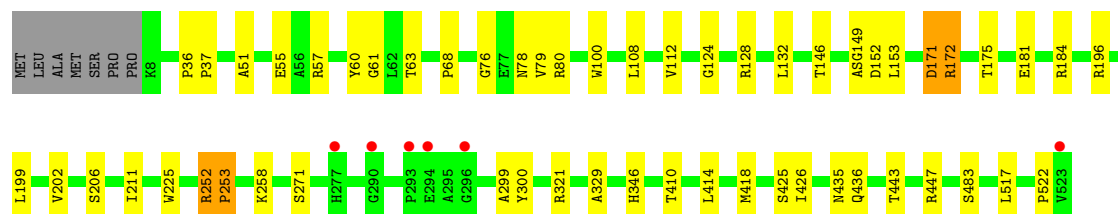
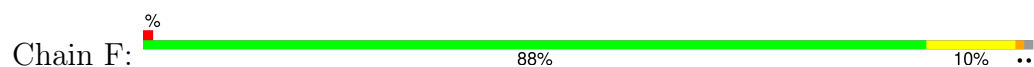
• Molecule 1: Putative histidine ammonia-lyase



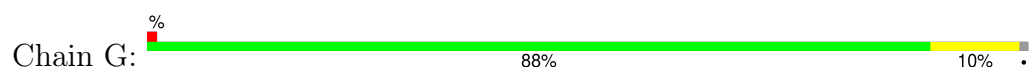
• Molecule 1: Putative histidine ammonia-lyase

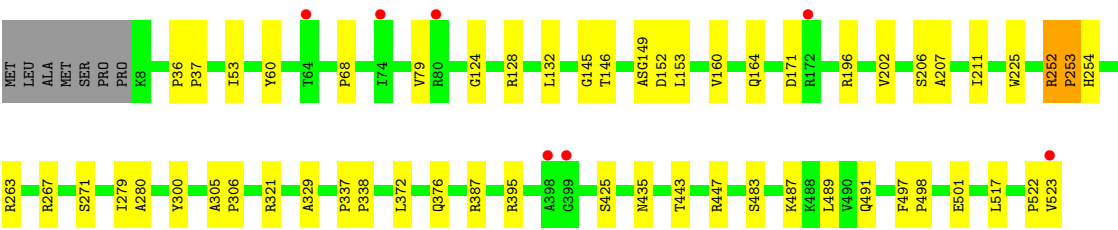


• Molecule 1: Putative histidine ammonia-lyase

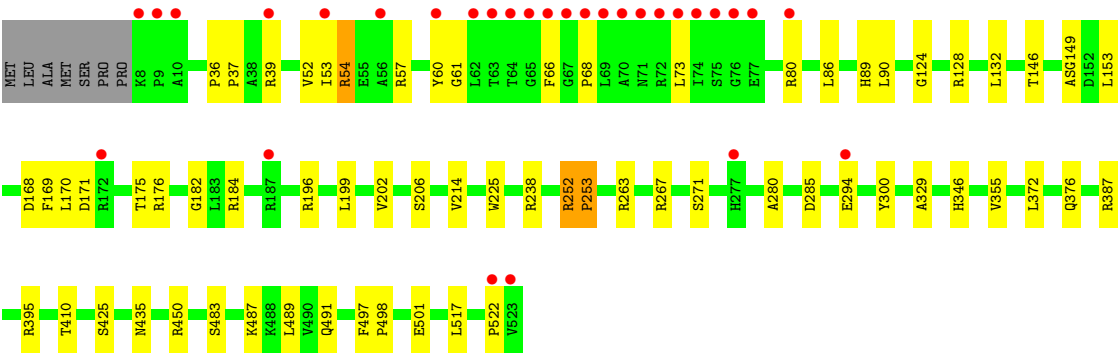
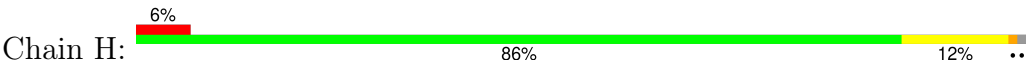


• Molecule 1: Putative histidine ammonia-lyase





● Molecule 1: Putative histidine ammonia-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.61Å 154.90Å 164.16Å 90.00° 94.06° 90.00°	Depositor
Resolution (Å)	500.00 – 1.90 163.75 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (500.00-1.90) 98.9 (163.75-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 1.85Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.175 , 0.198 0.173 , 0.196	Depositor DCC
R_{free} test set	17030 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	33789	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: MDO, DHC

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	0.36	0/3862	0.86	6/5253 (0.1%)
1	B	0.36	0/3862	0.86	7/5253 (0.1%)
1	C	0.38	0/3854	0.88	11/5242 (0.2%)
1	D	0.37	0/3854	0.87	10/5242 (0.2%)
1	E	0.37	0/3854	0.86	6/5242 (0.1%)
1	F	0.38	0/3854	0.88	8/5242 (0.2%)
1	G	0.38	0/3854	0.87	8/5242 (0.2%)
1	H	0.36	0/3854	0.84	7/5242 (0.1%)
All	All	0.37	0/30848	0.86	63/41958 (0.2%)

There are no bond length outliers.

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	252	ARG	CA-C-N	7.22	128.87	119.84
1	F	252	ARG	C-N-CA	7.22	128.87	119.84
1	C	497	PHE	CA-C-N	7.13	124.86	119.66
1	C	497	PHE	C-N-CA	7.13	124.86	119.66
1	E	252	ARG	CA-C-N	6.97	128.55	119.84
1	E	252	ARG	C-N-CA	6.97	128.55	119.84
1	D	497	PHE	CA-C-N	6.75	124.52	119.66
1	D	497	PHE	C-N-CA	6.75	124.52	119.66
1	D	425	SER	N-CA-C	6.40	119.07	111.71
1	G	252	ARG	CA-C-N	6.20	127.58	119.84
1	G	252	ARG	C-N-CA	6.20	127.58	119.84
1	F	425	SER	N-CA-C	6.14	119.61	111.75
1	F	253	PRO	N-CA-C	6.05	124.93	112.47
1	H	253	PRO	N-CA-C	6.03	124.89	112.47
1	C	252	ARG	CA-C-N	5.98	127.31	119.84
1	C	252	ARG	C-N-CA	5.98	127.31	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	425	SER	N-CA-C	5.98	119.40	111.75
1	C	171	ASP	N-CA-C	-5.97	101.93	110.59
1	E	425	SER	N-CA-C	5.96	118.56	111.71
1	B	254	HIS	N-CA-C	-5.95	102.15	109.65
1	A	252	ARG	CA-C-N	5.91	127.22	119.84
1	A	252	ARG	C-N-CA	5.91	127.22	119.84
1	D	253	PRO	N-CA-C	5.91	124.64	112.47
1	F	206	SER	N-CA-C	5.87	117.67	111.28
1	H	252	ARG	CA-C-N	5.83	127.13	119.84
1	H	252	ARG	C-N-CA	5.83	127.13	119.84
1	H	425	SER	N-CA-C	5.78	118.33	111.33
1	G	253	PRO	N-CA-C	5.74	124.29	112.47
1	C	253	PRO	N-CA-C	5.67	124.15	112.47
1	G	254	HIS	N-CA-C	-5.67	102.51	109.65
1	E	400	LEU	N-CA-C	-5.61	105.31	111.82
1	A	253	PRO	N-CA-C	5.61	124.02	112.47
1	B	253	PRO	N-CA-C	5.55	123.90	112.47
1	B	141	VAL	N-CA-C	5.54	114.20	107.61
1	C	300	TYR	N-CA-C	5.54	118.08	111.71
1	F	300	TYR	N-CA-C	5.48	118.01	111.71
1	H	395	ARG	N-CA-C	-5.47	101.03	109.52
1	B	300	TYR	N-CA-C	5.45	117.98	111.71
1	B	425	SER	N-CA-C	5.39	118.65	111.75
1	A	425	SER	N-CA-C	5.36	118.61	111.75
1	B	206	SER	N-CA-C	5.34	117.11	111.28
1	E	253	PRO	N-CA-C	5.32	123.43	112.47
1	H	206	SER	N-CA-C	5.31	116.75	111.07
1	A	387	ARG	N-CA-C	5.28	118.53	111.24
1	B	153	LEU	N-CA-C	5.28	116.72	111.07
1	E	206	SER	N-CA-C	5.28	117.03	111.28
1	D	300	TYR	N-CA-C	5.24	117.74	111.71
1	G	425	SER	N-CA-C	5.23	118.45	111.75
1	D	141	VAL	N-CA-C	5.21	113.81	107.61
1	G	206	SER	N-CA-C	5.21	117.64	111.33
1	D	395	ARG	N-CA-C	-5.21	101.49	109.41
1	A	300	TYR	N-CA-C	5.20	117.69	111.71
1	F	299	ALA	N-CA-C	-5.15	103.73	110.53
1	C	86	LEU	N-CA-C	-5.09	105.62	111.07
1	C	387	ARG	N-CA-C	5.08	118.25	111.24
1	C	206	SER	N-CA-C	5.06	117.45	111.33
1	H	300	TYR	N-CA-C	5.04	117.51	111.71
1	D	206	SER	N-CA-C	5.03	116.76	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	252	ARG	CA-C-N	5.02	126.12	119.84
1	D	252	ARG	C-N-CA	5.02	126.12	119.84
1	G	387	ARG	N-CA-C	5.02	118.17	111.24
1	F	171	ASP	N-CA-C	-5.01	103.32	110.59
1	G	171	ASP	N-CA-C	-5.01	103.05	110.46

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	A	3813	0	3857	35	0
1	B	3813	0	3857	52	0
1	C	3806	0	3849	43	0
1	D	3806	0	3849	46	0
1	E	3806	0	3849	33	0
1	F	3806	0	3849	38	0
1	G	3806	0	3849	32	0
1	H	3806	0	3849	54	0
2	A	13	0	7	0	0
2	B	13	0	7	1	0
2	C	13	0	6	1	0
2	D	13	0	5	1	0
2	E	13	0	6	1	0
2	F	13	0	6	1	0
2	G	13	0	6	1	0
2	H	13	0	6	1	0
3	A	360	0	0	3	0
3	B	369	0	0	5	0
3	C	407	0	0	5	0
3	D	404	0	0	6	0
3	E	382	0	0	5	0
3	F	491	0	0	4	0
3	G	431	0	0	2	0
3	H	379	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	33789	0	30857	303	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 (303) 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:F:153:LEU:HD22	1:F:202:VAL:HG12	1.63	0.80
1:D:153:LEU:HD22	1:D:202:VAL:HG12	1.64	0.79
1:E:487:LYS:O	1:E:491:GLN:HG3	1.83	0.78
1:B:153:LEU:HD22	1:B:202:VAL:HG12	1.70	0.74
1:B:487:LYS:O	1:B:491:GLN:HG3	1.87	0.74
1:A:153:LEU:HD22	1:A:202:VAL:HG12	1.69	0.74
1:H:153:LEU:HD22	1:H:202:VAL:HG12	1.72	0.72
1:C:487:LYS:O	1:C:491:GLN:HG3	1.90	0.71
1:H:53:ILE:HG21	1:H:196:ARG:HH11	1.56	0.70
1:D:61:GLY:HA3	1:D:199:LEU:HD11	1.73	0.70
1:F:79:VAL:HG11	1:F:196:ARG:HD3	1.75	0.69
1:D:50:GLY:O	1:D:54:ARG:HG3	1.93	0.68
1:B:51:ALA:O	1:B:55:GLU:HG3	1.94	0.68
1:B:53:ILE:HG21	1:B:196:ARG:HH11	1.57	0.68
1:H:146:THR:HG22	3:H:2163:HOH:O	1.94	0.67
1:G:53:ILE:HD13	1:G:196:ARG:HD2	1.78	0.66
1:G:487:LYS:O	1:G:491:GLN:HG3	1.95	0.65
1:C:153:LEU:HD22	1:C:202:VAL:HG12	1.77	0.65
1:F:146:THR:HG22	3:F:2088:HOH:O	1.97	0.64
1:E:153:LEU:HD22	1:E:202:VAL:HG12	1.80	0.63
1:B:372:LEU:O	1:B:376:GLN:HG3	1.98	0.62
1:G:146:THR:HG22	3:G:1967:HOH:O	1.98	0.62
1:B:61:GLY:HA3	1:B:199:LEU:HD11	1.80	0.62
1:H:214:VAL:HB	1:H:450:ARG:NH2	2.16	0.61
1:C:124:GLY:O	1:C:128:ARG:HG2	2.01	0.61
1:C:271:SER:HB2	1:C:483:SER:HB3	1.84	0.60
1:H:489:LEU:C	1:H:489:LEU:HD23	2.27	0.60
1:F:171:ASP:OD2	1:F:175:THR:HB	2.02	0.59
1:H:238:ARG:HH11	1:H:387:ARG:NH2	1.99	0.59
1:A:426:ILE:HD13	3:D:3398:HOH:O	2.01	0.59
1:D:52:VAL:HG13	1:D:57:ARG:HB2	1.83	0.59
1:D:53:ILE:HD13	1:D:196:ARG:HD2	1.82	0.59
1:D:51:ALA:O	1:D:55:GLU:HG3	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:GLY:O	1:B:128:ARG:HG2	2.03	0.58
1:B:251:LEU:HD13	1:C:335:VAL:HG21	1.84	0.58
1:D:225:TRP:CE2	1:D:517:LEU:HD22	2.39	0.57
1:F:124:GLY:O	1:F:128:ARG:HG2	2.05	0.57
1:H:54:ARG:HG2	1:H:54:ARG:HH11	1.69	0.56
1:C:225:TRP:CE2	1:C:517:LEU:HD22	2.39	0.56
1:H:238:ARG:NH1	1:H:387:ARG:NH2	2.54	0.56
1:B:258:LYS:HD2	3:B:3514:HOH:O	2.05	0.56
1:H:487:LYS:O	1:H:491:GLN:HG3	2.06	0.56
1:G:153:LEU:HD22	1:G:202:VAL:HG12	1.87	0.56
1:H:53:ILE:HG21	1:H:196:ARG:NH1	2.20	0.56
1:H:225:TRP:CE2	1:H:517:LEU:HD22	2.41	0.56
1:A:132:LEU:C	1:A:132:LEU:HD13	2.31	0.56
1:E:132:LEU:C	1:E:132:LEU:HD13	2.30	0.55
1:G:271:SER:HB2	1:G:483:SER:HB3	1.87	0.55
1:A:271:SER:HB2	1:A:483:SER:HB3	1.88	0.55
1:D:225:TRP:CE2	1:D:522:PRO:HD3	2.42	0.55
1:F:68:PRO:HG3	1:F:435:ASN:HB2	1.88	0.55
1:A:263:ARG:O	1:A:267:ARG:HG2	2.07	0.54
1:A:79:VAL:HG11	1:A:196:ARG:HD3	1.89	0.54
1:H:39:ARG:HG3	1:H:39:ARG:HH11	1.73	0.54
1:C:489:LEU:C	1:C:489:LEU:HD23	2.32	0.54
1:G:225:TRP:CE2	1:G:522:PRO:HD3	2.43	0.54
1:A:146:THR:HG22	3:A:2274:HOH:O	2.07	0.54
1:H:61:GLY:HA3	1:H:199:LEU:HD21	1.89	0.54
1:E:329:ALA:HB1	1:H:252:ARG:HA	1.90	0.53
1:A:52:VAL:HG13	1:A:57:ARG:HB2	1.90	0.53
1:H:52:VAL:HG13	1:H:57:ARG:HB2	1.90	0.53
1:E:271:SER:HB2	1:E:483:SER:HB3	1.91	0.53
1:F:329:ALA:HB1	1:G:252:ARG:HA	1.90	0.53
1:F:36:PRO:HB2	1:F:37:PRO:HD3	1.91	0.53
1:B:489:LEU:HD23	1:B:489:LEU:C	2.34	0.53
3:A:3436:HOH:O	1:D:426:ILE:HD13	2.09	0.53
1:B:252:ARG:HA	1:C:329:ALA:HB1	1.90	0.53
1:C:146:THR:HG22	3:C:1832:HOH:O	2.09	0.53
1:A:225:TRP:CE2	1:A:517:LEU:HD22	2.44	0.52
1:C:68:PRO:HG3	1:C:435:ASN:HB2	1.91	0.52
1:H:132:LEU:C	1:H:132:LEU:HD13	2.34	0.52
1:A:68:PRO:HG3	1:A:435:ASN:HB2	1.91	0.52
1:C:176:ARG:HD2	3:C:3285:HOH:O	2.10	0.52
1:A:252:ARG:HA	1:D:329:ALA:HB1	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:ALA:HB1	1:C:252:ARG:HA	1.92	0.51
1:A:170:LEU:HD23	1:A:176:ARG:HG2	1.91	0.51
1:F:426:ILE:HD13	3:G:3571:HOH:O	2.09	0.51
1:A:279:ILE:HD11	1:D:346:HIS:CE1	2.45	0.51
1:C:424:ALA:HB2	1:C:448:LEU:HD12	1.92	0.51
1:C:36:PRO:HB2	1:C:37:PRO:HD3	1.91	0.51
1:H:225:TRP:CE2	1:H:522:PRO:HD3	2.46	0.51
1:B:191:LEU:HD21	1:B:201:LEU:CD1	2.41	0.51
1:D:36:PRO:HB2	1:D:37:PRO:HD3	1.92	0.51
1:A:176:ARG:HD2	3:A:3332:HOH:O	2.11	0.50
1:D:132:LEU:HD13	1:D:132:LEU:C	2.36	0.50
1:G:523:VAL:OXT	1:G:523:VAL:HG12	2.10	0.50
1:A:152:ASP:CG	1:A:207:ALA:HB3	2.36	0.50
1:B:36:PRO:HB2	1:B:37:PRO:HD3	1.92	0.50
1:D:60:TYR:HA	1:D:64:THR:OG1	2.12	0.50
1:D:489:LEU:C	1:D:489:LEU:HD23	2.36	0.50
1:F:225:TRP:CE2	1:F:517:LEU:HD22	2.47	0.50
1:G:489:LEU:HD23	1:G:489:LEU:C	2.36	0.50
1:H:271:SER:HB2	1:H:483:SER:HB3	1.92	0.50
1:A:487:LYS:O	1:A:491:GLN:HG3	2.12	0.50
1:B:225:TRP:CE2	1:B:522:PRO:HD3	2.47	0.50
1:D:271:SER:HB2	1:D:483:SER:HB3	1.94	0.50
1:E:280:ALA:O	1:H:57:ARG:HD2	2.12	0.50
1:A:51:ALA:O	1:A:55:GLU:HG3	2.13	0.49
1:D:297:GLN:HG3	3:D:3086:HOH:O	2.12	0.49
1:F:57:ARG:HD2	1:G:280:ALA:O	2.12	0.49
1:F:171:ASP:C	1:F:171:ASP:OD1	2.55	0.49
1:B:271:SER:HB2	1:B:483:SER:HB3	1.95	0.49
1:E:60:TYR:OH	2:E:701:DHC:HC2	2.12	0.49
1:H:66:PHE:CZ	1:H:86:LEU:HD22	2.48	0.49
1:C:263:ARG:O	1:C:267:ARG:HG2	2.12	0.49
1:E:146:THR:HG22	3:E:1932:HOH:O	2.13	0.49
1:E:171:ASP:OD2	1:E:175:THR:HB	2.12	0.49
1:B:523:VAL:OXT	1:B:523:VAL:HG12	2.13	0.49
1:H:184:ARG:HG2	1:H:184:ARG:HH11	1.78	0.49
1:B:168:ASP:HB2	1:B:176:ARG:HH21	1.78	0.49
1:E:372:LEU:O	1:E:376:GLN:HG3	2.12	0.49
1:B:225:TRP:CE2	1:B:517:LEU:HD22	2.48	0.49
1:B:68:PRO:HG3	1:B:435:ASN:HB2	1.95	0.49
1:A:170:LEU:CD2	1:A:176:ARG:HG2	2.43	0.49
1:A:372:LEU:O	1:A:376:GLN:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:THR:HG22	3:B:2492:HOH:O	2.13	0.49
1:E:225:TRP:CE2	1:E:517:LEU:HD22	2.48	0.49
1:F:271:SER:HB2	1:F:483:SER:HB3	1.95	0.49
1:H:68:PRO:HG3	1:H:435:ASN:HB2	1.95	0.49
1:A:280:ALA:O	1:D:57:ARG:HD2	2.12	0.48
1:A:321:ARG:HH21	1:D:321:ARG:HH21	1.59	0.48
1:F:79:VAL:CG1	1:F:196:ARG:HD3	2.43	0.48
1:H:170:LEU:HD23	1:H:176:ARG:HG2	1.95	0.48
1:C:80:ARG:HE	1:C:194:SER:HA	1.79	0.48
1:D:66:PHE:CE2	1:D:86:LEU:HB2	2.48	0.48
1:D:211:ILE:HD13	1:D:447:ARG:HG3	1.95	0.48
1:F:132:LEU:C	1:F:132:LEU:HD13	2.38	0.48
1:C:53:ILE:HD13	1:C:196:ARG:HD2	1.95	0.48
1:H:450:ARG:HG2	1:H:450:ARG:HH11	1.77	0.48
1:A:145:GLY:HA2	1:B:410:THR:HG23	1.96	0.48
1:E:489:LEU:HD23	1:E:489:LEU:C	2.37	0.48
1:G:132:LEU:HD13	1:G:132:LEU:C	2.37	0.48
3:B:3548:HOH:O	1:C:426:ILE:HD13	2.14	0.48
1:F:258:LYS:HD2	3:F:5436:HOH:O	2.13	0.48
1:C:12:GLU:HA	1:C:33:VAL:HG13	1.96	0.48
1:F:436:GLN:HG2	1:G:300:TYR:CZ	2.49	0.48
1:F:61:GLY:HA3	1:F:199:LEU:HD21	1.95	0.47
1:D:67:GLY:HA2	2:D:701:DHC:C2	2.44	0.47
1:E:51:ALA:O	1:E:55:GLU:HG3	2.15	0.47
1:H:124:GLY:O	1:H:128:ARG:HG2	2.14	0.47
1:H:372:LEU:O	1:H:376:GLN:HG3	2.14	0.47
1:D:12:GLU:HA	1:D:33:VAL:HG13	1.95	0.47
1:G:68:PRO:HG3	1:G:435:ASN:HB2	1.97	0.47
1:D:184:ARG:HG2	1:D:184:ARG:HH11	1.79	0.47
1:E:79:VAL:HG21	3:E:2045:HOH:O	2.14	0.47
1:E:171:ASP:OD1	1:E:171:ASP:C	2.58	0.47
1:E:426:ILE:HD13	3:H:3422:HOH:O	2.12	0.47
1:B:53:ILE:CG2	1:B:196:ARG:HH11	2.26	0.47
1:E:145:GLY:HA2	1:F:410:THR:HG23	1.97	0.47
1:C:80:ARG:NE	1:C:194:SER:HA	2.30	0.47
1:D:12:GLU:HG2	1:D:35:ALA:HB2	1.97	0.47
1:E:12:GLU:HA	1:E:33:VAL:HG13	1.96	0.47
1:E:252:ARG:HA	1:H:329:ALA:HB1	1.97	0.47
1:C:523:VAL:OXT	1:C:523:VAL:HG12	2.14	0.47
1:B:132:LEU:HD13	1:B:132:LEU:C	2.40	0.46
1:E:263:ARG:O	1:E:267:ARG:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:400:LEU:HD21	1:F:78:ASN:HB3	1.96	0.46
1:D:152:ASP:OD1	1:D:443:THR:OG1	2.33	0.46
1:G:79:VAL:HG11	1:G:196:ARG:HD3	1.96	0.46
1:G:124:GLY:O	1:G:128:ARG:HG2	2.15	0.46
1:F:225:TRP:CE2	1:F:522:PRO:HD3	2.51	0.46
1:G:60:TYR:OH	2:G:701:DHC:HC2	2.16	0.46
1:H:285:ASP:OD2	1:H:285:ASP:C	2.59	0.46
1:B:53:ILE:HG21	1:B:196:ARG:NH1	2.29	0.46
1:B:170:LEU:CD2	1:B:176:ARG:HG2	2.45	0.46
1:E:176:ARG:HD2	3:E:3308:HOH:O	2.15	0.46
1:H:80:ARG:HH11	1:H:80:ARG:HG3	1.80	0.46
1:B:57:ARG:HD2	1:C:280:ALA:O	2.15	0.46
1:B:426:ILE:HD13	3:C:3493:HOH:O	2.15	0.46
1:A:53:ILE:HD13	1:A:196:ARG:HD2	1.98	0.45
1:G:36:PRO:N	1:G:37:PRO:HD2	2.32	0.45
1:H:36:PRO:N	1:H:37:PRO:HD2	2.30	0.45
1:D:225:TRP:CD2	1:D:517:LEU:HD22	2.50	0.45
1:H:214:VAL:HB	1:H:450:ARG:HH21	1.81	0.45
1:A:7:PRO:O	1:A:8:LYS:C	2.59	0.45
1:C:132:LEU:C	1:C:132:LEU:HD13	2.41	0.45
1:A:329:ALA:HB1	1:D:252:ARG:HA	1.98	0.45
1:A:160:VAL:O	1:A:164:GLN:HG3	2.17	0.45
1:F:80:ARG:HG2	3:F:2717:HOH:O	2.16	0.45
1:D:146:THR:HG22	3:D:2324:HOH:O	2.16	0.45
1:B:432:ASN:HB2	1:B:436:GLN:HE21	1.81	0.45
1:D:66:PHE:CZ	1:D:86:LEU:HD22	2.51	0.45
1:A:225:TRP:CD2	1:A:517:LEU:HD22	2.52	0.45
1:H:184:ARG:HG2	1:H:184:ARG:NH1	2.32	0.45
1:H:501:GLU:HB2	3:H:3619:HOH:O	2.17	0.45
1:B:305:ALA:N	1:B:306:PRO:CD	2.80	0.45
1:E:279:ILE:HD11	1:H:346:HIS:CE1	2.52	0.45
1:F:321:ARG:HH21	1:G:321:ARG:HH21	1.64	0.45
1:G:395:ARG:CZ	1:G:501:GLU:HG2	2.47	0.45
1:H:294:GLU:OE1	1:H:387:ARG:NH2	2.50	0.45
1:C:491:GLN:O	1:C:495:GLU:HG3	2.17	0.44
1:A:489:LEU:C	1:A:489:LEU:HD23	2.41	0.44
1:D:191:LEU:HD21	1:D:201:LEU:CD1	2.48	0.44
1:C:315:THR:HG21	3:C:2732:HOH:O	2.16	0.44
1:C:225:TRP:CD2	1:C:522:PRO:HG3	2.53	0.44
1:E:63:THR:HG22	3:E:5314:HOH:O	2.16	0.44
1:F:51:ALA:O	1:F:55:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:80:ARG:HG3	1:F:80:ARG:HH11	1.82	0.44
1:F:63:THR:HG22	3:F:5031:HOH:O	2.17	0.44
1:A:36:PRO:N	1:A:37:PRO:HD2	2.32	0.44
1:B:75:SER:OG	1:B:77:GLU:HG2	2.17	0.44
1:D:372:LEU:O	1:D:376:GLN:HG3	2.17	0.44
1:E:315:THR:HG21	3:E:3147:HOH:O	2.17	0.44
1:G:305:ALA:N	1:G:306:PRO:CD	2.81	0.44
1:B:170:LEU:HD23	1:B:176:ARG:HG2	1.99	0.44
1:F:211:ILE:HD13	1:F:447:ARG:HG3	2.00	0.44
1:G:372:LEU:O	1:G:376:GLN:HG3	2.18	0.44
1:B:15:ARG:HB2	3:B:5606:HOH:O	2.18	0.44
1:H:60:TYR:OH	2:H:701:DHC:HC2	2.18	0.44
1:B:285:ASP:C	1:B:285:ASP:OD2	2.61	0.43
1:D:48:ARG:NH2	1:D:338:PRO:O	2.51	0.43
1:A:61:GLY:HA3	1:A:199:LEU:HD21	2.00	0.43
1:B:53:ILE:HD13	1:B:196:ARG:HD2	1.99	0.43
1:C:152:ASP:CG	1:C:207:ALA:HB3	2.43	0.43
1:G:160:VAL:O	1:G:164:GLN:HG3	2.19	0.43
1:A:60:TYR:HA	1:A:64:THR:OG1	2.18	0.43
1:C:145:GLY:HA2	1:D:410:THR:HG23	2.00	0.43
1:C:225:TRP:CE2	1:C:522:PRO:HG3	2.53	0.43
1:E:57:ARG:HD2	1:H:280:ALA:O	2.18	0.43
1:E:225:TRP:CE2	1:E:522:PRO:HD3	2.53	0.43
1:F:252:ARG:HA	1:G:329:ALA:HB1	1.99	0.43
1:B:337:PRO:HA	1:B:338:PRO:HD3	1.90	0.43
1:F:414:LEU:O	1:F:418:MET:HG3	2.19	0.43
1:B:60:TYR:OH	2:B:701:DHC:HC2	2.19	0.43
1:B:278:VAL:HB	1:B:281:GLU:HG3	2.01	0.43
1:C:170:LEU:HD23	1:C:176:ARG:HG2	2.00	0.43
1:D:184:ARG:HG2	1:D:184:ARG:NH1	2.33	0.43
1:B:152:ASP:CG	1:B:207:ALA:HB3	2.43	0.43
1:C:48:ARG:HH11	1:C:48:ARG:HG2	1.83	0.43
1:G:497:PHE:HA	1:G:498:PRO:HD2	1.94	0.43
1:E:152:ASP:CG	1:E:207:ALA:HB3	2.44	0.43
1:E:288:ASP:O	1:H:73:LEU:HD12	2.18	0.43
1:D:335:VAL:HG11	3:D:2240:HOH:O	2.19	0.43
1:C:444:ILE:O	1:C:448:LEU:HG	2.18	0.43
1:H:171:ASP:C	1:H:171:ASP:OD1	2.61	0.43
1:B:31:ARG:HH12	1:B:33:VAL:HG21	1.83	0.42
1:D:12:GLU:CG	1:D:35:ALA:HB2	2.48	0.42
1:A:282:ARG:HD3	3:D:2298:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:LEU:HD13	1:B:153:LEU:HB3	2.01	0.42
1:B:238:ARG:HH21	1:B:387:ARG:HH21	1.66	0.42
1:G:225:TRP:CE2	1:G:517:LEU:HD22	2.54	0.42
1:G:263:ARG:O	1:G:267:ARG:HG2	2.19	0.42
1:H:497:PHE:HA	1:H:498:PRO:HD3	1.88	0.42
1:C:79:VAL:HG11	1:C:196:ARG:HD3	2.02	0.42
1:C:80:ARG:HH21	1:C:194:SER:CB	2.33	0.42
1:E:305:ALA:HB3	1:E:306:PRO:HD3	2.02	0.42
1:B:76:GLY:O	1:B:79:VAL:HG23	2.20	0.42
1:D:177:LEU:HD21	1:D:185:ARG:NH1	2.34	0.42
1:G:211:ILE:HD13	1:G:447:ARG:HG3	2.02	0.42
1:H:80:ARG:HG3	1:H:80:ARG:NH1	2.35	0.42
1:H:176:ARG:HD2	3:H:3379:HOH:O	2.18	0.42
1:B:48:ARG:NH2	1:B:338:PRO:O	2.52	0.42
1:C:12:GLU:HA	1:C:33:VAL:CG1	2.50	0.42
1:C:90:LEU:HD13	1:C:153:LEU:HB3	2.02	0.42
1:F:108:LEU:O	1:F:112:VAL:HG23	2.20	0.42
1:C:60:TYR:OH	2:C:701:DHC:HC2	2.20	0.42
1:D:124:GLY:O	1:D:128:ARG:HG2	2.20	0.42
1:H:86:LEU:HD12	1:H:89:HIS:CE1	2.54	0.42
1:F:60:TYR:OH	2:F:701:DHC:HC2	2.20	0.41
1:G:145:GLY:HA2	1:H:410:THR:HG23	2.01	0.41
1:B:79:VAL:HG21	3:B:5059:HOH:O	2.20	0.41
1:C:10:ALA:HB2	1:C:31:ARG:NH2	2.35	0.41
1:C:468:ALA:O	1:C:472:GLU:HG3	2.20	0.41
1:E:279:ILE:HD11	1:H:346:HIS:CG	2.55	0.41
1:D:79:VAL:HG21	3:D:5454:HOH:O	2.19	0.41
1:F:181:GLU:OE1	1:F:184:ARG:NH1	2.53	0.41
1:A:184:ARG:HG2	1:A:184:ARG:HH11	1.85	0.41
1:C:394:HIS:HE1	3:C:2881:HOH:O	2.03	0.41
1:A:285:ASP:OD1	1:A:288:ASP:OD2	2.38	0.41
1:E:100:TRP:CZ2	1:E:172:ARG:HG2	2.55	0.41
1:B:39:ARG:HD2	1:B:43:ARG:NH2	2.36	0.41
1:B:152:ASP:OD1	1:B:443:THR:OG1	2.36	0.41
1:E:68:PRO:HG3	1:E:435:ASN:HB2	2.02	0.41
1:F:346:HIS:CE1	1:G:279:ILE:HD11	2.56	0.41
1:B:263:ARG:O	1:B:267:ARG:HG2	2.20	0.41
1:F:100:TRP:CH2	1:F:172:ARG:HD3	2.56	0.41
1:H:90:LEU:HD13	1:H:153:LEU:HB3	2.02	0.41
1:H:171:ASP:OD2	1:H:175:THR:HB	2.21	0.41
1:B:178:ASP:OD2	1:B:178:ASP:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:ALA:HB2	1:C:31:ARG:HH21	1.86	0.41
1:C:391:PRO:HB2	1:D:69:LEU:HD21	2.02	0.41
1:F:346:HIS:CG	1:G:279:ILE:HD11	2.56	0.41
1:H:169:PHE:CD2	1:H:182:GLY:HA3	2.56	0.41
1:H:450:ARG:HG2	1:H:450:ARG:NH1	2.35	0.41
1:F:76:GLY:O	1:F:79:VAL:HG23	2.21	0.41
1:H:263:ARG:O	1:H:267:ARG:HG2	2.21	0.41
1:B:141:VAL:HG13	1:B:158:HIS:HB2	2.03	0.40
1:D:8:LYS:CG	1:D:31:ARG:HG3	2.50	0.40
1:D:90:LEU:HD13	1:D:153:LEU:HB3	2.03	0.40
1:D:141:VAL:HA	1:D:142:PRO:HD3	1.98	0.40
1:H:53:ILE:HD13	1:H:196:ARG:HD2	2.02	0.40
1:H:168:ASP:HB2	1:H:176:ARG:HH21	1.86	0.40
1:H:489:LEU:HD23	1:H:489:LEU:O	2.20	0.40
1:F:80:ARG:HG3	1:F:80:ARG:NH1	2.36	0.40
1:F:152:ASP:OD1	1:F:443:THR:OG1	2.38	0.40
1:H:355:VAL:HG13	3:H:2566:HOH:O	2.20	0.40
1:A:152:ASP:OD1	1:A:443:THR:OG1	2.37	0.40
1:B:80:ARG:HH11	1:B:80:ARG:HG3	1.87	0.40
1:D:152:ASP:CG	1:D:207:ALA:HB3	2.46	0.40
1:B:321:ARG:HH21	1:C:321:ARG:HH21	1.70	0.40
1:D:108:LEU:O	1:D:112:VAL:HG23	2.22	0.40
1:G:152:ASP:CG	1:G:207:ALA:HB3	2.46	0.40
1:G:337:PRO:HA	1:G:338:PRO:HD3	1.95	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	510/521 (98%)	499 (98%)	9 (2%)	2 (0%)	30 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	510/521 (98%)	503 (99%)	6 (1%)	1 (0%)	44	36
1	C	509/521 (98%)	503 (99%)	5 (1%)	1 (0%)	44	36
1	D	509/521 (98%)	499 (98%)	9 (2%)	1 (0%)	44	36
1	E	509/521 (98%)	501 (98%)	7 (1%)	1 (0%)	44	36
1	F	509/521 (98%)	502 (99%)	6 (1%)	1 (0%)	44	36
1	G	509/521 (98%)	503 (99%)	5 (1%)	1 (0%)	44	36
1	H	509/521 (98%)	500 (98%)	8 (2%)	1 (0%)	44	36
All	All	4074/4168 (98%)	4010 (98%)	55 (1%)	9 (0%)	44	36

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	253	PRO
1	F	253	PRO
1	A	8	LYS
1	C	253	PRO
1	D	253	PRO
1	G	253	PRO
1	H	253	PRO
1	A	253	PRO
1	B	253	PRO

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	384/389 (99%)	383 (100%)	1 (0%)	91	92
1	B	384/389 (99%)	383 (100%)	1 (0%)	91	92
1	C	383/389 (98%)	382 (100%)	1 (0%)	91	92
1	D	383/389 (98%)	383 (100%)	0	100	100
1	E	383/389 (98%)	382 (100%)	1 (0%)	91	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	383/389 (98%)	382 (100%)	1 (0%)	91	92
1	G	383/389 (98%)	382 (100%)	1 (0%)	91	92
1	H	383/389 (98%)	382 (100%)	1 (0%)	91	92
All	All	3066/3112 (98%)	3059 (100%)	7 (0%)	92	93

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	443	THR
1	B	443	THR
1	C	80	ARG
1	E	443	THR
1	F	172	ARG
1	G	443	THR
1	H	54	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	A	195	HIS
1	A	353	GLN
1	A	491	GLN
1	B	164	GLN
1	B	189	GLN
1	B	435	ASN
1	B	436	GLN
1	B	520	GLN
1	C	164	GLN
1	C	277	HIS
1	C	394	HIS
1	C	435	ASN
1	D	78	ASN
1	D	164	GLN
1	D	189	GLN
1	D	195	HIS
1	D	394	HIS
1	D	491	GLN
1	D	516	HIS
1	D	519	GLN

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Mol	Chain	Res	Type
1	E	164	GLN
1	E	189	GLN
1	E	394	HIS
1	E	436	GLN
1	E	520	GLN
1	F	164	GLN
1	F	394	HIS
1	F	436	GLN
1	F	491	GLN
1	G	164	GLN
1	G	353	GLN
1	G	435	ASN
1	G	436	GLN
1	H	58	HIS
1	H	78	ASN
1	H	164	GLN
1	H	195	HIS
1	H	394	HIS
1	H	436	GLN
1	H	508	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MDO	E	149	1	11,13,14	2.40	4 (36%)	15,18,20	2.67	5 (33%)
1	MDO	F	149	1	11,13,14	2.44	4 (36%)	15,18,20	2.68	5 (33%)
1	MDO	G	149	1	11,13,14	2.40	4 (36%)	15,18,20	2.75	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MDO	H	149	1	11,13,14	2.44	5 (45%)	15,18,20	2.65	5 (33%)
1	MDO	B	149	1	11,13,14	2.47	4 (36%)	15,18,20	2.70	5 (33%)
1	MDO	C	149	1	11,13,14	2.46	4 (36%)	15,18,20	2.59	5 (33%)
1	MDO	D	149	1	11,13,14	2.47	4 (36%)	15,18,20	2.64	5 (33%)
1	MDO	A	149	1	11,13,14	2.42	4 (36%)	15,18,20	2.73	5 (33%)

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
1	MDO	E	149	1	-	0/4/23/24	0/1/1/1
1	MDO	F	149	1	-	0/4/23/24	0/1/1/1
1	MDO	G	149	1	-	0/4/23/24	0/1/1/1
1	MDO	H	149	1	-	0/4/23/24	0/1/1/1
1	MDO	B	149	1	-	0/4/23/24	0/1/1/1
1	MDO	C	149	1	-	0/4/23/24	0/1/1/1
1	MDO	D	149	1	-	0/4/23/24	0/1/1/1
1	MDO	A	149	1	-	0/4/23/24	0/1/1/1

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	149	MDO	O2-C2	5.43	1.34	1.23
1	B	149	MDO	O2-C2	5.35	1.34	1.23
1	D	149	MDO	O2-C2	5.31	1.33	1.23
1	C	149	MDO	O2-C2	5.12	1.33	1.23
1	F	149	MDO	O2-C2	5.12	1.33	1.23
1	G	149	MDO	O2-C2	5.08	1.33	1.23
1	E	149	MDO	O2-C2	5.06	1.33	1.23
1	A	149	MDO	O2-C2	5.06	1.33	1.23
1	C	149	MDO	C2-N3	-3.87	1.31	1.40
1	B	149	MDO	C2-N3	-3.80	1.31	1.40
1	E	149	MDO	C2-N3	-3.77	1.31	1.40
1	A	149	MDO	C2-N3	-3.66	1.31	1.40
1	F	149	MDO	C2-N3	-3.65	1.31	1.40
1	D	149	MDO	C2-N3	-3.63	1.31	1.40
1	G	149	MDO	C2-N3	-3.60	1.31	1.40
1	H	149	MDO	C2-N3	-3.58	1.31	1.40
1	G	149	MDO	CA2-N2	-2.95	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	149	MDO	CA2-N2	-2.93	1.34	1.39
1	F	149	MDO	CA2-N2	-2.88	1.34	1.39
1	C	149	MDO	CA2-N2	-2.85	1.34	1.39
1	E	149	MDO	CA2-N2	-2.83	1.34	1.39
1	B	149	MDO	CA2-N2	-2.72	1.34	1.39
1	D	149	MDO	CA2-N2	-2.64	1.34	1.39
1	F	149	MDO	CA2-C2	-2.64	1.38	1.43
1	G	149	MDO	CA2-C2	-2.61	1.38	1.43
1	E	149	MDO	CA2-C2	-2.55	1.38	1.43
1	D	149	MDO	CA2-C2	-2.54	1.38	1.43
1	B	149	MDO	CA2-C2	-2.44	1.38	1.43
1	A	149	MDO	CA2-C2	-2.40	1.38	1.43
1	H	149	MDO	CA2-C2	-2.40	1.38	1.43
1	C	149	MDO	CA2-C2	-2.39	1.38	1.43
1	H	149	MDO	CA2-N2	-2.34	1.35	1.39
1	H	149	MDO	C1-N2	2.05	1.35	1.32

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	149	MDO	CA2-C2-N3	7.13	109.49	103.50
1	H	149	MDO	CA2-C2-N3	7.01	109.39	103.50
1	G	149	MDO	CA2-C2-N3	6.95	109.34	103.50
1	E	149	MDO	CA2-C2-N3	6.94	109.33	103.50
1	F	149	MDO	CA2-C2-N3	6.87	109.27	103.50
1	D	149	MDO	CA2-C2-N3	6.85	109.25	103.50
1	B	149	MDO	CA2-C2-N3	6.85	109.25	103.50
1	C	149	MDO	CA2-C2-N3	6.76	109.18	103.50
1	B	149	MDO	O2-C2-CA2	-4.72	128.01	131.02
1	F	149	MDO	O2-C2-CA2	-4.69	128.03	131.02
1	G	149	MDO	O2-C2-CA2	-4.68	128.03	131.02
1	D	149	MDO	O2-C2-CA2	-4.50	128.15	131.02
1	A	149	MDO	O2-C2-CA2	-4.46	128.18	131.02
1	E	149	MDO	O2-C2-CA2	-4.40	128.22	131.02
1	C	149	MDO	O2-C2-CA2	-4.21	128.34	131.02
1	H	149	MDO	O2-C2-CA2	-4.17	128.36	131.02
1	A	149	MDO	C2-CA2-N2	-3.92	106.14	108.95
1	H	149	MDO	C2-CA2-N2	-3.91	106.15	108.95
1	B	149	MDO	C2-CA2-N2	-3.90	106.15	108.95
1	E	149	MDO	C2-CA2-N2	-3.73	106.28	108.95
1	C	149	MDO	C2-CA2-N2	-3.69	106.31	108.95
1	D	149	MDO	C2-CA2-N2	-3.65	106.33	108.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	149	MDO	C2-CA2-N2	-3.61	106.36	108.95
1	G	149	MDO	C2-CA2-N2	-3.60	106.37	108.95
1	G	149	MDO	N3-C1-N2	-2.96	109.15	111.48
1	G	149	MDO	CA2-N2-C1	2.88	107.97	105.39
1	F	149	MDO	N3-C1-N2	-2.74	109.32	111.48
1	A	149	MDO	CA2-N2-C1	2.73	107.84	105.39
1	A	149	MDO	N3-C1-N2	-2.72	109.34	111.48
1	B	149	MDO	N3-C1-N2	-2.71	109.35	111.48
1	E	149	MDO	N3-C1-N2	-2.71	109.35	111.48
1	D	149	MDO	N3-C1-N2	-2.68	109.37	111.48
1	E	149	MDO	CA2-N2-C1	2.68	107.79	105.39
1	C	149	MDO	N3-C1-N2	-2.67	109.38	111.48
1	H	149	MDO	N3-C1-N2	-2.66	109.39	111.48
1	F	149	MDO	CA2-N2-C1	2.65	107.77	105.39
1	B	149	MDO	CA2-N2-C1	2.58	107.70	105.39
1	C	149	MDO	CA2-N2-C1	2.48	107.61	105.39
1	D	149	MDO	CA2-N2-C1	2.44	107.58	105.39
1	H	149	MDO	CA2-N2-C1	2.43	107.57	105.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

8 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
2	DHC	E	701	-	13,13,13	2.49	6 (46%)	17,17,17	0.82	0
2	DHC	G	701	-	13,13,13	2.44	6 (46%)	17,17,17	0.83	0
2	DHC	A	701	-	13,13,13	2.45	6 (46%)	17,17,17	0.82	0
2	DHC	C	701	-	13,13,13	2.49	7 (53%)	17,17,17	0.90	0
2	DHC	F	701	-	13,13,13	2.53	7 (53%)	17,17,17	0.93	0
2	DHC	B	701	-	13,13,13	2.53	5 (38%)	17,17,17	0.86	0
2	DHC	H	701	-	13,13,13	2.51	5 (38%)	17,17,17	0.83	0
2	DHC	D	701	-	13,13,13	2.55	6 (46%)	17,17,17	0.83	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
2	DHC	E	701	-	-	2/5/5/5	0/1/1/1
2	DHC	G	701	-	-	2/5/5/5	0/1/1/1
2	DHC	A	701	-	-	2/5/5/5	0/1/1/1
2	DHC	C	701	-	-	2/5/5/5	0/1/1/1
2	DHC	F	701	-	-	2/5/5/5	0/1/1/1
2	DHC	B	701	-	-	2/5/5/5	0/1/1/1
2	DHC	H	701	-	-	2/5/5/5	0/1/1/1
2	DHC	D	701	-	-	4/5/5/5	0/1/1/1

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	701	DHC	C2'-C3'	5.15	1.46	1.38
2	E	701	DHC	C2'-C3'	4.79	1.45	1.38
2	B	701	DHC	C6'-C5'	4.77	1.46	1.38
2	F	701	DHC	C2'-C3'	4.70	1.45	1.38
2	C	701	DHC	C6'-C5'	4.66	1.46	1.38
2	G	701	DHC	C2'-C3'	4.62	1.45	1.38
2	B	701	DHC	C2'-C3'	4.57	1.45	1.38
2	H	701	DHC	C6'-C5'	4.53	1.46	1.38
2	C	701	DHC	C2'-C3'	4.51	1.45	1.38
2	A	701	DHC	C2'-C3'	4.51	1.45	1.38
2	H	701	DHC	C2'-C3'	4.45	1.45	1.38
2	A	701	DHC	C6'-C5'	4.38	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	701	DHC	C6'-C5'	4.37	1.45	1.38
2	G	701	DHC	C6'-C5'	4.21	1.45	1.38
2	D	701	DHC	C6'-C5'	4.14	1.45	1.38
2	E	701	DHC	C6'-C5'	3.89	1.45	1.38
2	E	701	DHC	C2'-C1'	3.85	1.46	1.39
2	D	701	DHC	C2'-C1'	3.72	1.46	1.39
2	G	701	DHC	C2'-C1'	3.63	1.46	1.39
2	F	701	DHC	C2'-C1'	3.63	1.46	1.39
2	A	701	DHC	C2'-C1'	3.58	1.46	1.39
2	H	701	DHC	C2'-C1'	3.57	1.46	1.39
2	B	701	DHC	C2'-C1'	3.53	1.46	1.39
2	C	701	DHC	C2'-C1'	3.43	1.45	1.39
2	E	701	DHC	C6'-C1'	3.10	1.45	1.39
2	F	701	DHC	C6'-C1'	3.01	1.45	1.39
2	D	701	DHC	C6'-C1'	2.98	1.45	1.39
2	H	701	DHC	C6'-C1'	2.92	1.45	1.39
2	B	701	DHC	C5'-C4'	2.82	1.44	1.39
2	B	701	DHC	C6'-C1'	2.74	1.45	1.39
2	C	701	DHC	C6'-C1'	2.62	1.44	1.39
2	A	701	DHC	C6'-C1'	2.62	1.44	1.39
2	C	701	DHC	C5'-C4'	2.60	1.44	1.39
2	G	701	DHC	C6'-C1'	2.58	1.44	1.39
2	F	701	DHC	C5'-C4'	2.57	1.44	1.39
2	H	701	DHC	C5'-C4'	2.56	1.44	1.39
2	A	701	DHC	C5'-C4'	2.54	1.43	1.39
2	D	701	DHC	C5'-C4'	2.53	1.43	1.39
2	G	701	DHC	C4'-C3'	2.51	1.44	1.40
2	E	701	DHC	C5'-C4'	2.41	1.43	1.39
2	E	701	DHC	C4'-C3'	2.40	1.44	1.40
2	G	701	DHC	C5'-C4'	2.27	1.43	1.39
2	D	701	DHC	C4'-C3'	2.20	1.43	1.40
2	C	701	DHC	C4'-C3'	2.11	1.43	1.40
2	F	701	DHC	C4'-C3'	2.05	1.43	1.40
2	F	701	DHC	C1'-C3	2.03	1.53	1.47
2	A	701	DHC	C1'-C3	2.03	1.53	1.47
2	C	701	DHC	C1'-C3	2.00	1.53	1.47

There are no bond angle outliers.

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	701	DHC	O2-C1-C2-C3
2	F	701	DHC	O1-C1-C2-C3
2	G	701	DHC	O1-C1-C2-C3
2	E	701	DHC	O1-C1-C2-C3
2	E	701	DHC	O2-C1-C2-C3
2	G	701	DHC	O2-C1-C2-C3
2	B	701	DHC	O1-C1-C2-C3
2	B	701	DHC	O2-C1-C2-C3
2	D	701	DHC	O1-C1-C2-C3
2	A	701	DHC	O2-C1-C2-C3
2	D	701	DHC	O2-C1-C2-C3
2	A	701	DHC	O1-C1-C2-C3
2	C	701	DHC	O1-C1-C2-C3
2	C	701	DHC	O2-C1-C2-C3
2	D	701	DHC	C2'-C1'-C3-C2
2	D	701	DHC	C6'-C1'-C3-C2
2	H	701	DHC	O1-C1-C2-C3
2	H	701	DHC	O2-C1-C2-C3

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	701	DHC	1	0
2	G	701	DHC	1	0
2	C	701	DHC	1	0
2	F	701	DHC	1	0
2	B	701	DHC	1	0
2	H	701	DHC	1	0
2	D	701	DHC	1	0

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	514/521 (98%)	-0.02	23 (4%) 39 40	10, 20, 41, 61	0
1	B	514/521 (98%)	-0.09	8 (1%) 70 72	10, 20, 38, 53	0
1	C	513/521 (98%)	-0.21	9 (1%) 67 70	9, 18, 35, 48	0
1	D	513/521 (98%)	-0.05	26 (5%) 34 36	8, 18, 41, 55	0
1	E	513/521 (98%)	-0.14	18 (3%) 47 49	9, 18, 37, 66	0
1	F	513/521 (98%)	-0.35	6 (1%) 76 78	8, 15, 32, 46	0
1	G	513/521 (98%)	-0.26	7 (1%) 73 75	7, 17, 33, 47	0
1	H	513/521 (98%)	0.07	30 (5%) 30 31	9, 20, 43, 59	0
All	All	4106/4168 (98%)	-0.13	127 (3%) 51 53	7, 18, 38, 66	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	74	ILE	8.2
1	A	296	GLY	7.5
1	H	74	ILE	7.1
1	A	289	ILE	6.1
1	D	70	ALA	5.7
1	E	289	ILE	5.7
1	E	296	GLY	5.3
1	A	293	PRO	5.2
1	B	523	VAL	5.0
1	E	523	VAL	5.0
1	H	523	VAL	4.9
1	H	66	PHE	4.9
1	C	399	GLY	4.9
1	D	66	PHE	4.8
1	D	523	VAL	4.7
1	E	291	THR	4.7

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Mol	Chain	Res	Type	RSRZ
1	B	7	PRO	4.7
1	E	293	PRO	4.7
1	H	70	ALA	4.5
1	E	290	GLY	4.5
1	A	523	VAL	4.4
1	F	523	VAL	4.3
1	H	63	THR	4.3
1	F	293	PRO	4.2
1	G	523	VAL	4.2
1	A	286	ALA	4.2
1	G	399	GLY	4.2
1	H	77	GLU	4.2
1	D	64	THR	4.1
1	A	285	ASP	4.1
1	A	291	THR	4.1
1	D	73	LEU	4.0
1	B	277	HIS	3.9
1	C	523	VAL	3.9
1	H	60	TYR	3.9
1	D	71	ASN	3.9
1	H	73	LEU	3.9
1	A	7	PRO	3.8
1	A	294	GLU	3.8
1	D	63	THR	3.8
1	D	69	LEU	3.7
1	D	68	PRO	3.7
1	A	290	GLY	3.7
1	D	293	PRO	3.7
1	D	60	TYR	3.7
1	E	288	ASP	3.7
1	G	398	ALA	3.7
1	H	64	THR	3.6
1	H	9	PRO	3.5
1	E	294	GLU	3.5
1	D	294	GLU	3.4
1	A	172	ARG	3.4
1	F	294	GLU	3.3
1	D	75	SER	3.3
1	F	277	HIS	3.3
1	E	295	ALA	3.3
1	H	69	LEU	3.2
1	H	277	HIS	3.2

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Mol	Chain	Res	Type	RSRZ
1	E	285	ASP	3.2
1	E	286	ALA	3.2
1	C	296	GLY	3.1
1	H	75	SER	3.1
1	D	296	GLY	3.0
1	C	184	ARG	2.9
1	H	62	LEU	2.9
1	B	184	ARG	2.9
1	D	62	LEU	2.8
1	C	172	ARG	2.8
1	H	72	ARG	2.8
1	D	77	GLU	2.8
1	E	172	ARG	2.8
1	A	284	LEU	2.8
1	F	296	GLY	2.8
1	H	8	LYS	2.7
1	A	288	ASP	2.7
1	A	295	ALA	2.7
1	H	187	ARG	2.7
1	H	76	GLY	2.7
1	A	73	LEU	2.6
1	D	54	ARG	2.6
1	B	177	LEU	2.6
1	A	292	GLU	2.6
1	A	74	ILE	2.5
1	H	53	ILE	2.5
1	E	284	LEU	2.5
1	H	68	PRO	2.5
1	D	80	ARG	2.5
1	D	277	HIS	2.5
1	H	67	GLY	2.5
1	A	277	HIS	2.4
1	H	10	ALA	2.4
1	H	172	ARG	2.4
1	H	71	ASN	2.4
1	A	287	GLY	2.4
1	E	287	GLY	2.4
1	A	400	LEU	2.3
1	A	279	ILE	2.3
1	E	277	HIS	2.3
1	D	56	ALA	2.3
1	H	294	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	76	GLY	2.2
1	D	72	ARG	2.2
1	H	39	ARG	2.2
1	A	66	PHE	2.2
1	C	290	GLY	2.2
1	F	290	GLY	2.2
1	H	65	GLY	2.2
1	G	74	ILE	2.2
1	E	292	GLU	2.2
1	B	172	ARG	2.2
1	C	80	ARG	2.2
1	B	399	GLY	2.1
1	G	80	ARG	2.1
1	E	279	ILE	2.1
1	E	80	ARG	2.1
1	G	172	ARG	2.1
1	H	80	ARG	2.1
1	C	285	ASP	2.1
1	H	522	PRO	2.1
1	C	279	ILE	2.1
1	G	64	THR	2.1
1	D	67	GLY	2.1
1	B	33	VAL	2.0
1	A	171	ASP	2.0
1	D	51	ALA	2.0
1	H	56	ALA	2.0
1	D	172	ARG	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	MDO	H	149	13/14	0.82	0.12	19,23,29,30	0
1	MDO	B	149	13/14	0.85	0.11	19,22,27,28	0
1	MDO	F	149	13/14	0.89	0.10	15,19,23,27	0
1	MDO	E	149	13/14	0.89	0.09	13,17,22,23	0
1	MDO	A	149	13/14	0.90	0.09	14,19,21,24	0
1	MDO	C	149	13/14	0.90	0.09	13,15,20,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MDO	G	149	13/14	0.90	0.09	14,17,21,22	0
1	MDO	D	149	13/14	0.90	0.10	18,21,29,29	0

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(\AA^2)	Q<0.9
2	DHC	D	701	13/13	0.77	0.16	34,39,44,47	0
2	DHC	A	701	13/13	0.85	0.16	34,42,46,48	0
2	DHC	H	701	13/13	0.85	0.14	33,40,49,53	0
2	DHC	B	701	13/13	0.86	0.11	27,31,37,40	0
2	DHC	E	701	13/13	0.87	0.10	24,30,34,34	0
2	DHC	G	701	13/13	0.88	0.11	24,28,36,39	0
2	DHC	C	701	13/13	0.88	0.10	21,26,33,36	0
2	DHC	F	701	13/13	0.90	0.09	24,28,32,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.