



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 11:38 pm GMT

PDB ID : 4ELB
Title : Structure-activity relationship guides enantiomeric preference among potent inhibitors of B. anthracis dihydrofolate reductase
Authors : Bourne, C.R.; Barrow, W.W.
Deposited on : 2012-04-10
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

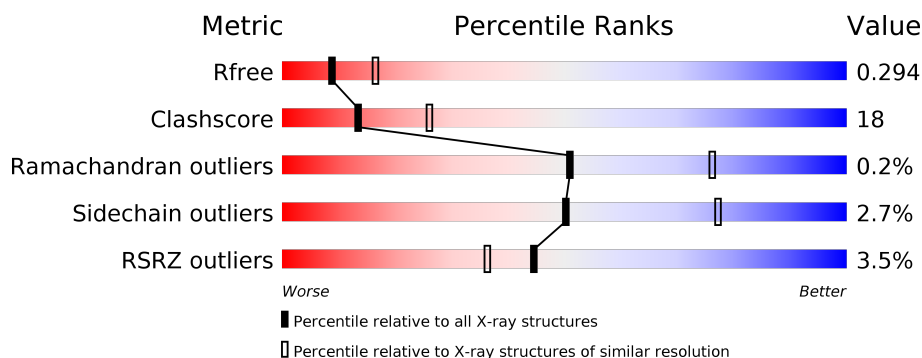
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	166	<div> <div>4%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>.</div> </div> </div>
1	B	166	<div> <div>80%</div> <div>19%</div> <div>.</div> </div>
1	C	166	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>17%</div> <div>.</div> </div> </div>
1	D	166	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>21%</div> <div>.</div> </div> </div>
1	E	166	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>24%</div> <div>.</div> </div> </div>
1	F	166	<div> <div>4%</div> <div> <div></div> <div>77%</div> <div>23%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	166	
1	H	166	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	B	202	-	-	X	-
3	CL	G	202	-	-	X	-
3	CL	H	203	-	-	X	-
4	34S	A	203	-	-	X	-
4	34S	B	203	-	-	-	X
4	34S	F	203[A]	-	-	X	-
5	34R	F	204[B]	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12054 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 Dihydrofolate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	0	0	0
			1374	889	225	251	9			
1	H	166	Total	C	N	O	S	0	0	0
			1380	892	228	251	9			
1	C	166	Total	C	N	O	S	0	0	0
			1380	892	228	251	9			
1	B	166	Total	C	N	O	S	0	0	0
			1374	889	225	251	9			
1	G	166	Total	C	N	O	S	0	0	0
			1380	892	228	251	9			
1	F	166	Total	C	N	O	S	0	0	0
			1380	892	228	251	9			
1	D	166	Total	C	N	O	S	0	0	0
			1380	892	228	251	9			
1	E	166	Total	C	N	O	S	0	0	0
			1380	892	228	251	9			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	163	LEU	-	EXPRESSION TAG	UNP Q81R22
A	164	VAL	-	EXPRESSION TAG	UNP Q81R22
A	165	PRO	-	EXPRESSION TAG	UNP Q81R22
A	166	ARG	-	EXPRESSION TAG	UNP Q81R22
H	163	LEU	-	EXPRESSION TAG	UNP Q81R22
H	164	VAL	-	EXPRESSION TAG	UNP Q81R22
H	165	PRO	-	EXPRESSION TAG	UNP Q81R22
H	166	ARG	-	EXPRESSION TAG	UNP Q81R22
C	163	LEU	-	EXPRESSION TAG	UNP Q81R22
C	164	VAL	-	EXPRESSION TAG	UNP Q81R22
C	165	PRO	-	EXPRESSION TAG	UNP Q81R22
C	166	ARG	-	EXPRESSION TAG	UNP Q81R22
B	163	LEU	-	EXPRESSION TAG	UNP Q81R22

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Chain	Residue	Modelled	Actual	Comment	Reference
B	164	VAL	-	EXPRESSION TAG	UNP Q81R22
B	165	PRO	-	EXPRESSION TAG	UNP Q81R22
B	166	ARG	-	EXPRESSION TAG	UNP Q81R22
G	163	LEU	-	EXPRESSION TAG	UNP Q81R22
G	164	VAL	-	EXPRESSION TAG	UNP Q81R22
G	165	PRO	-	EXPRESSION TAG	UNP Q81R22
G	166	ARG	-	EXPRESSION TAG	UNP Q81R22
F	163	LEU	-	EXPRESSION TAG	UNP Q81R22
F	164	VAL	-	EXPRESSION TAG	UNP Q81R22
F	165	PRO	-	EXPRESSION TAG	UNP Q81R22
F	166	ARG	-	EXPRESSION TAG	UNP Q81R22
D	163	LEU	-	EXPRESSION TAG	UNP Q81R22
D	164	VAL	-	EXPRESSION TAG	UNP Q81R22
D	165	PRO	-	EXPRESSION TAG	UNP Q81R22
D	166	ARG	-	EXPRESSION TAG	UNP Q81R22
E	163	LEU	-	EXPRESSION TAG	UNP Q81R22
E	164	VAL	-	EXPRESSION TAG	UNP Q81R22
E	165	PRO	-	EXPRESSION TAG	UNP Q81R22
E	166	ARG	-	EXPRESSION TAG	UNP Q81R22

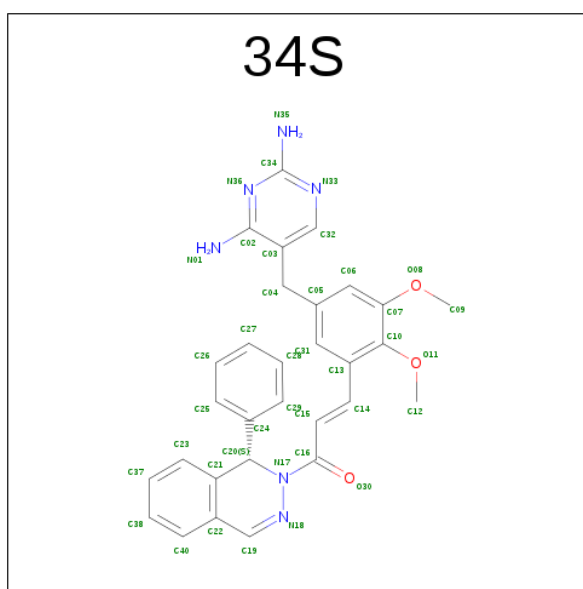
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0
2	H	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	F	1	Total Ca 1 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	E	1	Total Cl 1 1	0	0
3	H	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	F	1	Total Cl 1 1	0	0

- Molecule 4 is (2E)-3-{5-[(2,4-DIAMINOPYRIMIDIN-5-YL)METHYL]-2,3-DIMETHOXY PHENYL}-1-[(1S)-1-PHENYLPHthalAZIN-2(1H)-YL]PROP-2-EN-1-ONE (three-letter code: 34S) (formula: C₃₀H₂₈N₆O₃).



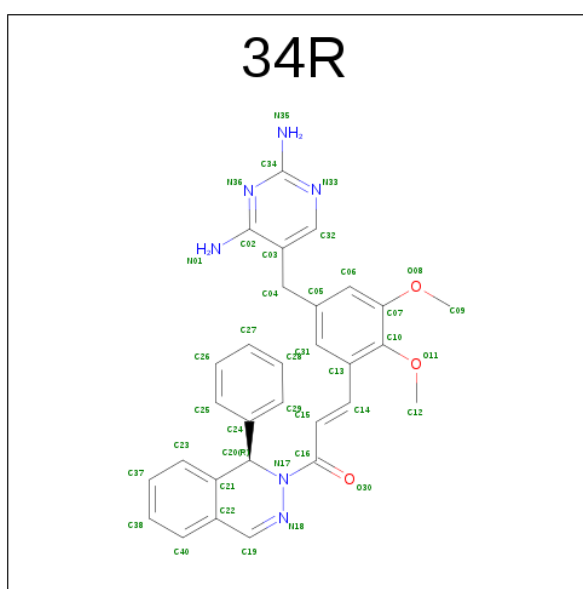
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 39 30 6 3	0	0
4	H	1	Total C N O 39 30 6 3	0	0
4	B	1	Total C N O 39 30 6 3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	G	1	Total	C	N	O	0	1
			39	30	6	3		
4	F	1	Total	C	N	O	0	1
			39	30	6	3		
4	E	1	Total	C	N	O	0	1
			39	30	6	3		

- Molecule 5 is (2E)-3-{5-[(2,4-DIAMINOPYRIMIDIN-5-YL)METHYL]-2,3-DIMETHOXY PHENYL}-1-[(1R)-1-PHENYLPHthalazin-2(1H)-YL]PROP-2-EN-1-ONE (three-letter code: 34R) (formula: C₃₀H₂₈N₆O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			39	30	6	3		
5	F	1	Total	C	N	O	0	1
			39	30	6	3		
5	D	1	Total	C	N	O	0	0
			39	30	6	3		
5	E	1	Total	C	N	O	0	1
			39	30	6	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	96	Total	O	0	0
			96	96		

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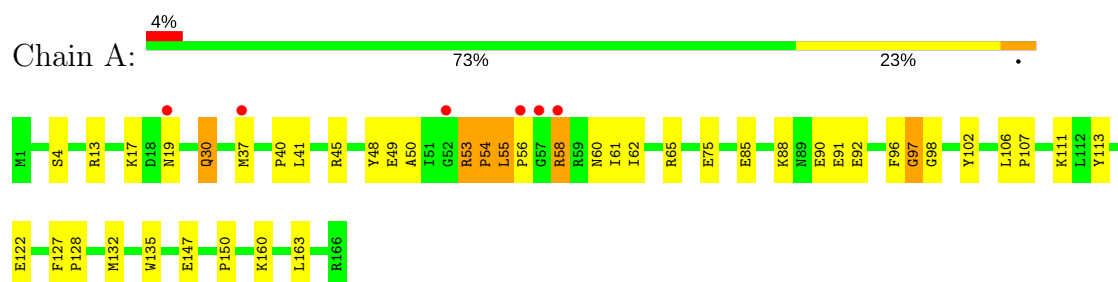
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	58	Total 58	O 58	0	0
6	C	102	Total 102	O 102	0	0
6	B	60	Total 60	O 60	0	0
6	G	72	Total 72	O 72	0	0
6	F	58	Total 58	O 58	0	0
6	D	82	Total 82	O 82	0	0
6	E	92	Total 92	O 92	0	0

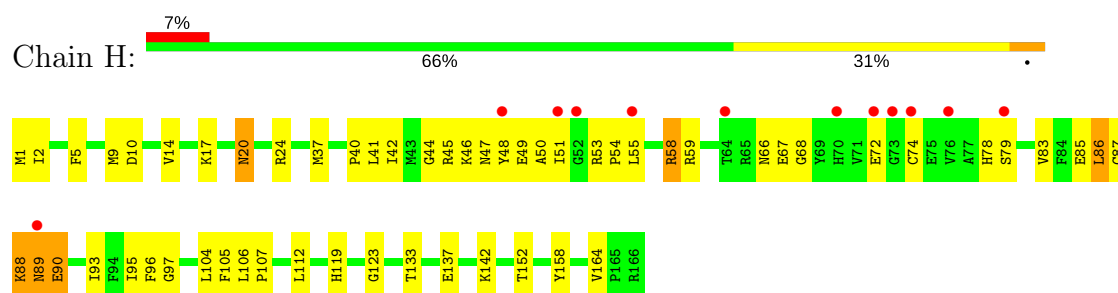
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

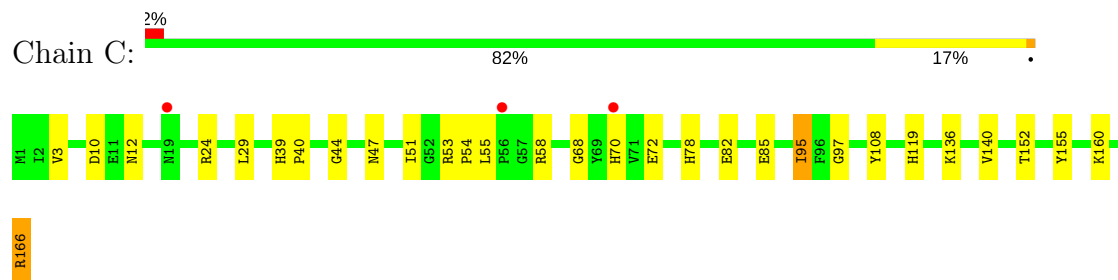
- Molecule 1: Dihydrofolate reductase



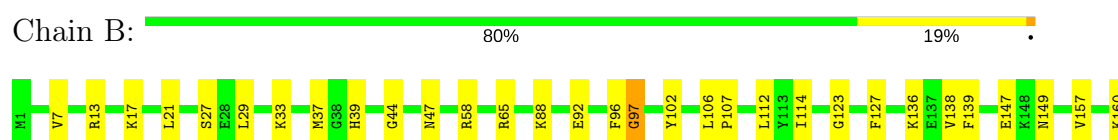
- Molecule 1: Dihydrofolate reductase



- Molecule 1: Dihydrofolate reductase

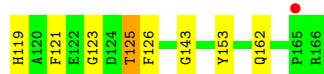
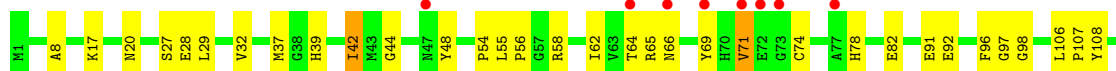
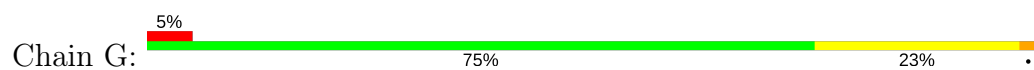


- Molecule 1: Dihydrofolate reductase

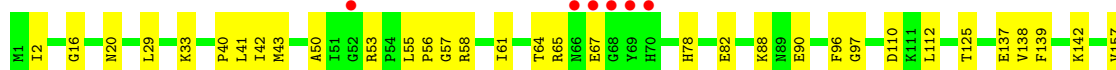
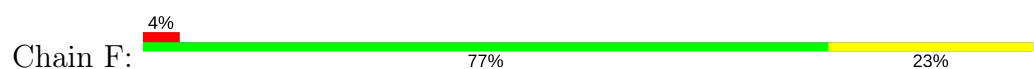




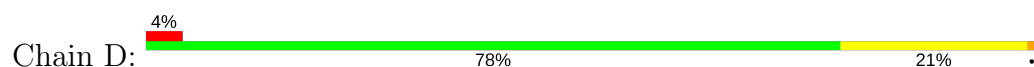
- Molecule 1: Dihydrofolate reductase



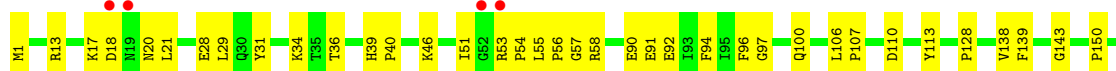
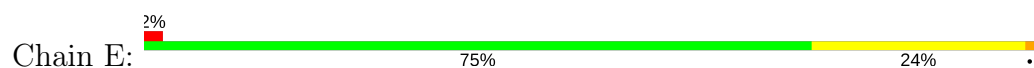
- Molecule 1: Dihydrofolate reductase



- Molecule 1: Dihydrofolate reductase



- Molecule 1: Dihydrofolate reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.87Å 135.44Å 168.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.94 – 2.60 71.45 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.94-2.60) 99.6 (71.45-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.25 (at 2.62Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.243 , 0.309 0.229 , 0.294	Depositor DCC
R_{free} test set	2459 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.0	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	12054	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.26 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.4095e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: CA, CL, 34R, 34S

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	0.27	0/1412	0.55	0/1911
1	B	0.28	0/1412	0.54	0/1911
1	C	0.29	0/1418	0.55	0/1918
1	D	0.29	0/1418	0.56	0/1918
1	E	0.29	0/1418	0.56	0/1918
1	F	0.29	0/1418	0.55	0/1918
1	G	0.28	0/1418	0.54	0/1918
1	H	0.31	0/1418	0.56	0/1918
All	All	0.29	0/11332	0.55	0/15330

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
All	All	0	8

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	97	GLY	Peptide
1	B	97	GLY	Peptide
1	C	97	GLY	Peptide
1	D	97	GLY	Peptide
1	E	97	GLY	Peptide
1	F	97	GLY	Peptide
1	G	97	GLY	Peptide
1	H	97	GLY	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	1374	0	1335	54	1
1	B	1374	0	1335	35	0
1	C	1380	0	1346	28	0
1	D	1380	0	1346	31	0
1	E	1380	0	1346	50	1
1	F	1380	0	1346	63	0
1	G	1380	0	1346	40	0
1	H	1380	0	1346	58	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	1	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	1	0
3	B	1	0	0	2	0
3	C	1	0	0	1	0
3	D	1	0	0	1	0
3	E	1	0	0	1	0
3	F	1	0	0	0	0
3	G	1	0	0	2	0
3	H	1	0	0	3	0
4	A	39	0	28	22	0
4	B	39	0	28	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	39	0	28	6	0
4	F	39	0	28	24	0
4	G	39	0	28	9	0
4	H	39	0	28	18	0
5	C	39	0	28	5	0
5	D	39	0	28	10	0
5	E	39	0	28	13	0
5	F	39	0	28	25	0
6	A	96	0	0	3	1
6	B	60	0	0	5	0
6	C	102	0	0	5	0
6	D	82	0	0	4	0
6	E	92	0	0	3	0
6	F	58	0	0	4	0
6	G	72	0	0	4	0
6	H	58	0	0	2	0
All	All	12054	0	11026	404	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (404) 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:53:ARG:NH2	5:F:204[B]:34R:H26	1.51	1.23
1:A:41:LEU:CD2	1:A:55:LEU:HD11	1.72	1.19
1:A:56:PRO:HD2	4:A:203:34S:H4	1.28	1.15
1:F:53:ARG:NH2	5:F:204[B]:34R:C27	2.12	1.12
1:F:53:ARG:CZ	5:F:204[B]:34R:H26	1.80	1.09
1:A:61:ILE:HD12	1:A:75:GLU:HB2	1.37	1.06
4:A:203:34S:H12	4:A:203:34S:C12	1.90	1.02
1:E:31:TYR:HA	1:E:34:LYS:HE3	1.39	1.00
4:H:202:34S:N18	4:H:202:34S:H13	1.77	0.99
1:F:55:LEU:HD13	4:F:203[A]:34S:C40	1.94	0.97
1:F:20:ASN:HA	5:F:204[B]:34R:H6	1.46	0.95
1:C:166:ARG:CG	1:C:166:ARG:HH11	1.80	0.95
1:H:55:LEU:HD22	4:H:202:34S:C21	1.97	0.94
1:A:41:LEU:HD23	1:A:55:LEU:HD11	1.46	0.93
1:H:37:MET:HA	1:H:58:ARG:HH11	1.30	0.93
1:F:53:ARG:HH21	5:F:204[B]:34R:C26	1.83	0.92
1:F:53:ARG:HH21	5:F:204[B]:34R:C27	1.83	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:20:ASN:HA	4:F:203[A]:34S:H17	1.52	0.92
4:F:203[A]:34S:H13	4:F:203[A]:34S:N18	1.84	0.91
1:H:67:GLU:HA	1:H:78:HIS:CE1	2.07	0.90
1:A:55:LEU:HB3	4:A:203:34S:C37	2.01	0.90
1:C:51:ILE:HD13	5:C:203:34R:H1	1.50	0.90
1:D:96:PHE:CE2	5:D:203:34R:H10	2.06	0.89
1:H:55:LEU:HD22	4:H:202:34S:C22	2.03	0.88
4:A:203:34S:N18	4:A:203:34S:H13	1.89	0.88
1:A:55:LEU:HB3	4:A:203:34S:C38	2.05	0.87
1:E:51:ILE:HG21	1:E:55:LEU:HD21	1.55	0.87
4:F:203[A]:34S:H11	4:F:203[A]:34S:O30	1.75	0.86
1:E:110:ASP:OD1	6:E:321:HOH:O	1.95	0.85
1:A:41:LEU:CD2	1:A:55:LEU:CD1	2.56	0.84
1:E:55:LEU:HA	5:E:204[B]:34R:H25	1.57	0.84
1:B:96:PHE:CE2	4:B:203:34S:H28	2.13	0.83
4:A:203:34S:H15	4:A:203:34S:H12	1.62	0.82
1:E:90:GLU:OE2	6:E:384:HOH:O	1.96	0.82
4:F:203[A]:34S:H12	4:F:203[A]:34S:O11	1.77	0.82
1:H:48:TYR:OH	1:H:54:PRO:HD3	1.81	0.81
1:B:162:GLN:HG2	6:B:357:HOH:O	1.79	0.81
1:F:139:PHE:HB3	1:F:157:VAL:HG12	1.63	0.80
1:F:139:PHE:HB3	1:F:157:VAL:CG1	2.12	0.80
1:F:41:LEU:HD21	1:F:96:PHE:CD2	2.17	0.79
1:B:139:PHE:HB3	1:B:157:VAL:HG12	1.65	0.79
1:A:61:ILE:CD1	1:A:75:GLU:HB2	2.12	0.79
1:A:55:LEU:CB	4:A:203:34S:C38	2.61	0.79
1:A:41:LEU:HD22	1:A:55:LEU:HD11	1.63	0.79
1:E:17:LYS:O	1:E:18:ASP:OD1	2.01	0.79
4:A:203:34S:O11	4:A:203:34S:H12	1.80	0.79
1:E:55:LEU:HD22	5:E:204[B]:34R:C25	2.13	0.78
4:H:202:34S:O11	4:H:202:34S:H12	1.84	0.78
1:F:50:ALA:O	6:F:308:HOH:O	2.00	0.78
1:F:55:LEU:CD2	5:F:204[B]:34R:C28	2.62	0.78
1:H:37:MET:HA	1:H:58:ARG:NH1	1.99	0.77
1:A:41:LEU:HD22	1:A:55:LEU:CD1	2.15	0.77
1:E:139:PHE:HB3	1:E:157:VAL:CG1	2.13	0.77
1:C:166:ARG:HH11	1:C:166:ARG:HG3	1.50	0.77
5:F:204[B]:34R:O08	5:F:204[B]:34R:H5	1.86	0.76
1:D:48:TYR:OH	1:D:54:PRO:HG3	1.85	0.76
1:E:139:PHE:HB3	1:E:157:VAL:HG12	1.66	0.76
1:C:166:ARG:HH11	1:C:166:ARG:HG2	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:24:ARG:NH2	1:B:88:LYS:HZ2	1.84	0.76
4:F:203[A]:34S:O08	4:F:203[A]:34S:H16	1.86	0.75
1:F:55:LEU:HD13	4:F:203[A]:34S:C38	2.16	0.75
1:A:58:ARG:HH11	4:A:203:34S:H3	1.52	0.74
1:A:56:PRO:HD2	4:A:203:34S:C37	2.14	0.74
1:G:20:ASN:OD1	6:G:337:HOH:O	2.05	0.74
4:H:202:34S:C12	4:H:202:34S:O08	2.36	0.73
1:B:96:PHE:CZ	4:B:203:34S:H28	2.23	0.73
1:D:29:LEU:O	5:D:203:34R:H19	1.87	0.73
1:G:62:ILE:CD1	1:G:74:CYS:HB3	2.18	0.73
1:H:59:ARG:NH2	1:H:86:LEU:HD23	2.03	0.72
1:F:55:LEU:HD21	5:F:204[B]:34R:C29	2.18	0.72
1:G:55:LEU:HD13	4:G:203[A]:34S:C22	2.19	0.71
1:A:85:GLU:OE2	1:A:88:LYS:NZ	2.23	0.71
1:E:1:MET:O	6:E:391:HOH:O	2.09	0.70
4:H:202:34S:H16	4:H:202:34S:O08	1.90	0.70
5:E:204[B]:34R:O08	5:E:204[B]:34R:C12	2.39	0.70
1:A:13:ARG:NH1	1:A:128:PRO:O	2.26	0.69
4:B:203:34S:O08	4:B:203:34S:H16	1.92	0.69
1:H:89:ASN:O	1:H:89:ASN:CG	2.30	0.69
1:H:55:LEU:HD22	4:H:202:34S:C23	2.22	0.69
1:A:132:MET:HE2	1:A:135:TRP:CD1	2.28	0.69
1:E:53:ARG:CD	1:E:54:PRO:HD2	2.23	0.69
1:F:20:ASN:OD1	6:F:308:HOH:O	2.11	0.68
1:D:42:ILE:HD12	1:D:42:ILE:N	2.09	0.68
1:A:37:MET:HA	1:A:58:ARG:HE	1.59	0.68
1:D:127:PHE:CD1	1:D:128:PRO:HD2	2.29	0.68
1:C:95:ILE:HD12	1:C:95:ILE:N	2.07	0.68
4:B:203:34S:O08	4:B:203:34S:C12	2.41	0.68
1:E:56:PRO:O	1:E:58:ARG:NH1	2.27	0.67
1:A:58:ARG:NH1	4:A:203:34S:H3	2.09	0.67
1:F:53:ARG:HH21	5:F:204[B]:34R:H25	1.59	0.67
1:D:96:PHE:CZ	5:D:203:34R:H10	2.30	0.67
1:F:55:LEU:CD1	4:F:203[A]:34S:C40	2.73	0.67
1:H:106:LEU:O	1:H:106:LEU:HD23	1.95	0.66
4:A:203:34S:H23	4:A:203:34S:C31	2.26	0.66
1:F:41:LEU:HD21	1:F:96:PHE:CG	2.30	0.66
1:B:139:PHE:HB3	1:B:157:VAL:CG1	2.25	0.66
4:H:202:34S:C31	4:H:202:34S:H23	2.25	0.66
6:B:352:HOH:O	1:F:163:LEU:HD21	1.95	0.65
1:H:53:ARG:HB2	1:H:54:PRO:HD2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:ARG:NH1	1:F:164:VAL:O	2.29	0.65
1:F:58:ARG:NH2	4:F:203[A]:34S:H3	2.11	0.65
4:F:203[A]:34S:O08	4:F:203[A]:34S:C12	2.44	0.65
1:A:55:LEU:CB	4:A:203:34S:C37	2.73	0.65
1:F:162:GLN:HG2	6:F:354:HOH:O	1.97	0.64
2:D:201:CA:CA	6:D:381:HOH:O	1.73	0.64
5:D:203:34R:H24	5:D:203:34R:C23	2.26	0.64
5:F:204[B]:34R:O08	5:F:204[B]:34R:C12	2.46	0.63
1:A:48:TYR:OH	1:A:54:PRO:HG3	1.98	0.63
1:H:55:LEU:CD2	4:H:202:34S:C21	2.73	0.63
1:C:68:GLY:O	1:C:70:HIS:CD2	2.52	0.63
1:G:107:PRO:HG2	1:G:108:TYR:CE2	2.33	0.63
1:A:132:MET:HE2	1:A:132:MET:HA	1.81	0.63
1:G:62:ILE:HD11	1:G:74:CYS:HB3	1.80	0.63
1:H:24:ARG:NH2	1:B:88:LYS:NZ	2.47	0.63
1:C:12:ASN:ND2	6:C:345:HOH:O	2.27	0.62
1:F:29:LEU:HD22	5:F:204[B]:34R:H2	1.79	0.62
4:B:203:34S:H19	6:B:358:HOH:O	1.98	0.62
1:D:39:HIS:HB3	1:D:92:GLU:O	2.00	0.62
5:D:203:34R:H4	5:D:203:34R:O08	1.98	0.62
5:F:204[B]:34R:C32	5:F:204[B]:34R:C31	2.75	0.62
1:C:51:ILE:CD1	5:C:203:34R:H1	2.28	0.62
1:C:3:VAL:HG13	1:C:95:ILE:HD11	1.81	0.61
1:F:55:LEU:CD1	4:F:203[A]:34S:C22	2.77	0.61
1:E:17:LYS:C	1:E:18:ASP:OD1	2.37	0.61
1:F:55:LEU:CD2	5:F:204[B]:34R:C29	2.78	0.61
4:A:203:34S:C32	4:A:203:34S:C31	2.77	0.61
1:E:55:LEU:HD13	4:E:203[A]:34S:C22	2.29	0.61
1:H:55:LEU:HB3	4:H:202:34S:C38	2.31	0.61
1:G:106:LEU:N	1:G:107:PRO:HD2	2.15	0.61
5:E:204[B]:34R:O08	5:E:204[B]:34R:H5	2.00	0.61
1:G:44:GLY:HA3	3:G:202:CL:CL	2.38	0.60
4:H:202:34S:H11	4:H:202:34S:O30	2.00	0.60
1:B:96:PHE:O	4:B:203:34S:N01	2.34	0.60
1:B:136:LYS:HE2	1:B:161:GLN:HA	1.83	0.60
1:G:98:GLY:HA3	3:G:202:CL:CL	2.39	0.60
4:H:202:34S:N18	4:H:202:34S:C14	2.52	0.60
1:A:55:LEU:HB2	4:A:203:34S:C38	2.32	0.59
1:E:53:ARG:HG3	1:E:54:PRO:HD2	1.82	0.59
1:F:55:LEU:CD2	5:F:204[B]:34R:H27	2.31	0.59
1:G:96:PHE:CE2	4:G:203[A]:34S:H21	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:55:LEU:HD22	4:F:203[A]:34S:C23	2.33	0.59
1:D:122:GLU:HG2	6:D:358:HOH:O	2.02	0.59
1:H:40:PRO:CG	1:H:90:GLU:HG2	2.32	0.59
1:A:17:LYS:NZ	6:A:330:HOH:O	2.22	0.58
1:C:166:ARG:NH1	1:C:166:ARG:HG3	2.15	0.58
1:G:28:GLU:OE2	4:G:203[A]:34S:N35	2.29	0.58
1:H:55:LEU:HD22	4:H:202:34S:C40	2.33	0.58
1:F:55:LEU:HD11	4:F:203[A]:34S:C22	2.33	0.58
1:A:60:ASN:O	1:A:61:ILE:HD13	2.04	0.58
1:B:138:VAL:HG23	1:B:157:VAL:HG13	1.85	0.58
4:H:202:34S:C31	4:H:202:34S:C32	2.79	0.58
1:B:27:SER:HB2	1:B:149:ASN:HD21	1.67	0.57
1:D:59:ARG:NH1	1:D:90:GLU:OE2	2.32	0.57
1:H:45:ARG:CZ	1:H:49:GLU:OE2	2.52	0.57
1:C:136:LYS:HE3	1:C:160:LYS:O	2.05	0.57
4:F:203[A]:34S:O11	4:F:203[A]:34S:C15	2.51	0.57
1:C:152:THR:HA	6:C:310:HOH:O	2.03	0.57
1:H:55:LEU:HB3	4:H:202:34S:C37	2.34	0.56
1:E:55:LEU:HD22	5:E:204[B]:34R:C26	2.35	0.56
1:G:107:PRO:HG2	1:G:108:TYR:CD2	2.40	0.56
1:A:13:ARG:HD3	1:A:127:PHE:O	2.05	0.56
1:A:13:ARG:NH1	1:A:127:PHE:CD2	2.72	0.56
1:F:33:LYS:HB2	5:F:204[B]:34R:H19	1.88	0.56
1:H:48:TYR:OH	1:H:54:PRO:CD	2.54	0.56
1:H:45:ARG:NH2	1:H:49:GLU:OE2	2.39	0.55
1:B:29:LEU:HD22	4:B:203:34S:H12	1.87	0.55
1:E:53:ARG:CG	1:E:54:PRO:HD2	2.35	0.55
1:A:96:PHE:CZ	4:A:203:34S:H28	2.42	0.55
1:F:41:LEU:HD22	1:F:43:MET:HE2	1.89	0.55
1:H:85:GLU:OE1	1:H:88:LYS:NZ	2.37	0.55
4:F:203[A]:34S:C31	4:F:203[A]:34S:C32	2.84	0.55
4:F:203[A]:34S:C16	4:F:203[A]:34S:H11	2.36	0.55
1:H:40:PRO:CD	1:H:90:GLU:HG2	2.36	0.55
1:E:55:LEU:HD22	5:E:204[B]:34R:H24	1.89	0.55
1:F:55:LEU:HD22	5:F:204[B]:34R:H27	1.88	0.55
1:H:106:LEU:N	1:H:107:PRO:HD2	2.22	0.55
1:B:47:ASN:HB2	3:B:202:CL:CL	2.44	0.54
1:A:91:GLU:HG3	1:A:92:GLU:N	2.22	0.54
1:D:28:GLU:OE2	5:D:203:34R:N35	2.36	0.54
1:E:31:TYR:CA	1:E:34:LYS:HE3	2.26	0.54
5:F:204[B]:34R:C31	5:F:204[B]:34R:H12	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:LEU:HD13	4:A:203:34S:C40	2.38	0.54
1:D:29:LEU:O	5:D:203:34R:C40	2.56	0.54
1:G:39:HIS:ND1	1:G:92:GLU:HB3	2.22	0.54
1:F:55:LEU:HD21	5:F:204[B]:34R:C28	2.33	0.54
1:B:13:ARG:HD3	6:B:320:HOH:O	2.07	0.53
1:D:28:GLU:CD	5:D:203:34R:H13	2.10	0.53
1:G:8:ALA:HB2	4:G:203[A]:34S:N35	2.23	0.53
1:H:66:ASN:C	1:H:66:ASN:OD1	2.47	0.53
1:E:46:LYS:HB2	3:E:202:CL:CL	2.46	0.53
1:F:41:LEU:HD22	1:F:43:MET:CE	2.39	0.53
1:E:139:PHE:HB3	1:E:157:VAL:HG11	1.90	0.53
1:F:112:LEU:O	1:F:157:VAL:HA	2.09	0.53
5:F:204[B]:34R:C32	5:F:204[B]:34R:H17	2.38	0.53
1:B:138:VAL:CG2	1:B:157:VAL:HG13	2.39	0.53
1:B:44:GLY:HA3	3:B:202:CL:CL	2.45	0.52
1:F:67:GLU:HA	1:F:78:HIS:CD2	2.44	0.52
4:A:203:34S:N18	4:A:203:34S:C14	2.61	0.52
1:D:111:LYS:HG3	1:D:159:GLU:HG2	1.91	0.52
1:E:29:LEU:HD22	4:E:203[A]:34S:H13	1.90	0.52
1:G:78:HIS:ND1	1:G:82:GLU:OE1	2.31	0.52
1:H:50:ALA:HA	6:H:350:HOH:O	2.09	0.52
1:E:13:ARG:NH1	1:E:128:PRO:O	2.42	0.52
1:B:33:LYS:HG3	4:B:203:34S:C38	2.39	0.52
1:G:56:PRO:O	1:G:58:ARG:NH1	2.43	0.52
1:G:27:SER:HB3	1:G:153:TYR:OH	2.09	0.52
1:C:95:ILE:CD1	1:C:95:ILE:N	2.73	0.51
1:H:55:LEU:CD2	4:H:202:34S:C23	2.88	0.51
1:A:13:ARG:NH1	1:A:127:PHE:HD2	2.09	0.51
1:C:24:ARG:NH1	6:C:363:HOH:O	2.44	0.51
1:F:55:LEU:HD22	5:F:204[B]:34R:C28	2.40	0.51
1:E:57:GLY:O	1:E:58:ARG:HG3	2.10	0.51
1:G:62:ILE:HD11	1:G:74:CYS:CB	2.40	0.51
1:D:131:ASP:OD1	1:D:133:THR:OG1	2.24	0.51
1:H:142:LYS:HE2	1:F:137:GLU:O	2.11	0.51
1:A:48:TYR:CD1	1:A:62:ILE:HD11	2.46	0.51
1:F:78:HIS:ND1	1:F:82:GLU:OE2	2.31	0.51
1:F:58:ARG:NH2	4:F:203[A]:34S:C38	2.74	0.50
1:E:51:ILE:HG12	5:E:204[B]:34R:H1	1.93	0.50
1:G:29:LEU:HD22	4:G:203[A]:34S:H12	1.92	0.50
1:D:36:THR:O	1:D:58:ARG:HD3	2.12	0.50
4:E:203[A]:34S:H16	4:E:203[A]:34S:O08	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:110:ASP:OD1	1:F:160:LYS:NZ	2.44	0.50
4:H:202:34S:O11	4:H:202:34S:C15	2.55	0.50
1:D:164:VAL:HG23	1:D:164:VAL:O	2.11	0.50
1:A:150:PRO:HA	6:A:306:HOH:O	2.11	0.50
1:F:40:PRO:HG2	1:F:90:GLU:HG3	1.94	0.50
1:E:20:ASN:OD1	1:E:21:LEU:N	2.43	0.49
1:H:89:ASN:O	1:H:89:ASN:OD1	2.30	0.49
1:A:98:GLY:HA3	3:A:202:CL:CL	2.50	0.49
1:H:47:ASN:HB2	3:H:203:CL:CL	2.49	0.49
1:D:44:GLY:HA3	3:D:202:CL:CL	2.50	0.49
1:G:66:ASN:HB3	1:G:69:TYR:HB2	1.94	0.49
1:A:30:GLN:OE1	4:A:203:34S:H8	2.13	0.49
1:E:55:LEU:HD13	4:E:203[A]:34S:C40	2.43	0.49
1:F:2:ILE:HG13	6:F:309:HOH:O	2.12	0.49
1:H:1:MET:CE	1:H:87:CYS:HB2	2.43	0.49
1:A:132:MET:CE	1:A:132:MET:HA	2.42	0.49
1:C:44:GLY:HA3	3:C:202:CL:CL	2.49	0.49
1:B:96:PHE:CE2	4:B:203:34S:C31	2.92	0.49
1:G:58:ARG:NH1	6:G:347:HOH:O	2.46	0.49
1:H:2:ILE:N	1:H:2:ILE:HD12	2.27	0.49
1:E:40:PRO:HG2	1:E:90:GLU:HG3	1.95	0.48
1:H:59:ARG:HH22	1:H:86:LEU:HD23	1.77	0.48
1:F:56:PRO:O	1:F:58:ARG:NH2	2.46	0.48
1:C:95:ILE:HD12	1:C:95:ILE:H	1.77	0.48
1:F:58:ARG:CZ	4:F:203[A]:34S:H3	2.42	0.48
1:G:54:PRO:HG3	1:G:74:CYS:SG	2.54	0.48
1:H:42:ILE:N	1:H:42:ILE:HD12	2.28	0.48
1:A:111:LYS:HD3	1:A:113:TYR:CZ	2.48	0.48
1:H:41:LEU:HD12	1:H:55:LEU:HD12	1.95	0.48
1:F:64:THR:O	1:F:78:HIS:HA	2.14	0.48
1:C:166:ARG:NH1	1:C:166:ARG:HG2	2.24	0.48
1:D:161:GLN:NE2	6:D:356:HOH:O	2.35	0.48
1:F:139:PHE:HB3	1:F:157:VAL:HG11	1.94	0.48
4:A:203:34S:C15	4:A:203:34S:O11	2.50	0.47
4:F:203[A]:34S:H23	4:F:203[A]:34S:C31	2.43	0.47
1:H:104:LEU:HD23	1:H:105:PHE:CE2	2.50	0.47
1:D:37:MET:O	1:D:37:MET:HG3	2.14	0.47
1:F:57:GLY:O	1:F:58:ARG:HG3	2.15	0.47
1:B:147:GLU:CD	1:B:147:GLU:H	2.18	0.47
1:H:48:TYR:HE1	1:H:54:PRO:HA	1.79	0.47
1:A:163:LEU:N	1:A:163:LEU:HD12	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:ILE:CD1	1:C:95:ILE:H	2.27	0.47
1:A:56:PRO:HG3	6:A:387:HOH:O	2.15	0.47
1:B:112:LEU:O	1:B:157:VAL:HA	2.15	0.47
1:B:136:LYS:HE3	1:B:160:LYS:O	2.14	0.47
1:E:96:PHE:CZ	5:E:204[B]:34R:H17	2.50	0.47
1:D:160:LYS:HD2	6:D:310:HOH:O	2.14	0.47
1:A:45:ARG:HD3	1:A:49:GLU:OE2	2.14	0.47
1:B:39:HIS:CD2	1:B:92:GLU:HB3	2.50	0.47
1:C:10:ASP:HB2	1:C:119:HIS:O	2.15	0.47
1:E:46:LYS:NZ	1:E:100:GLN:OE1	2.47	0.47
4:A:203:34S:H15	4:A:203:34S:C15	2.40	0.46
1:A:61:ILE:HD12	1:A:75:GLU:CB	2.26	0.46
1:A:60:ASN:C	1:A:61:ILE:HD13	2.36	0.46
1:E:31:TYR:HA	1:E:34:LYS:CE	2.28	0.46
1:F:96:PHE:O	5:F:204[B]:34R:N01	2.48	0.46
1:H:66:ASN:OD1	1:H:68:GLY:N	2.48	0.46
1:C:29:LEU:HD22	5:C:203:34R:H2	1.97	0.46
1:B:17:LYS:HB2	1:B:123:GLY:HA2	1.98	0.46
1:H:137:GLU:O	1:F:142:LYS:HE3	2.15	0.46
1:D:122:GLU:O	1:D:122:GLU:HG3	2.16	0.46
1:A:4:SER:OG	1:A:111:LYS:HB3	2.15	0.46
1:B:127:PHE:O	6:B:320:HOH:O	2.21	0.46
1:B:138:VAL:HG23	1:B:157:VAL:CG1	2.45	0.46
1:H:9:MET:HA	1:H:14:VAL:O	2.14	0.46
1:C:72:GLU:HA	6:C:335:HOH:O	2.16	0.46
1:E:91:GLU:HG3	1:E:92:GLU:N	2.30	0.46
1:G:106:LEU:N	1:G:107:PRO:CD	2.79	0.46
1:H:40:PRO:HG2	1:H:90:GLU:HG2	1.97	0.46
1:F:29:LEU:CD2	5:F:204[B]:34R:H2	2.45	0.46
1:E:94:PHE:HE1	1:E:113:TYR:CE2	2.33	0.45
1:A:19:ASN:O	1:A:50:ALA:HB1	2.17	0.45
1:G:125:THR:C	1:G:126:PHE:CD2	2.90	0.45
1:A:147:GLU:OE2	1:C:108:TYR:HB3	2.17	0.45
4:E:203[A]:34S:C14	4:E:203[A]:34S:N18	2.80	0.45
5:E:204[B]:34R:H12	5:E:204[B]:34R:C31	2.47	0.45
1:A:55:LEU:HB3	4:A:203:34S:C23	2.44	0.45
5:E:204[B]:34R:C32	5:E:204[B]:34R:C31	2.94	0.45
1:E:53:ARG:HG3	1:E:54:PRO:CD	2.45	0.45
1:H:46:LYS:HB2	3:H:203:CL:CL	2.54	0.45
1:B:7:VAL:HG12	1:B:114:ILE:HA	1.99	0.45
1:D:106:LEU:N	1:D:107:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:HIS:HD2	1:B:92:GLU:HB3	1.82	0.45
4:F:203[A]:34S:N18	4:F:203[A]:34S:C14	2.58	0.44
1:E:55:LEU:HD23	1:E:55:LEU:N	2.33	0.44
1:F:55:LEU:HD22	4:F:203[A]:34S:C37	2.47	0.44
1:F:29:LEU:O	5:F:204[B]:34R:C40	2.65	0.44
1:H:85:GLU:OE2	1:H:88:LYS:NZ	2.50	0.44
1:A:97:GLY:HA2	1:A:102:TYR:CZ	2.52	0.44
1:G:37:MET:O	1:G:39:HIS:HD2	2.00	0.44
1:H:17:LYS:HD3	1:H:123:GLY:HA2	2.00	0.44
1:F:42:ILE:HD13	1:F:61:ILE:HB	1.99	0.44
1:E:53:ARG:CD	1:E:54:PRO:CD	2.95	0.44
1:G:39:HIS:CE1	1:G:92:GLU:HB3	2.52	0.44
5:C:203:34R:H28	5:C:203:34R:C16	2.47	0.44
1:D:160:LYS:O	1:D:162:GLN:NE2	2.51	0.44
1:F:16:GLY:O	1:F:125:THR:HG22	2.18	0.44
4:F:203[A]:34S:C29	4:F:203[A]:34S:C16	2.96	0.44
1:B:7:VAL:CG1	1:B:114:ILE:HG23	2.47	0.44
1:A:106:LEU:N	1:A:107:PRO:HD2	2.33	0.43
1:E:36:THR:HG22	1:E:94:PHE:CG	2.54	0.43
1:F:55:LEU:CD2	4:F:203[A]:34S:C23	2.95	0.43
1:E:55:LEU:HB3	4:E:203[A]:34S:C37	2.48	0.43
1:E:56:PRO:HD2	5:E:204[B]:34R:H25	2.00	0.43
1:D:48:TYR:OH	1:D:54:PRO:CG	2.62	0.43
1:E:138:VAL:HG23	1:E:157:VAL:HG13	1.99	0.43
1:E:20:ASN:CG	1:E:21:LEU:N	2.72	0.43
1:A:17:LYS:HG2	1:A:122:GLU:HG3	2.00	0.43
1:B:7:VAL:HG21	1:B:127:PHE:CD1	2.54	0.43
1:G:119:HIS:HB3	1:G:121:PHE:CE2	2.53	0.43
1:G:58:ARG:HG3	6:G:347:HOH:O	2.18	0.43
1:H:44:GLY:HA3	3:H:203:CL:CL	2.56	0.43
1:B:106:LEU:N	1:B:107:PRO:CD	2.81	0.43
1:G:55:LEU:HA	1:G:56:PRO:HD3	1.85	0.43
1:F:55:LEU:HD13	4:F:203[A]:34S:C22	2.37	0.43
1:H:85:GLU:CD	1:H:88:LYS:NZ	2.72	0.43
1:C:39:HIS:HA	1:C:40:PRO:HD3	1.85	0.43
1:D:42:ILE:CD1	1:D:42:ILE:N	2.78	0.43
1:H:106:LEU:N	1:H:107:PRO:CD	2.82	0.43
1:H:51:ILE:HD11	1:H:96:PHE:HE2	1.84	0.43
1:E:143:GLY:HA3	1:E:153:TYR:CE1	2.54	0.42
1:H:20:ASN:ND2	6:H:350:HOH:O	2.51	0.42
1:H:10:ASP:HB2	1:H:119:HIS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:142:LYS:NZ	1:H:152:THR:HG23	2.34	0.42
1:F:20:ASN:CA	5:F:204[B]:34R:H6	2.34	0.42
1:G:32:VAL:HG12	4:G:203[A]:34S:H1	2.01	0.42
1:H:41:LEU:CD1	1:H:55:LEU:HD12	2.49	0.42
1:G:143:GLY:O	6:G:369:HOH:O	2.21	0.42
1:G:17:LYS:HB2	1:G:123:GLY:HA2	2.00	0.42
1:A:163:LEU:N	1:A:163:LEU:CD1	2.83	0.42
1:B:21:LEU:HG	4:B:203:34S:O08	2.20	0.42
1:G:64:THR:C	1:G:66:ASN:H	2.22	0.42
1:G:96:PHE:CZ	4:G:203[A]:34S:H21	2.54	0.42
1:G:56:PRO:HD2	4:G:203[A]:34S:H4	2.02	0.42
1:D:7:VAL:HG11	1:D:127:PHE:CE1	2.54	0.42
1:E:106:LEU:N	1:E:107:PRO:CD	2.82	0.42
1:F:138:VAL:HG23	1:F:157:VAL:HG13	2.02	0.42
1:C:166:ARG:CG	1:C:166:ARG:NH1	2.50	0.42
4:G:203[A]:34S:O30	4:G:203[A]:34S:H11	2.19	0.42
5:D:203:34R:C12	5:D:203:34R:O08	2.67	0.42
1:H:54:PRO:HB3	1:H:74:CYS:SG	2.60	0.42
1:C:53:ARG:HB2	1:C:54:PRO:CD	2.50	0.41
1:H:42:ILE:HD13	1:H:93:ILE:HB	2.02	0.41
1:D:10:ASP:OD2	1:D:14:VAL:HB	2.20	0.41
1:D:10:ASP:CG	1:D:14:VAL:HB	2.41	0.41
5:D:203:34R:H22	5:D:203:34R:H24	2.02	0.41
1:E:51:ILE:HG23	5:E:204[B]:34R:H1	2.02	0.41
1:A:48:TYR:HB2	1:A:62:ILE:HD12	2.02	0.41
1:A:127:PHE:CD1	1:A:128:PRO:HD2	2.56	0.41
1:C:78:HIS:ND1	1:C:82:GLU:OE2	2.49	0.41
1:A:111:LYS:HD3	1:A:113:TYR:OH	2.20	0.41
5:C:203:34R:C23	5:C:203:34R:H24	2.49	0.41
1:D:9:MET:HB2	1:D:13:ARG:HA	2.03	0.41
1:E:53:ARG:HD3	1:E:54:PRO:CD	2.51	0.41
1:G:126:PHE:N	1:G:126:PHE:CD2	2.89	0.41
1:B:97:GLY:HA2	1:B:102:TYR:CZ	2.56	0.41
1:E:36:THR:HG22	1:E:94:PHE:CD2	2.56	0.41
1:H:55:LEU:HD22	4:H:202:34S:C37	2.51	0.41
1:G:42:ILE:N	1:G:42:ILE:CD1	2.84	0.41
1:F:55:LEU:HD23	1:F:55:LEU:HA	1.52	0.41
1:G:62:ILE:HD12	1:G:62:ILE:N	2.36	0.41
1:G:39:HIS:HD1	1:G:92:GLU:HB3	1.85	0.41
1:D:119:HIS:HB3	1:D:121:PHE:CE2	2.56	0.40
1:D:40:PRO:HD2	1:D:92:GLU:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:112:LEU:HB2	1:H:158:TYR:HB2	2.01	0.40
1:A:53:ARG:HA	1:A:54:PRO:HD3	1.68	0.40
1:A:40:PRO:HG2	1:A:90:GLU:HG3	2.02	0.40
1:C:140:VAL:HA	1:C:155:TYR:O	2.21	0.40
1:E:39:HIS:HB3	1:E:92:GLU:O	2.21	0.40
1:F:16:GLY:CA	1:F:125:THR:CG2	3.00	0.40
1:F:164:VAL:HA	1:F:165:PRO:HD3	1.94	0.40
1:H:5:PHE:CD1	1:H:95:ILE:HB	2.56	0.40
1:B:37:MET:HA	1:B:58:ARG:NH2	2.37	0.40
1:E:163:LEU:HD23	1:E:163:LEU:HA	1.80	0.40
1:E:166:ARG:CZ	1:E:166:ARG:HB2	2.51	0.40
1:E:28:GLU:CD	5:E:204[B]:34R:H13	2.24	0.40
1:G:48:TYR:OH	1:G:71:VAL:HG21	2.21	0.40
1:B:27:SER:HB2	1:B:149:ASN:ND2	2.33	0.40
1:C:58:ARG:NH1	6:C:352:HOH:O	2.54	0.40
1:G:29:LEU:HA	1:G:29:LEU:HD23	1.89	0.40
1:H:79:SER:O	1:H:83:VAL:HG23	2.21	0.40
1:F:16:GLY:C	1:F:125:THR:HG22	2.42	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:ARG:O	1:H:89:ASN:ND2[2_554]	1.91	0.29
1:E:150:PRO:O	6:A:319:HOH:O[2_555]	2.08	0.12

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	164/166 (99%)	160 (98%)	3 (2%)	1 (1%)	28 53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	164/166 (99%)	159 (97%)	4 (2%)	1 (1%)	28	53
1	C	164/166 (99%)	161 (98%)	3 (2%)	0	100	100
1	D	164/166 (99%)	161 (98%)	3 (2%)	0	100	100
1	E	164/166 (99%)	161 (98%)	3 (2%)	0	100	100
1	F	164/166 (99%)	160 (98%)	4 (2%)	0	100	100
1	G	164/166 (99%)	161 (98%)	3 (2%)	0	100	100
1	H	164/166 (99%)	158 (96%)	6 (4%)	0	100	100
All	All	1312/1328 (99%)	1281 (98%)	29 (2%)	2 (0%)	51	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	162	GLN
1	A	54	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	149/150 (99%)	144 (97%)	5 (3%)	42	69
1	B	149/150 (99%)	148 (99%)	1 (1%)	87	96
1	C	150/150 (100%)	145 (97%)	5 (3%)	43	70
1	D	150/150 (100%)	147 (98%)	3 (2%)	60	83
1	E	150/150 (100%)	149 (99%)	1 (1%)	87	96
1	F	150/150 (100%)	148 (99%)	2 (1%)	73	90
1	G	150/150 (100%)	144 (96%)	6 (4%)	36	64
1	H	150/150 (100%)	141 (94%)	9 (6%)	22	44
All	All	1198/1200 (100%)	1166 (97%)	32 (3%)	50	77

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	53	ARG
1	A	55	LEU
1	A	58	ARG
1	A	160	LYS
1	H	20	ASN
1	H	58	ARG
1	H	72	GLU
1	H	86	LEU
1	H	88	LYS
1	H	89	ASN
1	H	90	GLU
1	H	133	THR
1	H	164	VAL
1	C	47	ASN
1	C	55	LEU
1	C	85	GLU
1	C	95	ILE
1	C	166	ARG
1	B	163	LEU
1	G	42	ILE
1	G	65	ARG
1	G	71	VAL
1	G	91	GLU
1	G	125	THR
1	G	162	GLN
1	F	65	ARG
1	F	88	LYS
1	D	53	ARG
1	D	58	ARG
1	D	162	GLN
1	E	166	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	19	ASN
1	H	20	ASN
1	H	60	ASN
1	C	70	HIS
1	B	162	GLN
1	F	20	ASN
1	D	162	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 16 are monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
4	34S	A	203	-	43,43,43	2.46	6 (13%)	55,60,60	1.78	12 (21%)
4	34S	B	203	-	43,43,43	2.45	6 (13%)	55,60,60	1.76	14 (25%)
5	34R	C	203	-	43,43,43	1.54	5 (11%)	55,60,60	1.77	13 (23%)
5	34R	D	203	-	43,43,43	1.59	5 (11%)	55,60,60	1.74	12 (21%)
4	34S	E	203[A]	-	43,43,43	2.50	6 (13%)	55,60,60	1.94	16 (29%)
5	34R	E	204[B]	-	43,43,43	1.59	6 (13%)	55,60,60	1.75	10 (18%)
4	34S	F	203[A]	-	43,43,43	2.46	6 (13%)	55,60,60	1.81	13 (23%)
5	34R	F	204[B]	-	43,43,43	1.58	6 (13%)	55,60,60	1.73	12 (21%)
4	34S	G	203[A]	-	43,43,43	2.47	6 (13%)	55,60,60	1.85	14 (25%)
4	34S	H	202	-	43,43,43	2.45	6 (13%)	55,60,60	1.78	11 (20%)

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
4	34S	A	203	-	-	0/20/34/34	0/4/5/5
4	34S	B	203	-	-	0/20/34/34	0/4/5/5
5	34R	C	203	-	-	0/20/34/34	0/4/5/5
5	34R	D	203	-	-	0/20/34/34	0/4/5/5
4	34S	E	203[A]	-	-	0/20/34/34	0/4/5/5
5	34R	E	204[B]	-	-	0/20/34/34	0/4/5/5
4	34S	F	203[A]	-	-	0/20/34/34	0/4/5/5
5	34R	F	204[B]	-	-	0/20/34/34	0/4/5/5
4	34S	G	203[A]	-	-	0/20/34/34	0/4/5/5
4	34S	H	202	-	-	0/20/34/34	0/4/5/5

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	203	34S	C22-C21	-7.77	1.31	1.40
4	H	202	34S	C22-C21	-7.68	1.32	1.40
4	F	203[A]	34S	C22-C21	-7.66	1.32	1.40
4	E	203[A]	34S	C22-C21	-7.47	1.32	1.40
4	B	203	34S	C22-C21	-7.43	1.32	1.40
4	G	203[A]	34S	C22-C21	-7.41	1.32	1.40
5	E	204[B]	34R	C22-C21	-3.55	1.36	1.40
5	F	204[B]	34R	C22-C21	-3.48	1.36	1.40
5	D	203	34R	C22-C21	-3.34	1.36	1.40
5	C	203	34R	C22-C21	-3.14	1.37	1.40
5	E	204[B]	34R	C21-C20	-2.26	1.49	1.51
5	F	204[B]	34R	C24-C20	-2.20	1.50	1.52
5	D	203	34R	C24-C20	-2.18	1.50	1.52
5	C	203	34R	C24-C20	-2.10	1.50	1.52
5	F	204[B]	34R	C21-C20	-2.10	1.49	1.51
5	E	204[B]	34R	C24-C20	-2.04	1.50	1.52
4	G	203[A]	34S	C02-N01	2.87	1.41	1.34
4	F	203[A]	34S	C02-N01	2.87	1.41	1.34
4	H	202	34S	C02-N01	2.92	1.41	1.34
4	A	203	34S	C02-N01	2.93	1.41	1.34
4	B	203	34S	C02-N01	2.96	1.41	1.34
4	E	203[A]	34S	C02-N01	3.01	1.42	1.34
4	A	203	34S	C23-C21	3.22	1.43	1.39
4	F	203[A]	34S	C23-C21	3.26	1.43	1.39
4	B	203	34S	C23-C21	3.26	1.43	1.39
4	H	202	34S	C23-C21	3.27	1.44	1.39
4	E	203[A]	34S	C23-C21	3.30	1.44	1.39
4	G	203[A]	34S	C23-C21	3.39	1.44	1.39
5	D	203	34R	C02-N01	3.64	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	204[B]	34R	C02-N01	3.65	1.43	1.34
5	F	204[B]	34R	C02-N01	3.65	1.43	1.34
5	C	203	34R	C02-N01	3.76	1.44	1.34
4	A	203	34S	C16-N17	4.04	1.42	1.35
4	F	203[A]	34S	C16-N17	4.09	1.42	1.35
4	B	203	34S	C16-N17	4.16	1.43	1.35
4	G	203[A]	34S	C16-N17	4.18	1.43	1.35
4	H	202	34S	C16-N17	4.24	1.43	1.35
4	A	203	34S	C34-N35	4.52	1.43	1.34
4	E	203[A]	34S	C16-N17	4.53	1.43	1.35
4	B	203	34S	C34-N35	4.54	1.43	1.34
4	H	202	34S	C34-N35	4.54	1.43	1.34
5	F	204[B]	34R	C34-N35	4.54	1.43	1.34
5	E	204[B]	34R	C34-N35	4.55	1.43	1.34
5	D	203	34R	C34-N35	4.57	1.43	1.34
4	F	203[A]	34S	C34-N35	4.57	1.43	1.34
4	G	203[A]	34S	C34-N35	4.62	1.43	1.34
5	C	203	34R	C34-N35	4.65	1.43	1.34
4	E	203[A]	34S	C34-N35	4.68	1.43	1.34
5	C	203	34R	C16-N17	4.70	1.43	1.35
5	F	204[B]	34R	C16-N17	4.74	1.44	1.35
5	E	204[B]	34R	C16-N17	4.79	1.44	1.35
5	D	203	34R	C16-N17	4.93	1.44	1.35
4	H	202	34S	C19-N18	10.67	1.41	1.29
4	A	203	34S	C19-N18	10.75	1.41	1.29
4	B	203	34S	C19-N18	10.78	1.41	1.29
4	F	203[A]	34S	C19-N18	10.79	1.41	1.29
4	G	203[A]	34S	C19-N18	10.93	1.41	1.29
4	E	203[A]	34S	C19-N18	11.07	1.42	1.29

All (127) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	203[A]	34S	C22-C19-N18	-6.36	117.94	125.75
4	H	202	34S	C22-C19-N18	-6.18	118.16	125.75
4	E	203[A]	34S	C22-C19-N18	-6.10	118.26	125.75
4	A	203	34S	C22-C19-N18	-5.82	118.59	125.75
4	G	203[A]	34S	C22-C19-N18	-5.42	119.09	125.75
4	B	203	34S	C22-C19-N18	-5.27	119.27	125.75
5	E	204[B]	34R	C22-C19-N18	-5.21	119.34	125.75
5	C	203	34R	C22-C19-N18	-5.21	119.35	125.75
5	F	204[B]	34R	C22-C19-N18	-5.07	119.52	125.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	203	34R	N33-C34-N36	-4.97	120.61	125.82
5	F	204[B]	34R	N33-C34-N36	-4.94	120.64	125.82
5	D	203	34R	N33-C34-N36	-4.94	120.64	125.82
4	E	203[A]	34S	N33-C34-N36	-4.92	120.66	125.82
5	E	204[B]	34R	N33-C34-N36	-4.91	120.67	125.82
4	G	203[A]	34S	N33-C34-N36	-4.86	120.73	125.82
4	A	203	34S	N33-C34-N36	-4.70	120.89	125.82
5	D	203	34R	C22-C19-N18	-4.66	120.03	125.75
4	H	202	34S	N33-C34-N36	-4.64	120.95	125.82
4	F	203[A]	34S	N33-C34-N36	-4.62	120.98	125.82
4	B	203	34S	N33-C34-N36	-4.58	121.02	125.82
5	E	204[B]	34R	C13-C14-C15	-4.12	118.82	126.90
4	F	203[A]	34S	C13-C14-C15	-3.69	119.66	126.90
4	A	203	34S	C13-C14-C15	-3.61	119.83	126.90
5	F	204[B]	34R	C13-C14-C15	-3.58	119.89	126.90
4	E	203[A]	34S	C04-C03-C02	-3.55	117.78	122.28
5	C	203	34R	C13-C14-C15	-3.40	120.24	126.90
5	D	203	34R	C13-C14-C15	-3.30	120.44	126.90
4	G	203[A]	34S	C13-C14-C15	-3.27	120.48	126.90
4	E	203[A]	34S	O08-C07-C06	-3.25	118.69	124.17
4	H	202	34S	C13-C14-C15	-3.14	120.73	126.90
4	E	203[A]	34S	C03-C32-N33	-3.04	118.73	123.87
4	G	203[A]	34S	C04-C03-C02	-2.95	118.54	122.28
4	H	202	34S	C03-C32-N33	-2.92	118.92	123.87
4	F	203[A]	34S	C03-C32-N33	-2.91	118.95	123.87
4	B	203	34S	C13-C14-C15	-2.90	121.21	126.90
4	A	203	34S	C03-C32-N33	-2.84	119.06	123.87
4	B	203	34S	C03-C32-N33	-2.84	119.07	123.87
5	D	203	34R	C24-C20-C21	-2.76	108.25	112.93
4	G	203[A]	34S	C03-C32-N33	-2.75	119.22	123.87
4	G	203[A]	34S	C24-C20-N17	-2.68	107.25	110.94
4	B	203	34S	O08-C07-C06	-2.66	119.68	124.17
4	E	203[A]	34S	C13-C14-C15	-2.56	121.88	126.90
4	A	203	34S	O08-C07-C06	-2.53	119.91	124.17
4	H	202	34S	O08-C07-C06	-2.49	119.98	124.17
5	C	203	34R	C03-C32-N33	-2.45	119.72	123.87
4	F	203[A]	34S	O08-C07-C06	-2.42	120.09	124.17
4	G	203[A]	34S	O08-C07-C06	-2.42	120.10	124.17
4	G	203[A]	34S	C13-C31-C05	-2.41	119.47	122.29
5	D	203	34R	C03-C32-N33	-2.40	119.81	123.87
5	E	204[B]	34R	C03-C32-N33	-2.37	119.86	123.87
5	F	204[B]	34R	C03-C32-N33	-2.37	119.87	123.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	204[B]	34R	O08-C07-C06	-2.25	120.37	124.17
5	E	204[B]	34R	O08-C07-C06	-2.24	120.39	124.17
5	C	203	34R	C13-C31-C05	-2.24	119.67	122.29
4	B	203	34S	C24-C20-N17	-2.23	107.87	110.94
5	E	204[B]	34R	C13-C31-C05	-2.21	119.70	122.29
5	F	204[B]	34R	C24-C20-C21	-2.14	109.30	112.93
5	C	203	34R	O08-C07-C06	-2.12	120.61	124.17
5	D	203	34R	C13-C31-C05	-2.09	119.84	122.29
5	D	203	34R	O08-C07-C06	-2.08	120.67	124.17
5	F	204[B]	34R	C13-C31-C05	-2.07	119.87	122.29
4	F	203[A]	34S	C24-C20-N17	-2.03	108.14	110.94
4	B	203	34S	C13-C31-C05	-2.01	119.94	122.29
4	E	203[A]	34S	C13-C31-C05	-2.01	119.94	122.29
4	G	203[A]	34S	N01-C02-N36	2.04	120.02	117.00
5	F	204[B]	34R	C21-C22-C19	2.05	119.42	117.70
5	C	203	34R	C21-C22-C19	2.06	119.43	117.70
4	F	203[A]	34S	C21-C22-C19	2.10	119.46	117.70
4	E	203[A]	34S	C32-C03-C02	2.11	118.48	115.68
5	C	203	34R	C40-C22-C21	2.14	120.68	118.64
4	E	203[A]	34S	C21-C22-C19	2.16	119.52	117.70
4	A	203	34S	N01-C02-N36	2.18	120.22	117.00
4	A	203	34S	C32-C03-C02	2.19	118.59	115.68
5	C	203	34R	C09-O08-C07	2.20	120.70	117.54
4	H	202	34S	N01-C02-N36	2.24	120.31	117.00
4	H	202	34S	C32-C03-C02	2.25	118.67	115.68
4	F	203[A]	34S	C32-C03-C02	2.30	118.73	115.68
4	A	203	34S	C21-C22-C19	2.30	119.64	117.70
4	B	203	34S	C32-C03-C02	2.32	118.76	115.68
4	B	203	34S	N35-C34-N33	2.32	119.62	117.39
4	F	203[A]	34S	N35-C34-N33	2.34	119.64	117.39
4	F	203[A]	34S	N01-C02-N36	2.37	120.51	117.00
5	D	203	34R	O08-C07-C10	2.48	119.59	115.22
4	E	203[A]	34S	C12-O11-C10	2.48	121.61	114.81
4	A	203	34S	N35-C34-N33	2.52	119.81	117.39
5	F	204[B]	34R	N35-C34-N33	2.55	119.84	117.39
4	B	203	34S	N01-C02-N36	2.60	120.84	117.00
5	F	204[B]	34R	O08-C07-C10	2.60	119.79	115.22
5	D	203	34R	C21-C22-C19	2.61	119.89	117.70
4	E	203[A]	34S	N01-C02-N36	2.61	120.86	117.00
4	F	203[A]	34S	O08-C07-C10	2.62	119.83	115.22
4	G	203[A]	34S	C21-C22-C19	2.62	119.90	117.70
4	E	203[A]	34S	N35-C34-N33	2.63	119.92	117.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	203	34R	O08-C07-C10	2.65	119.88	115.22
5	D	203	34R	N35-C34-N33	2.66	119.95	117.39
5	F	204[B]	34R	C32-N33-C34	2.68	120.94	116.27
5	E	204[B]	34R	C32-N33-C34	2.68	120.94	116.27
4	H	202	34S	O08-C07-C10	2.71	119.99	115.22
5	E	204[B]	34R	O08-C07-C10	2.71	120.00	115.22
4	H	202	34S	N35-C34-N33	2.72	120.00	117.39
5	D	203	34R	C32-N33-C34	2.72	121.02	116.27
4	B	203	34S	C32-N33-C34	2.72	121.02	116.27
4	A	203	34S	O08-C07-C10	2.73	120.02	115.22
4	G	203[A]	34S	C32-N33-C34	2.74	121.05	116.27
5	C	203	34R	C32-N33-C34	2.76	121.08	116.27
4	B	203	34S	O08-C07-C10	2.77	120.10	115.22
5	E	204[B]	34R	N35-C34-N33	2.78	120.06	117.39
4	B	203	34S	C21-C22-C19	2.80	120.05	117.70
4	F	203[A]	34S	C32-N33-C34	2.80	121.16	116.27
4	H	202	34S	C32-N33-C34	2.85	121.24	116.27
4	A	203	34S	C32-N33-C34	2.85	121.24	116.27
4	E	203[A]	34S	C16-N17-N18	2.88	121.80	117.70
4	G	203[A]	34S	O08-C07-C10	2.89	120.31	115.22
4	E	203[A]	34S	C32-N33-C34	3.06	121.62	116.27
5	C	203	34R	N35-C34-N33	3.19	120.45	117.39
4	E	203[A]	34S	C34-N36-C02	3.44	120.81	116.99
4	G	203[A]	34S	N35-C34-N33	3.48	120.73	117.39
4	E	203[A]	34S	O08-C07-C10	3.50	121.38	115.22
4	H	202	34S	C34-N36-C02	3.64	121.04	116.99
4	F	203[A]	34S	C34-N36-C02	3.68	121.08	116.99
4	A	203	34S	C34-N36-C02	3.75	121.16	116.99
4	B	203	34S	C34-N36-C02	3.75	121.16	116.99
4	G	203[A]	34S	C34-N36-C02	3.96	121.39	116.99
5	D	203	34R	C34-N36-C02	4.66	122.16	116.99
5	C	203	34R	C34-N36-C02	4.66	122.17	116.99
5	E	204[B]	34R	C34-N36-C02	4.67	122.18	116.99
5	F	204[B]	34R	C34-N36-C02	4.72	122.23	116.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 142 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	203	34S	22	0
4	B	203	34S	10	0
5	C	203	34R	5	0
5	D	203	34R	10	0
4	E	203[A]	34S	6	0
5	E	204[B]	34R	13	0
4	F	203[A]	34S	24	0
5	F	204[B]	34R	25	0
4	G	203[A]	34S	9	0
4	H	202	34S	18	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	166/166 (100%)	0.36	6 (3%) 43 35	5, 31, 72, 99	0
1	B	166/166 (100%)	-0.03	0 100 100	14, 30, 58, 69	0
1	C	166/166 (100%)	0.23	3 (1%) 69 63	15, 29, 53, 71	0
1	D	166/166 (100%)	0.29	6 (3%) 43 35	8, 33, 73, 90	0
1	E	166/166 (100%)	0.30	4 (2%) 59 52	8, 32, 67, 90	0
1	F	166/166 (100%)	0.22	6 (3%) 43 35	10, 35, 76, 106	0
1	G	166/166 (100%)	0.31	9 (5%) 26 20	14, 37, 67, 82	0
1	H	166/166 (100%)	0.39	12 (7%) 16 12	10, 37, 88, 103	0
All	All	1328/1328 (100%)	0.26	46 (3%) 44 36	5, 33, 73, 106	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	52	GLY	6.5
1	H	89	ASN	6.5
1	A	57	GLY	6.2
1	H	52	GLY	5.5
1	H	64	THR	5.0
1	F	52	GLY	4.8
1	H	72	GLU	4.0
1	H	73	GLY	4.0
1	G	64	THR	3.5
1	E	18	ASP	3.4
1	D	51	ILE	3.3
1	A	19	ASN	3.2
1	A	56	PRO	3.2
1	G	71	VAL	3.1
1	A	37	MET	3.1
1	A	58	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	H	74	CYS	3.0
1	F	69	TYR	2.9
1	F	70	HIS	2.9
1	E	53	ARG	2.7
1	D	19	ASN	2.7
1	H	48	TYR	2.6
1	H	70	HIS	2.6
1	G	66	ASN	2.6
1	G	69	TYR	2.5
1	A	52	GLY	2.5
1	F	67	GLU	2.5
1	H	79	SER	2.4
1	G	73	GLY	2.4
1	C	70	HIS	2.3
1	C	19	ASN	2.3
1	H	51	ILE	2.3
1	H	76	VAL	2.3
1	G	72	GLU	2.3
1	C	56	PRO	2.2
1	D	161	GLN	2.2
1	F	68	GLY	2.2
1	G	47	ASN	2.2
1	D	52	GLY	2.2
1	F	66	ASN	2.2
1	G	165	PRO	2.2
1	D	69	TYR	2.1
1	G	77	ALA	2.1
1	E	19	ASN	2.1
1	D	63	VAL	2.0
1	H	55	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	34S	B	203	39/39	0.84	0.29	3.49	21,66,86,91	0
5	34R	F	204[B]	39/39	0.84	0.27	1.48	39,59,66,68	39
4	34S	F	203[A]	39/39	0.83	0.28	1.35	38,59,67,70	39
4	34S	G	203[A]	39/39	0.90	0.26	1.30	7,21,43,48	39
5	34R	C	203	39/39	0.86	0.28	0.95	10,52,81,85	0
4	34S	H	202	39/39	0.84	0.26	0.95	10,62,97,98	0
3	CL	C	202	1/1	0.97	0.20	0.80	27,27,27,27	0
4	34S	A	203	39/39	0.80	0.30	0.65	20,52,75,76	0
5	34R	E	204[B]	39/39	0.85	0.26	0.51	14,37,49,54	39
4	34S	E	203[A]	39/39	0.83	0.24	0.40	13,34,44,50	39
5	34R	D	203	39/39	0.87	0.24	0.33	17,51,67,71	0
3	CL	H	203	1/1	0.83	0.15	-1.29	87,87,87,87	0
3	CL	E	202	1/1	0.97	0.17	-1.31	35,35,35,35	0
3	CL	D	202	1/1	0.98	0.12	-1.45	28,28,28,28	0
3	CL	B	202	1/1	0.90	0.13	-1.48	49,49,49,49	0
3	CL	F	202	1/1	0.90	0.12	-1.53	58,58,58,58	0
3	CL	G	202	1/1	0.96	0.12	-1.56	51,51,51,51	0
2	CA	G	201	1/1	0.79	0.12	-1.94	27,27,27,27	0
3	CL	A	202	1/1	0.97	0.13	-2.08	33,33,33,33	0
2	CA	E	201	1/1	0.94	0.10	-2.80	34,34,34,34	0
2	CA	C	201	1/1	0.90	0.08	-3.16	23,23,23,23	0
2	CA	B	201	1/1	0.88	0.10	-3.48	32,32,32,32	0
2	CA	H	201	1/1	0.74	0.11	-4.38	106,106,106,106	0
2	CA	D	201	1/1	0.93	0.06	-6.90	43,43,43,43	0
2	CA	A	201	1/1	0.74	0.13	-	61,61,61,61	0
2	CA	F	201	1/1	0.94	0.11	-	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.