Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 12:06 AM GMT

PDB ID	:	3CDA
Title	:	Thermodynamic and structure guided design of statin hmg-coa reductase inhibitors
Authors	:	Pavlovsky, A.; Sarver, R.W.; Harris, M.S.; Finzel, B.C.
Deposited on	:	2008-02-26
Resolution	:	2.07 Å(reported)

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

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.07 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	Percentile Ranks	Value
Rfree		0.257
Clashscore		2
Ramachandran outliers		0.2%
Sidechain outliers		4.9%
RSRZ outliers		7.1%

Worse — *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
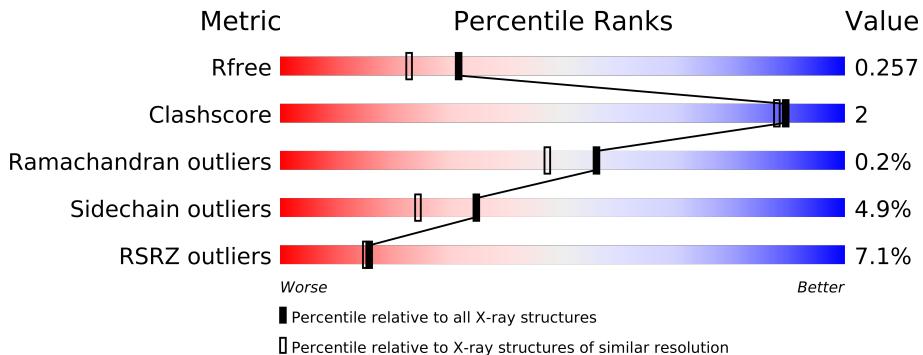
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1224 (2.08-2.04)
Clashscore	79885	1390 (2.08-2.04)
Ramachandran outliers	78287	1381 (2.08-2.04)
Sidechain outliers	78261	1381 (2.08-2.04)
RSRZ outliers	66119	1225 (2.08-2.04)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	441	
1	B	441	
1	C	441	
1	D	441	
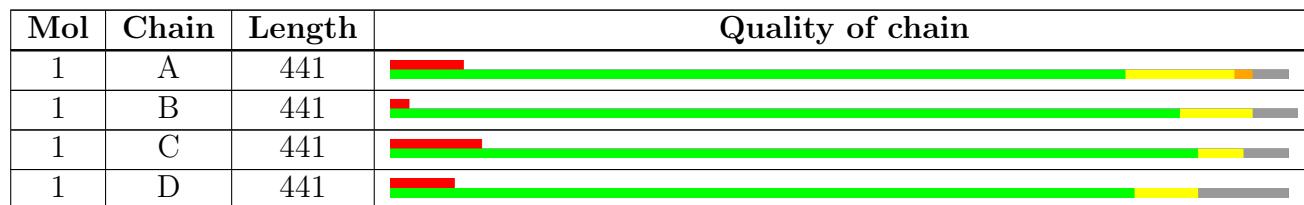
2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 12971 atoms, of which 0 are hydrogen and 0 are deuterium.

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 3-hydroxy-3-methylglutaryl-coenzymeA reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	422	Total	C	N	O	S	0	0	0
			3141	1957	552	602	30			
1	B	421	Total	C	N	O	S	0	0	0
			3133	1951	551	601	30			
1	C	417	Total	C	N	O	S	0	0	0
			3096	1929	542	595	30			
1	D	395	Total	C	N	O	S	0	0	0
			2928	1824	515	560	29			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	435	HIS	-	expression tag	UNP P04035
A	436	HIS	-	expression tag	UNP P04035
A	437	HIS	-	expression tag	UNP P04035
A	438	HIS	-	expression tag	UNP P04035
A	439	HIS	-	expression tag	UNP P04035
A	440	HIS	-	expression tag	UNP P04035
A	485	ILE	MET	engineered	UNP P04035
B	435	HIS	-	expression tag	UNP P04035
B	436	HIS	-	expression tag	UNP P04035
B	437	HIS	-	expression tag	UNP P04035
B	438	HIS	-	expression tag	UNP P04035
B	439	HIS	-	expression tag	UNP P04035
B	440	HIS	-	expression tag	UNP P04035
B	485	ILE	MET	engineered	UNP P04035
C	435	HIS	-	expression tag	UNP P04035
C	436	HIS	-	expression tag	UNP P04035
C	437	HIS	-	expression tag	UNP P04035
C	438	HIS	-	expression tag	UNP P04035
C	439	HIS	-	expression tag	UNP P04035
C	440	HIS	-	expression tag	UNP P04035
C	485	ILE	MET	engineered	UNP P04035

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	435	HIS	-	expression tag	UNP P04035
D	436	HIS	-	expression tag	UNP P04035
D	437	HIS	-	expression tag	UNP P04035
D	438	HIS	-	expression tag	UNP P04035
D	439	HIS	-	expression tag	UNP P04035
D	440	HIS	-	expression tag	UNP P04035
D	485	ILE	MET	engineered	UNP P04035

- Molecule 2 is (3R,5R)-7-{3-(4-FLUOROPHENYL)-1-(1-METHYLETHYL)-4-PHENYL-5-[(4-SULFAMOYLPHENYL)CARBAMOYL]-1H-PYRROL-2-YL}-3,5-DIHYDROXYHEPT ANOICACID (three-letter code: 8HI) (formula: $C_{33}H_{36}FN_3O_7S$).
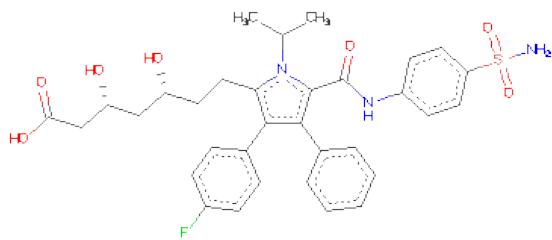
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			45	33	1	3	7	1		
2	B	1	Total	C	F	N	O	S	0	0
			45	33	1	3	7	1		
2	C	1	Total	C	F	N	O	S	0	0
			45	33	1	3	7	1		
2	D	1	Total	C	F	N	O	S	0	0
			45	33	1	3	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	129	Total	O	0	0
			129	129		

WORLDWIDE
PDB
PROTEIN DATA BANK

Continued from previous page...

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	134	Total 134	O 134	0	0
3	C	98	Total 98	O 98	0	0
3	D	132	Total 132	O 132	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: 3-hydroxy-3-methylglutaryl-coenzymeA reductase
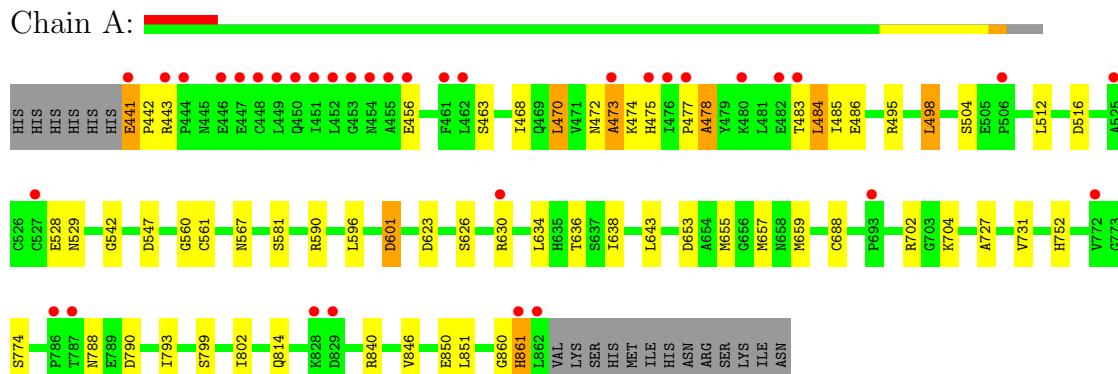
Chain A:

- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzymeA reductase

Chain B:


- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzymeA reductase

Chain C:

- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzymeA reductase

Chain D:

M523 G524 A525 C526 C527 E528 N529 D547 R571 T589 R595 D601 G614 V617 S626 R627 K633 N642 F647 M657 K666 V731 G747 H752 N788 E789 D790 L791 T796 K828 L851 A859 GLY HIS LEU VAL LYS SER HIS

MET ILE HIS ASN ARG SER LYS ILE ASN
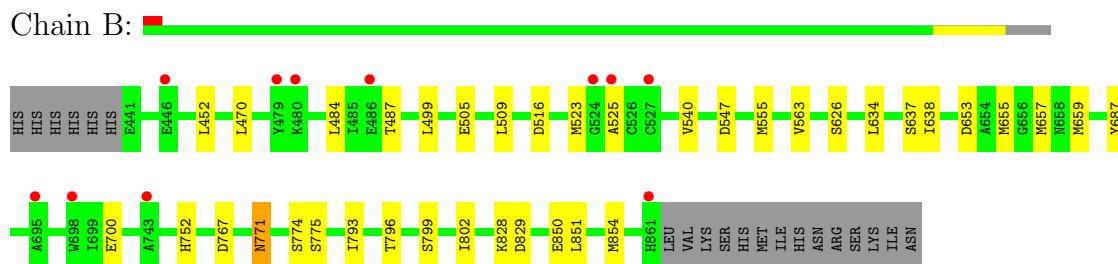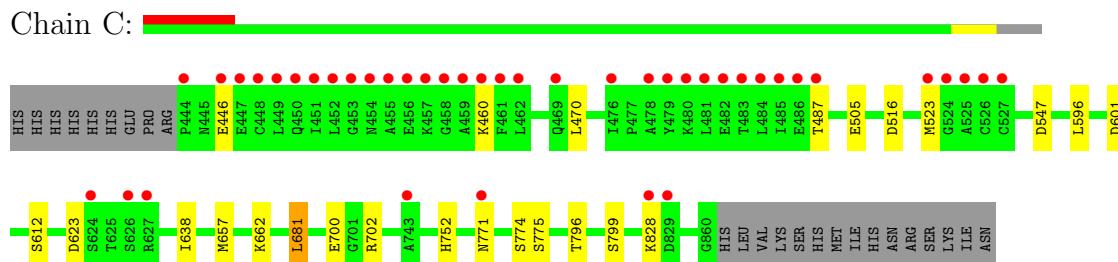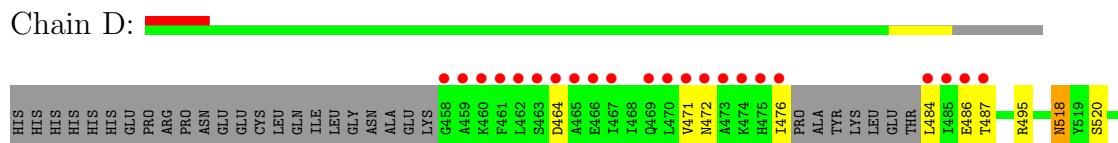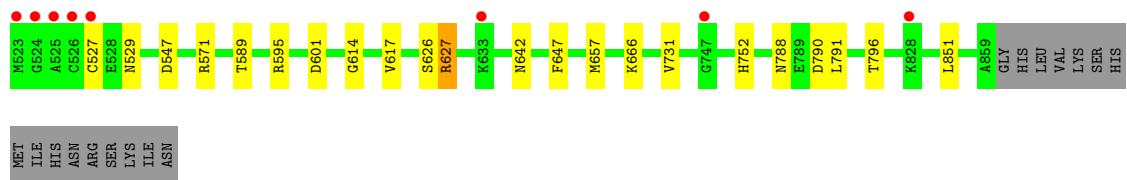
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	72.61Å 172.25Å 75.62Å 90.00° 118.04° 90.00°	Depositor
Resolution (Å)	50.00 – 2.07 43.53 – 2.07	Depositor EDS
% Data completeness (in resolution range)	90.5 (50.00-2.07) 90.5 (43.53-2.07)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.78 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.213 , 0.257 0.216 , 0.257	Depositor DCC
R_{free} test set	2066 reflections (2.34%)	DCC
Wilson B-factor (Å^2)	29.8	Xtriage
Anisotropy	0.862	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 33.0	EDS
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	0 of 90192 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	12971	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 8HI

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$>5	RMSZ	#$|Z|$>5
1	A	0.37	0/3187	0.64	6/4309 (0.1%)
1	B	0.36	0/3179	0.62	5/4298 (0.1%)
1	C	0.36	0/3140	0.61	4/4244 (0.1%)
1	D	0.37	0/2968	0.63	4/4010 (0.1%)
All	All	0.37	0/12474	0.63	19/16861 (0.1%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	547	ASP	CB-CG-OD2	5.90	123.61	118.30
1	C	623	ASP	CB-CG-OD2	5.82	123.54	118.30
1	A	547	ASP	CB-CG-OD2	5.82	123.54	118.30
1	A	623	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	790	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	516	ASP	CB-CG-OD2	5.60	123.34	118.30
1	B	547	ASP	CB-CG-OD2	5.33	123.10	118.30
1	C	516	ASP	CB-CG-OD2	5.32	123.09	118.30
1	C	547	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	516	ASP	CB-CG-OD2	5.30	123.07	118.30
1	B	829	ASP	CB-CG-OD2	5.17	122.95	118.30
1	B	767	ASP	CB-CG-OD2	5.13	122.92	118.30
1	B	653	ASP	CB-CG-OD2	5.13	122.91	118.30
1	D	790	ASP	CB-CG-OD2	5.08	122.87	118.30
1	A	653	ASP	CB-CG-OD2	5.07	122.86	118.30
1	D	601	ASP	CB-CG-OD2	5.03	122.83	118.30
1	A	601	ASP	CB-CG-OD2	5.03	122.82	118.30
1	C	601	ASP	CB-CG-OD2	5.02	122.82	118.30
1	D	464	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3141	0	3178	26	0
1	B	3133	0	3167	16	0
1	C	3096	0	3135	7	0
1	D	2928	0	2968	10	0
2	A	45	0	35	0	0
2	B	45	0	35	0	0
2	C	45	0	35	1	0
2	D	45	0	35	1	0
3	A	129	0	0	1	0
3	B	134	0	0	2	0
3	C	98	0	0	0	0
3	D	132	0	0	1	0
All	All	12971	0	12588	55	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (55) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:655:MET:SD	1:A:657:MET:HG2	2.14	0.87
1:C:771:ASN:OD1	1:C:775:SER:OG	1.96	0.83
1:B:775:SER:OG	3:B:993:HOH:O	2.02	0.76
1:B:771:ASN:HB2	3:B:993:HOH:O	1.92	0.69
1:B:655:MET:SD	1:B:657:MET:HG2	2.34	0.67
1:A:470:LEU:O	1:A:474:LYS:O	2.22	0.58
1:A:590:ARG:NH2	1:A:657:MET:HE3	2.21	0.56
1:C:681:LEU:HD22	1:D:731:VAL:HG22	1.87	0.55
1:A:636:THR:HG23	1:A:643:LEU:HD11	1.89	0.55
1:B:555:MET:HE3	1:B:563:VAL:HG22	1.88	0.55
1:B:700:GLU:OE2	1:C:700:GLU:OE2	2.25	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:555:MET:CE	1:B:563:VAL:HA	2.38	0.54
1:A:477:PRO:O	1:A:478:ALA:HB2	2.08	0.54
1:A:472:ASN:O	1:A:473:ALA:CB	2.57	0.52
1:C:702:ARG:O	1:C:799:SER:HA	2.10	0.51
1:D:627:ARG:HG2	3:D:911:HOH:O	2.09	0.51
2:D:3:8HI:H24A	2:D:3:8HI:C16	2.40	0.51
1:A:477:PRO:O	1:A:478:ALA:CB	2.60	0.49
1:B:638:ILE:O	1:C:796:THR:HG21	2.13	0.48
1:B:796:THR:HG21	1:C:638:ILE:O	2.13	0.48
1:C:774:SER:HA	1:C:799:SER:O	2.13	0.48
1:A:638:ILE:O	1:D:796:THR:HG21	2.12	0.48
1:D:495:ARG:HG2	1:D:529:ASN:OD1	2.13	0.48
1:A:793:ILE:HD13	1:A:851:LEU:HG	1.96	0.48
1:A:474:LYS:O	1:A:475:HIS:HB2	2.13	0.48
1:A:727:ALA:O	1:A:731:VAL:HG23	2.14	0.47
1:A:441:GLU:N	1:A:442:PRO:CD	2.77	0.47
1:D:471:VAL:HA	1:D:476:ILE:HG23	1.96	0.47
2:C:4:8HI:H25A	2:C:4:8HI:O	2.14	0.47
1:A:581:SER:OG	1:A:840:ARG:HD2	2.16	0.46
1:D:589:THR:HA	1:D:647:PHE:O	2.16	0.46
1:A:529:ASN:ND2	1:B:540:VAL:O	2.47	0.46
1:A:636:THR:HG23	1:A:643:LEU:CD1	2.46	0.45
1:A:860:GLY:O	1:A:861:HIS:HB2	2.16	0.45
1:A:774:SER:HA	1:A:799:SER:O	2.16	0.45
1:B:555:MET:HE3	1:B:563:VAL:HA	1.98	0.44
1:A:542:GLY:H	1:A:567:ASN:HD22	1.65	0.44
1:A:702:ARG:O	1:A:799:SER:HA	2.17	0.44
1:A:590:ARG:NH2	1:A:657:MET:CE	2.81	0.43
1:D:518:ASN:ND2	1:D:520:SER:OG	2.47	0.43
1:B:850:GLU:O	1:B:854:MET:HG2	2.19	0.43
1:D:614:GLY:O	1:D:617:VAL:HG22	2.20	0.42
1:A:596:LEU:HB3	1:A:601:ASP:HB2	2.00	0.42
1:B:655:MET:HA	1:B:802:ILE:O	2.19	0.42
1:B:637:SER:HB2	1:B:687:TYR:OH	2.19	0.42
1:B:499:LEU:HD23	1:B:509:LEU:HD11	2.02	0.41
1:A:560:GLY:O	1:A:561:CYS:HB2	2.20	0.41
1:B:774:SER:HA	1:B:799:SER:O	2.21	0.41
1:D:642:ASN:N	1:D:642:ASN:HD22	2.17	0.41
1:A:468:ILE:HG12	1:A:498:LEU:CD1	2.50	0.41
1:A:846:VAL:O	1:A:850:GLU:HG2	2.22	0.40
1:A:474:LYS:O	1:A:475:HIS:CB	2.70	0.40
1:B:793:ILE:HD13	1:B:851:LEU:HG	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:657:MET:HE2	3:A:978:HOH:O	2.21	0.40
1:D:595:ARG:HE	1:D:642:ASN:ND2	2.19	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	420/441 (95%)	398 (95%)	19 (4%)	3 (1%)	30	16
1	B	419/441 (95%)	404 (96%)	14 (3%)	1 (0%)	56	47
1	C	415/441 (94%)	399 (96%)	16 (4%)	0	100	100
1	D	391/441 (89%)	376 (96%)	15 (4%)	0	100	100
All	All	1645/1764 (93%)	1577 (96%)	64 (4%)	4 (0%)	56	47

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	473	ALA
1	A	478	ALA
1	A	484	LEU
1	B	525	ALA

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	336/355 (95%)	311 (93%)	25 (7%)	20	10

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	335/355 (94%)	323 (96%)	12 (4%)	47	39
1	C	331/355 (93%)	318 (96%)	13 (4%)	43	35
1	D	313/355 (88%)	298 (95%)	15 (5%)	35	25
All	All	1315/1420 (93%)	1250 (95%)	65 (5%)	35	24

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	441	GLU
1	A	443	ARG
1	A	456	GLU
1	A	463	SER
1	A	470	LEU
1	A	483	THR
1	A	484	LEU
1	A	485	ILE
1	A	486	GLU
1	A	495	ARG
1	A	498	LEU
1	A	504	SER
1	A	512	LEU
1	A	528	GLU
1	A	626	SER
1	A	630	ARG
1	A	634	LEU
1	A	659	MET
1	A	688	CYS
1	A	704	LYS
1	A	752	HIS
1	A	788	ASN
1	A	802	ILE
1	A	814	GLN
1	A	861	HIS
1	B	452	LEU
1	B	470	LEU
1	B	484	LEU
1	B	487	THR
1	B	505	GLU
1	B	523	MET
1	B	626	SER
1	B	634	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	659	MET
1	B	752	HIS
1	B	771	ASN
1	B	828	LYS
1	C	446	GLU
1	C	460	LYS
1	C	470	LEU
1	C	487	THR
1	C	505	GLU
1	C	523	MET
1	C	596	LEU
1	C	612	SER
1	C	657	MET
1	C	662	LYS
1	C	681	LEU
1	C	752	HIS
1	C	828	LYS
1	D	472	ASN
1	D	484	LEU
1	D	486	GLU
1	D	487	THR
1	D	518	ASN
1	D	527	CYS
1	D	571	ARG
1	D	626	SER
1	D	627	ARG
1	D	657	MET
1	D	666	LYS
1	D	752	HIS
1	D	788	ASN
1	D	791	LEU
1	D	851	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	488	HIS
1	A	518	ASN
1	A	567	ASN
1	A	632	GLN
1	A	635	HIS
1	A	788	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	472	ASN
1	B	510	GLN
1	B	819	GLN
1	B	830	ASN
1	C	472	ASN
1	C	679	GLN
1	D	472	ASN
1	D	518	ASN
1	D	632	GLN
1	D	642	ASN
1	D	672	HIS
1	D	810	ASN

5.3.3　RNA ⓘ

There are no RNA chains 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 ⓘ

4 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	8HI	A	2	-	48,48,48	1.81	4 (8%)	69,69,69	1.76	13 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	8HI	B	1	-	48,48,48	1.69	5 (10%)	69,69,69	2.10	15 (21%)
2	8HI	C	4	-	48,48,48	1.75	5 (10%)	69,69,69	1.89	11 (15%)
2	8HI	D	3	-	48,48,48	1.74	4 (8%)	69,69,69	1.72	12 (17%)

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	8HI	A	2	-	-	1/36/39/39	0/4/4/4
2	8HI	B	1	-	-	1/36/39/39	0/4/4/4
2	8HI	C	4	-	-	1/36/39/39	0/4/4/4
2	8HI	D	3	-	-	1/36/39/39	0/4/4/4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2	8HI	C20-S	-10.00	1.60	1.77
2	C	4	8HI	C20-S	-9.81	1.61	1.77
2	D	3	8HI	C20-S	-9.45	1.61	1.77
2	B	1	8HI	C20-S	-9.39	1.61	1.77
2	A	2	8HI	C8-N	-3.83	1.36	1.40
2	D	3	8HI	C8-N	-3.38	1.36	1.40
2	C	4	8HI	C8-N	-3.28	1.36	1.40
2	D	3	8HI	O6-C32	3.14	1.33	1.22
2	C	4	8HI	O6-C32	3.10	1.33	1.22
2	A	2	8HI	O6-C32	3.06	1.33	1.22
2	B	1	8HI	O6-C32	3.01	1.33	1.22
2	D	3	8HI	C17-N1	-2.66	1.36	1.41
2	C	4	8HI	C17-N1	-2.54	1.36	1.41
2	A	2	8HI	C17-N1	-2.51	1.36	1.41
2	B	1	8HI	C17-N1	-2.44	1.37	1.41
2	B	1	8HI	O5-C32	-2.29	1.22	1.30
2	B	1	8HI	C8-N	-2.27	1.38	1.40
2	C	4	8HI	O5-C32	-2.15	1.22	1.30

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	8HI	C16-C8-N	10.05	129.10	123.32

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	4	8HI	C16-C8-N	8.60	128.26	123.32
2	D	3	8HI	C16-C8-N	7.26	127.50	123.32
2	A	2	8HI	C16-C8-N	7.11	127.41	123.32
2	B	1	8HI	O1-S-O2	-6.69	107.16	118.78
2	C	4	8HI	O1-S-O2	-5.74	108.81	118.78
2	A	2	8HI	O1-S-O2	-5.29	109.59	118.78
2	D	3	8HI	O1-S-O2	-4.97	110.15	118.78
2	C	4	8HI	C26-C7-C6	-3.84	125.77	130.95
2	C	4	8HI	C26-C7-N	3.79	128.26	123.15
2	D	3	8HI	C26-C7-C6	-3.63	126.06	130.95
2	A	2	8HI	O1-S-C20	3.63	112.28	107.39
2	A	2	8HI	C26-C7-C6	-3.57	126.14	130.95
2	D	3	8HI	C26-C7-N	3.39	127.72	123.15
2	B	1	8HI	C26-C7-N	3.33	127.63	123.15
2	B	1	8HI	O2-S-C20	3.27	111.79	107.39
2	B	1	8HI	C9-C8-C16	-3.25	124.38	130.67
2	B	1	8HI	C26-C7-C6	-3.15	126.70	130.95
2	B	1	8HI	C8-N-C7	3.10	110.85	108.70
2	C	4	8HI	C9-C8-C16	-3.07	124.73	130.67
2	B	1	8HI	C6-C7-N	-3.05	105.64	107.82
2	D	3	8HI	O1-S-C20	3.04	111.48	107.39
2	D	3	8HI	C9-C8-C16	-2.94	124.98	130.67
2	A	2	8HI	C26-C7-N	2.93	127.09	123.15
2	A	2	8HI	C9-C8-C16	-2.91	125.04	130.67
2	B	1	8HI	C7-N-C23	-2.69	121.47	126.89
2	C	4	8HI	C2-C3-C6	-2.69	116.28	120.77
2	C	4	8HI	C6-C7-N	-2.68	105.91	107.82
2	A	2	8HI	C26-C27-C28	-2.65	109.91	115.40
2	C	4	8HI	C8-N-C7	2.65	110.54	108.70
2	B	1	8HI	C2-C3-C6	-2.57	116.47	120.77
2	B	1	8HI	C9-C6-C7	2.55	110.07	107.00
2	A	2	8HI	C30-C29-C28	-2.50	111.10	114.65
2	B	1	8HI	C24-C23-N	-2.42	108.68	111.52
2	D	3	8HI	C26-C27-C28	-2.39	110.44	115.40
2	A	2	8HI	O1-S-N2	2.37	110.95	107.28
2	D	3	8HI	C2-C3-C6	-2.34	116.86	120.77
2	D	3	8HI	C30-C29-C28	-2.31	111.38	114.65
2	A	2	8HI	C2-C3-C6	-2.30	116.92	120.77
2	D	3	8HI	C6-C7-N	-2.27	106.20	107.82
2	C	4	8HI	C26-C27-C28	-2.22	110.80	115.40
2	D	3	8HI	C9-C6-C7	2.18	109.63	107.00
2	A	2	8HI	C7-N-C23	-2.17	122.51	126.89

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	8HI	C1-C-C5	-2.16	119.96	122.90
2	C	4	8HI	O1-S-C20	2.16	110.30	107.39
2	B	1	8HI	C30-C29-C28	-2.13	111.64	114.65
2	D	3	8HI	C8-N-C7	2.11	110.16	108.70
2	A	2	8HI	C30-C31-C32	-2.09	108.68	112.90
2	B	1	8HI	C1-C-C5	-2.05	120.11	122.90
2	B	1	8HI	O1-S-C20	2.05	110.15	107.39
2	A	2	8HI	C1-C-C5	-2.03	120.14	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2	8HI	O-C16-C8-C9
2	D	3	8HI	O-C16-C8-C9
2	B	1	8HI	O-C16-C8-C9
2	C	4	8HI	O-C16-C8-C9

There are no ring outliers.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	422/441 (95%)	0.37	35 (8%)	11	11	24, 35, 56, 63	0
1	B	421/441 (95%)	0.22	11 (2%)	53	55	25, 35, 48, 57	0
1	C	417/441 (94%)	0.52	42 (10%)	7	8	23, 36, 59, 65	0
1	D	395/441 (89%)	0.46	30 (7%)	14	13	24, 35, 59, 64	0
All	All	1655/1764 (93%)	0.39	118 (7%)	16	15	23, 35, 56, 65	0

All (118) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	527	CYS	10.7
1	D	461	PHE	9.2
1	C	455	ALA	8.4
1	D	470	LEU	8.0
1	D	475	HIS	7.9
1	D	486	GLU	7.6
1	C	525	ALA	7.5
1	B	861	HIS	7.4
1	D	525	ALA	7.2
1	A	861	HIS	7.0
1	D	458	GLY	7.0
1	D	485	ILE	6.8
1	D	465	ALA	6.8
1	C	461	PHE	6.6
1	C	483	THR	6.5
1	D	459	ALA	6.1
1	D	484	LEU	6.0
1	C	452	LEU	5.9
1	C	458	GLY	5.4
1	D	523	MET	5.2
1	A	527	CYS	5.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	456	GLU	5.1
1	C	451	ILE	5.1
1	C	524	GLY	5.1
1	D	476	ILE	5.1
1	C	457	LYS	5.0
1	C	479	TYR	4.8
1	D	469	GLN	4.8
1	A	862	LEU	4.7
1	D	460	LYS	4.7
1	A	452	LEU	4.7
1	C	527	CYS	4.7
1	C	481	LEU	4.6
1	C	462	LEU	4.4
1	C	484	LEU	4.4
1	D	466	GLU	4.3
1	A	456	GLU	4.3
1	D	473	ALA	4.3
1	A	476	ILE	4.2
1	D	463	SER	4.2
1	C	485	ILE	4.2
1	A	444	PRO	4.2
1	D	462	LEU	4.1
1	A	455	ALA	3.9
1	C	487	THR	3.7
1	A	461	PHE	3.5
1	C	450	GLN	3.4
1	C	453	GLY	3.4
1	C	478	ALA	3.4
1	A	447	GLU	3.4
1	D	487	THR	3.3
1	D	474	LYS	3.3
1	D	524	GLY	3.3
1	A	475	HIS	3.3
1	B	524	GLY	3.2
1	A	446	GLU	3.2
1	A	450	GLN	3.2
1	D	471	VAL	3.1
1	B	486	GLU	3.1
1	D	464	ASP	3.1
1	A	525	ALA	3.1
1	C	460	LYS	3.1
1	C	444	PRO	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	480	LYS	3.0
1	B	446	GLU	3.0
1	A	462	LEU	3.0
1	C	526	CYS	3.0
1	D	472	ASN	2.9
1	C	448	CYS	2.9
1	A	449	LEU	2.9
1	C	486	GLU	2.8
1	C	469	GLN	2.8
1	D	828	LYS	2.8
1	B	527	CYS	2.7
1	A	453	GLY	2.7
1	C	523	MET	2.7
1	C	828	LYS	2.7
1	C	449	LEU	2.7
1	C	829	ASP	2.7
1	A	483	THR	2.6
1	A	454	ASN	2.6
1	A	448	CYS	2.5
1	C	459	ALA	2.5
1	A	828	LYS	2.5
1	C	454	ASN	2.5
1	B	479	TYR	2.5
1	A	443	ARG	2.5
1	A	451	ILE	2.5
1	C	743	ALA	2.4
1	C	476	ILE	2.4
1	D	467	ILE	2.4
1	D	526	CYS	2.3
1	B	525	ALA	2.3
1	C	771	ASN	2.3
1	A	630	ARG	2.3
1	A	482	GLU	2.2
1	C	446	GLU	2.2
1	C	626	SER	2.2
1	A	693	PRO	2.2
1	B	698	TRP	2.2
1	C	480	LYS	2.2
1	A	829	ASP	2.2
1	A	772	VAL	2.1
1	D	747	GLY	2.1
1	A	441	GLU	2.1

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	480	LYS	2.1
1	A	473	ALA	2.1
1	D	633	LYS	2.1
1	B	695	ALA	2.1
1	B	743	ALA	2.1
1	A	506	PRO	2.1
1	C	627	ARG	2.1
1	C	447	GLU	2.0
1	C	482	GLU	2.0
1	A	786	PRO	2.0
1	C	624	SER	2.0
1	A	787	THR	2.0
1	A	477	PRO	2.0

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 ⓘ

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	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	8HI	D	3	45/45	0.12	-0.28	25,32,34,36	0
2	8HI	A	2	45/45	0.12	-0.34	26,30,35,36	0
2	8HI	B	1	45/45	0.11	-0.47	27,34,37,38	0
2	8HI	C	4	45/45	0.11	-0.59	28,31,36,37	0

6.5 Other polymers ⓘ

There are no such residues in this entry.