



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:22 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 wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

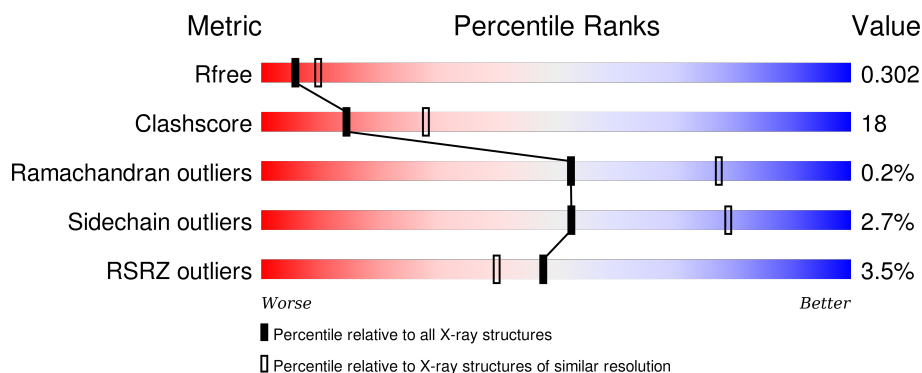
# 1 Overall quality at a glance

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))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (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  $\geq 3$ , 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>73%</div> <div>23%</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>82%</div> <div>17%</div> <div>.</div> </div>
1	D	166	<div> <div>4%</div> <div>78%</div> <div>21%</div> <div>.</div> </div>
1	E	166	<div> <div>2%</div> <div>75%</div> <div>24%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	166	<div> <div>4%</div> <div> <div></div> <div>77%</div> <div>23%</div> </div> </div>
1	G	166	<div> <div>5%</div> <div> <div></div> <div>75%</div> <div>23%</div> </div> </div>
1	H	166	<div> <div>7%</div> <div> <div></div> <div>66%</div> <div>31%</div> </div> </div>

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

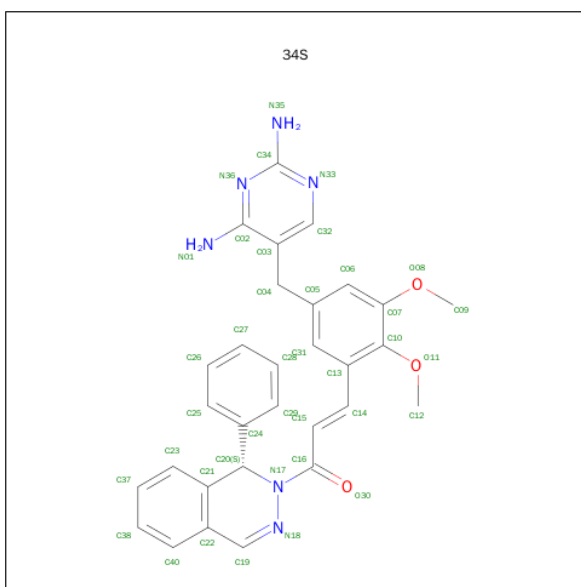
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

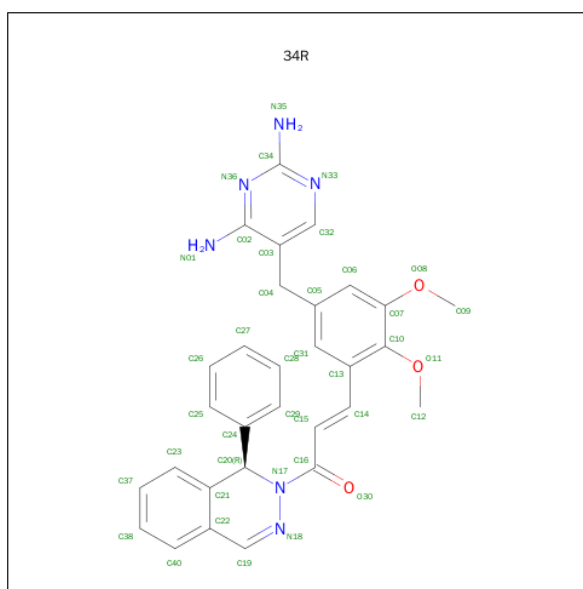
- Molecule 4 is (2E)-3-{5-[(2,4-DIAMINOPYRIMIDIN-5-YL)METHYL]-2,3-DIMETHOXY PHENYL}-1-[(1S)-1-PHENYLPHthalAZIN-2(1H)-YL]PROP-2-EN-1-ONE (three-letter code: 34S) (formula: C<sub>30</sub>H<sub>28</sub>N<sub>6</sub>O<sub>3</sub>).



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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: C<sub>30</sub>H<sub>28</sub>N<sub>6</sub>O<sub>3</sub>).



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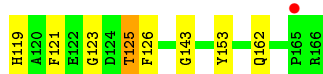
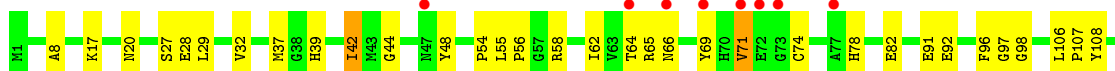
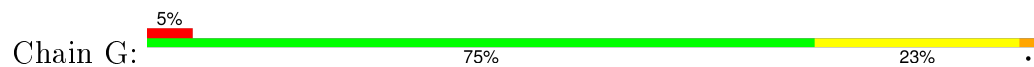
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	58	Total 58	O 58	0	0
6	C	102	Total 102	O 102	0	0
6	B	60	Total 60	O 60	0	0
6	G	72	Total 72	O 72	0	0
6	F	58	Total 58	O 58	0	0
6	D	82	Total 82	O 82	0	0
6	E	92	Total 92	O 92	0	0



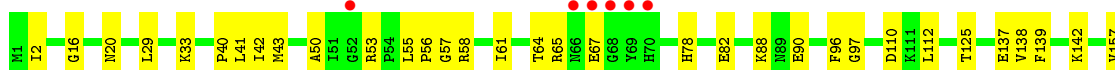
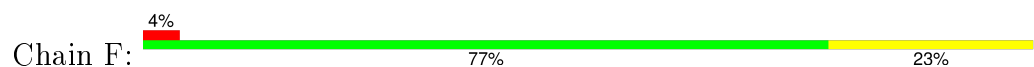




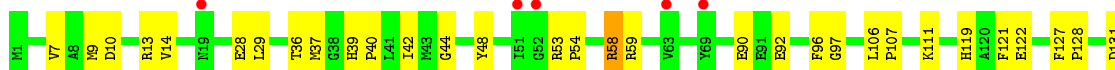
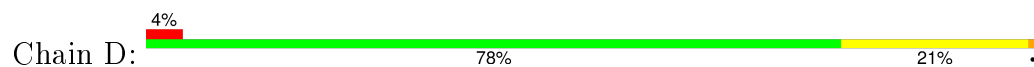
- Molecule 1: Dihydrofolate reductase



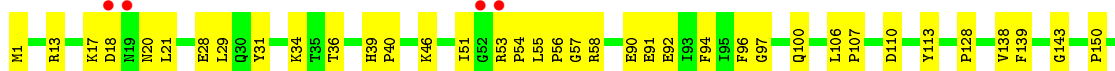
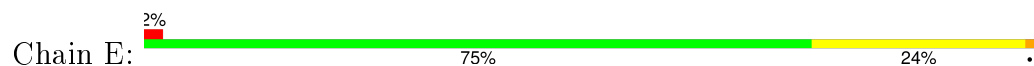
- Molecule 1: Dihydrofolate reductase



- 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, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.25 (at 2.62Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.243 , 0.309 0.243 , 0.302	Depositor DCC
$R_{free}$ test set	2463 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.9	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 58.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 48511 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	12054	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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.

5 of 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	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
4	E	39	0	28	6	0
4	F	39	0	28	24	0
4	G	39	0	28	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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.

The worst 5 of 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

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%)	30	56
1	B	164/166 (99%)	159 (97%)	4 (2%)	1 (1%)	30	56
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%)	52	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	162	GLN
1	A	54	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	149/150 (99%)	144 (97%)	5 (3%)	44	72
1	B	149/150 (99%)	148 (99%)	1 (1%)	88	96
1	C	150/150 (100%)	145 (97%)	5 (3%)	45	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	150/150 (100%)	147 (98%)	3 (2%)	63	85
1	E	150/150 (100%)	149 (99%)	1 (1%)	88	96
1	F	150/150 (100%)	148 (99%)	2 (1%)	76	91
1	G	150/150 (100%)	144 (96%)	6 (4%)	38	67
1	H	150/150 (100%)	141 (94%)	9 (6%)	24	47
All	All	1198/1200 (100%)	1166 (97%)	32 (3%)	52	79

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	47	ASN
1	C	95	ILE
1	D	58	ARG
1	C	85	GLU
1	C	166	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

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	2.42	6 (13%)	54,60,60	1.81	13 (24%)
4	34S	B	203	-	43,43,43	2.41	6 (13%)	54,60,60	1.80	15 (27%)
5	34R	C	203	-	43,43,43	1.51	5 (11%)	54,60,60	1.81	14 (25%)
5	34R	D	203	-	43,43,43	1.55	5 (11%)	54,60,60	1.76	13 (24%)
4	34S	E	203[A]	-	43,43,43	2.46	6 (13%)	54,60,60	2.00	14 (25%)
5	34R	E	204[B]	-	43,43,43	1.55	5 (11%)	54,60,60	1.78	11 (20%)
4	34S	F	203[A]	-	43,43,43	2.42	6 (13%)	54,60,60	1.86	14 (25%)
5	34R	F	204[B]	-	43,43,43	1.54	6 (13%)	54,60,60	1.76	11 (20%)
4	34S	G	203[A]	-	43,43,43	2.44	6 (13%)	54,60,60	1.88	14 (25%)
4	34S	H	202	-	43,43,43	2.42	6 (13%)	54,60,60	1.82	14 (25%)

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

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	203	34S	C22-C21	-7.13	1.31	1.40
4	H	202	34S	C22-C21	-7.05	1.32	1.40
4	F	203[A]	34S	C22-C21	-7.03	1.32	1.40
4	E	203[A]	34S	C22-C21	-6.86	1.32	1.40
4	B	203	34S	C22-C21	-6.83	1.32	1.40

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	203[A]	34S	C22-C19-N18	-6.25	117.94	125.69
4	H	202	34S	C22-C19-N18	-6.07	118.16	125.69
4	E	203[A]	34S	C22-C19-N18	-5.99	118.26	125.69
4	A	203	34S	C22-C19-N18	-5.72	118.59	125.69
4	G	203[A]	34S	C22-C19-N18	-5.32	119.09	125.69

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	166/166 (100%)	0.40	7 (4%) 40 32	5, 31, 72, 99	0
1	B	166/166 (100%)	0.00	0 100 100	14, 30, 58, 69	0
1	C	166/166 (100%)	0.26	3 (1%) 71 66	15, 29, 53, 71	0
1	D	166/166 (100%)	0.33	6 (3%) 46 38	8, 33, 73, 90	0
1	E	166/166 (100%)	0.34	4 (2%) 62 56	8, 32, 67, 90	0
1	F	166/166 (100%)	0.25	6 (3%) 46 38	10, 35, 76, 106	0
1	G	166/166 (100%)	0.35	9 (5%) 29 22	14, 37, 67, 82	0
1	H	166/166 (100%)	0.42	12 (7%) 18 13	10, 37, 88, 103	0
All	All	1328/1328 (100%)	0.29	47 (3%) 48 40	5, 33, 73, 106	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	52	GLY	6.6
1	H	89	ASN	6.6
1	A	57	GLY	6.3
1	H	52	GLY	5.6
1	H	64	THR	5.0

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

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

### 6.3 Carbohydrates ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	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	-1.95	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	-3.47	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.