



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 08:27 AM GMT

PDB ID : 2R4F  
Title : Substituted Pyrazoles as Hepatselective HMG-COA reductase inhibitors  
Authors : Pavlovsky, A.; Pfefferkorn, J.A.; Harris, M.S.; Finzel, B.C.  
Deposited on : 2007-08-31  
Resolution : 1.70 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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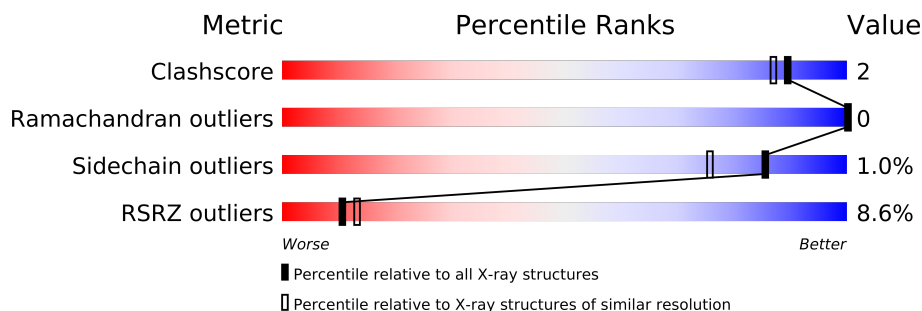
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 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




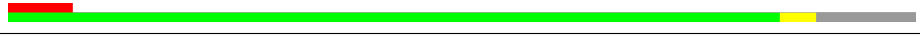
The reported resolution of this entry is 1.70 Å.

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))
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)
RSRZ outliers	66119	2456 (1.70-1.70)

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. 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	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	B	2	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13374 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	420	Total	C	N	O	S	0	0	0
			3123	1945	548	600	30			
1	B	405	Total	C	N	O	S	0	2	0
			3013	1874	529	580	30			
1	C	404	Total	C	N	O	S	0	3	0
			2997	1862	524	579	32			
1	D	394	Total	C	N	O	S	0	3	0
			2921	1815	512	564	30			

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

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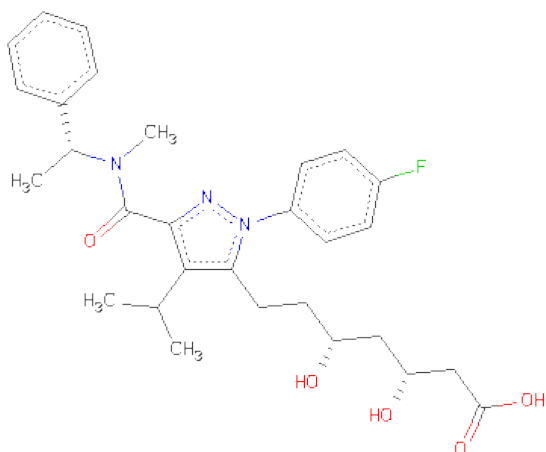
Chain	Residue	Modelled	Actual	Comment	Reference
D	435	HIS	-	EXPRESSION TAG	UNP P04035
D	436	HIS	-	EXPRESSION TAG	UNP P04035
D	437	HIS	-	EXPRESSION TAG	UNP P04035
D	438	HIS	-	EXPRESSION TAG	UNP P04035
D	439	HIS	-	EXPRESSION TAG	UNP P04035
D	440	HIS	-	EXPRESSION TAG	UNP P04035
D	485	ILE	MET	ENGINEERED	UNP P04035

- Molecule 2 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is (3R,5R)-7-[1-(4-FLUOROPHENYL)-4-(1-METHYLETHYL)-3-{METHYL[(1R)-1-PHENYLETHYL]CARBAMOYL}-1H-PYRAZOL-5-YL]-3,5-DIHYDROXYHEPTANOICACID (three-letter code: RIE) (formula: C<sub>29</sub>H<sub>36</sub>FN<sub>3</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			38	29	1	3	5		
3	B	1	Total	C	F	N	O	0	0
			38	29	1	3	5		
3	C	1	Total	C	F	N	O	0	0
			38	29	1	3	5		
3	D	1	Total	C	F	N	O	0	0
			38	29	1	3	5		

- Molecule 4 is water.

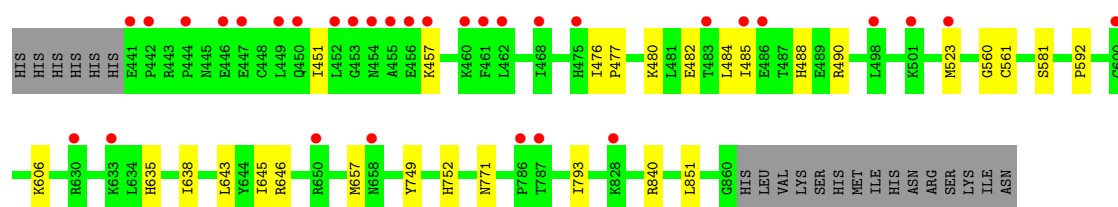
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	299	Total	O	0	0
			299	299		
4	B	291	Total	O	0	0
			291	291		
4	C	271	Total	O	0	0
			271	271		
4	D	287	Total	O	0	0
			287	287		

### 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.

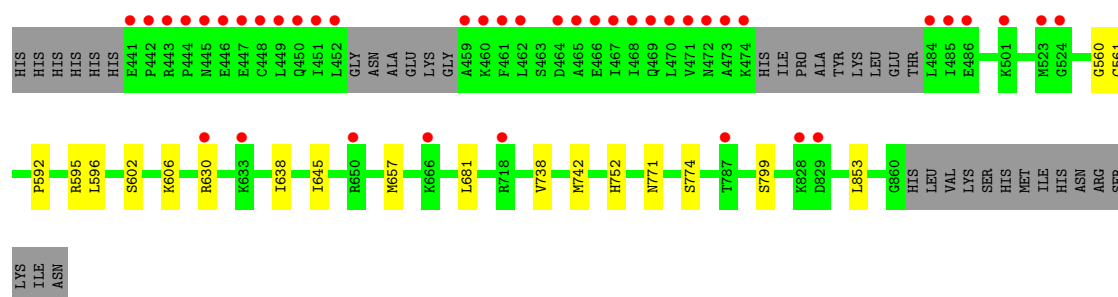
- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzymeA reductase

Chain A: 



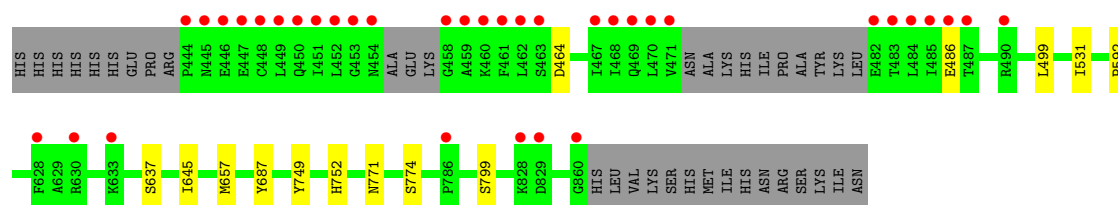
- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzymeA reductase

Chain B: 



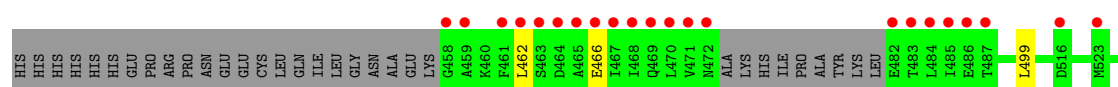
- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzymeA reductase

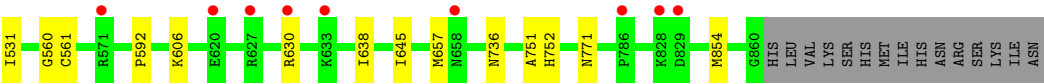
Chain C: 



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

Chain D: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.62Å 135.33Å 82.84Å 90.00° 97.53° 90.00°	Depositor
Resolution (Å)	39.54 – 1.70 39.54 – 1.70	Depositor EDS
% Data completeness (in resolution range)	93.7 (39.54-1.70) 89.0 (39.54-1.70)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.49 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.214 , 0.234 0.195 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	21.4	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 30.6	EDS
Estimated twinning fraction	0.144 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 186474 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13374	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>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: RIE, SO4

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	0.30	0/3168	0.45	0/4283
1	B	0.30	0/3063	0.44	0/4138
1	C	0.30	0/3051	0.44	0/4121
1	D	0.30	0/2975	0.45	0/4020
All	All	0.30	0/12257	0.45	0/16562

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 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	3123	0	3160	15	0
1	B	3013	0	3049	10	0
1	C	2997	0	3025	13	0
1	D	2921	0	2951	21	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	38	0	35	3	0
3	B	38	0	35	2	0
3	C	38	0	35	2	0
3	D	38	0	35	1	0
4	A	299	0	0	0	0
4	B	291	0	0	0	0
4	C	271	0	0	0	0
4	D	287	0	0	0	0
All	All	13374	0	12325	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:D:736:ASN:HD21	1:D:854:MET:HE3	1.16	1.08
1:D:751:ALA:HB2	1:D:854:MET:CE	1.87	1.04
1:D:736:ASN:ND2	1:D:854:MET:HE3	1.73	1.03
1:D:751:ALA:HB2	1:D:854:MET:HE2	1.48	0.93
1:D:736:ASN:HD21	1:D:854:MET:CE	1.92	0.81
1:D:751:ALA:HB2	1:D:854:MET:HE1	1.62	0.80
1:C:771[A]:ASN:OD1	1:D:771[A]:ASN:ND2	2.25	0.69
1:C:771[A]:ASN:CG	1:D:771[A]:ASN:HD21	1.98	0.67
1:C:771[A]:ASN:ND2	1:D:771[A]:ASN:OD1	2.30	0.64
1:C:771[A]:ASN:HD21	1:D:771[A]:ASN:CG	2.02	0.62
1:B:595:ARG:HD2	1:B:681:LEU:HD22	1.82	0.60
1:C:771[A]:ASN:ND2	1:D:771[A]:ASN:HD21	2.04	0.55
1:A:606:LYS:HD2	1:A:638:ILE:HD12	1.88	0.54
1:C:771[A]:ASN:HD21	1:D:771[A]:ASN:ND2	2.06	0.54
3:D:876:RIE:H7	3:D:876:RIE:H12B	1.89	0.54
1:B:606:LYS:HD2	1:B:638:ILE:HD12	1.90	0.53
3:C:876:RIE:H12B	3:C:876:RIE:H7	1.91	0.53
1:C:771[A]:ASN:ND2	1:D:771[A]:ASN:ND2	2.57	0.53
3:B:876:RIE:H7	3:B:876:RIE:H12B	1.90	0.53
3:A:876:RIE:H7	3:A:876:RIE:H12B	1.91	0.52
1:A:581:SER:OG	1:A:840:ARG:HD2	2.11	0.51
1:D:751:ALA:CB	1:D:854:MET:HE2	2.31	0.51
1:A:476:ILE:HG23	1:A:484:LEU:HD13	1.94	0.50
1:A:749:TYR:OH	1:C:749:TYR:OH	2.30	0.50
1:A:592:PRO:HD2	1:A:645:ILE:O	2.13	0.49
1:A:771:ASN:CG	1:B:771[B]:ASN:HD21	2.17	0.48
1:B:592:PRO:HD2	1:B:645:ILE:O	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:771:ASN:OD1	1:B:771[B]:ASN:ND2	2.43	0.46
1:D:592:PRO:HD2	1:D:645:ILE:O	2.16	0.45
1:A:482:GLU:HB3	1:A:488:HIS:HD2	1.82	0.44
1:C:499:LEU:HD22	1:C:531:ILE:HG21	2.00	0.44
1:A:638:ILE:HG13	1:A:643:LEU:HD13	2.00	0.43
1:B:560:GLY:O	1:B:561:CYS:HB2	2.18	0.42
3:B:876:RIE:H16B	3:B:876:RIE:H14	1.79	0.42
1:C:592:PRO:HD2	1:C:645:ILE:O	2.19	0.42
1:C:774:SER:HA	1:C:799:SER:O	2.19	0.42
1:D:606:LYS:HD2	1:D:638:ILE:HD12	2.00	0.42
1:A:485:ILE:HG21	1:A:490:ARG:HD3	2.00	0.42
1:B:596:LEU:HD13	1:B:602:SER:HA	2.01	0.42
1:D:499:LEU:HD22	1:D:531:ILE:HG21	2.01	0.42
1:C:771[A]:ASN:ND2	1:D:771[A]:ASN:CG	2.71	0.42
1:D:736:ASN:ND2	1:D:854:MET:CE	2.60	0.42
1:A:793:ILE:HD13	1:A:851:LEU:HG	2.02	0.42
1:B:774:SER:HA	1:B:799:SER:O	2.20	0.41
1:A:451:ILE:HG23	1:A:457:LYS:HD3	2.02	0.41
1:A:560:GLY:O	1:A:561:CYS:HB2	2.19	0.41
1:A:477:PRO:HG2	1:A:480:LYS:HB2	2.03	0.41
1:C:637:SER:HB2	1:C:687:TYR:OH	2.20	0.41
3:A:876:RIE:H14	3:A:876:RIE:H16B	1.80	0.41
1:B:738:VAL:O	1:B:742:MET:HG2	2.21	0.41
3:A:876:RIE:H21	1:B:853:LEU:HD11	2.02	0.41
1:A:635:HIS:HB3	1:A:646:ARG:HB3	2.03	0.40
1:D:462:LEU:HD22	1:D:466:GLU:HG2	2.02	0.40
3:C:876:RIE:H16B	3:C:876:RIE:H14	1.79	0.40
1:D:560:GLY:O	1:D:561:CYS:HB2	2.22	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	418/441 (95%)	405 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	401/441 (91%)	388 (97%)	13 (3%)	0	100	100
1	C	401/441 (91%)	387 (96%)	14 (4%)	0	100	100
1	D	393/441 (89%)	381 (97%)	12 (3%)	0	100	100
All	All	1613/1764 (91%)	1561 (97%)	52 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	334/355 (94%)	331 (99%)	3 (1%)	87	79
1	B	325/355 (92%)	322 (99%)	3 (1%)	87	79
1	C	324/355 (91%)	320 (99%)	4 (1%)	82	69
1	D	315/355 (89%)	312 (99%)	3 (1%)	85	76
All	All	1298/1420 (91%)	1285 (99%)	13 (1%)	85	76

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	523	MET
1	A	657	MET
1	A	752	HIS
1	B	630	ARG
1	B	657	MET
1	B	752	HIS
1	C	464	ASP
1	C	486	GLU
1	C	657	MET
1	C	752	HIS
1	D	630	ARG
1	D	657	MET
1	D	752	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	488	HIS
1	B	488	HIS
1	B	510	GLN
1	B	658	ASN
1	C	635	HIS
1	D	510	GLN
1	D	635	HIS
1	D	736	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 ⓘ

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	A	1	-	4,4,4	0.20	0	6,6,6	0.06	0
3	RIE	A	876	-	40,40,40	1.56	3 (7%)	56,56,56	1.85	9 (16%)
2	SO4	B	2	-	4,4,4	0.21	0	6,6,6	0.06	0
3	RIE	B	876	-	40,40,40	1.56	4 (10%)	56,56,56	1.82	9 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	3	-	4,4,4	0.23	0	6,6,6	0.08	0
3	RIE	C	876	-	40,40,40	1.56	3 (7%)	56,56,56	1.82	10 (17%)
2	SO4	D	4	-	4,4,4	0.23	0	6,6,6	0.09	0
3	RIE	D	876	-	40,40,40	1.56	4 (10%)	56,56,56	1.82	8 (14%)

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	SO4	A	1	-	-	0/0/0/0	0/0/0/0
3	RIE	A	876	-	-	0/36/37/37	0/3/3/3
2	SO4	B	2	-	-	0/0/0/0	0/0/0/0
3	RIE	B	876	-	-	0/36/37/37	0/3/3/3
2	SO4	C	3	-	-	0/0/0/0	0/0/0/0
3	RIE	C	876	-	-	0/36/37/37	0/3/3/3
2	SO4	D	4	-	-	0/0/0/0	0/0/0/0
3	RIE	D	876	-	-	0/36/37/37	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	876	RIE	C4-C5	6.97	1.50	1.38
3	C	876	RIE	C4-C5	6.97	1.50	1.38
3	B	876	RIE	C4-C5	6.94	1.50	1.38
3	A	876	RIE	C4-C5	6.90	1.50	1.38
3	A	876	RIE	C27-N3	-4.62	1.34	1.43
3	B	876	RIE	C27-N3	-4.50	1.34	1.43
3	D	876	RIE	C27-N3	-4.49	1.34	1.43
3	C	876	RIE	C27-N3	-4.47	1.34	1.43
3	D	876	RIE	C5-C6	-2.51	1.49	1.53
3	B	876	RIE	C5-C6	-2.49	1.49	1.53
3	A	876	RIE	C5-C6	-2.48	1.49	1.53
3	C	876	RIE	C5-C6	-2.40	1.49	1.53
3	D	876	RIE	C2-C5	2.03	1.50	1.42
3	B	876	RIE	C2-C5	2.02	1.50	1.42

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	876	RIE	C4-N3-N4	6.15	116.75	111.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	876	RIE	C4-N3-N4	6.03	116.64	111.17
3	B	876	RIE	C4-N3-N4	5.91	116.53	111.17
3	C	876	RIE	C4-N3-N4	5.85	116.48	111.17
3	A	876	RIE	C5-C4-N3	-5.14	103.43	106.69
3	D	876	RIE	C5-C4-N3	-5.08	103.47	106.69
3	B	876	RIE	C5-C4-N3	-4.86	103.61	106.69
3	A	876	RIE	C32-C1-N2	4.81	116.29	109.33
3	C	876	RIE	C32-C1-N2	4.81	116.30	109.33
3	C	876	RIE	C5-C4-N3	-4.73	103.69	106.69
3	B	876	RIE	C32-C1-N2	4.67	116.10	109.33
3	D	876	RIE	C32-C1-N2	4.46	115.78	109.33
3	D	876	RIE	C18-C27-C21	-3.75	115.56	121.29
3	B	876	RIE	C18-C27-C21	-3.69	115.65	121.29
3	C	876	RIE	C18-C27-C21	-3.69	115.65	121.29
3	A	876	RIE	C18-C27-C21	-3.60	115.79	121.29
3	D	876	RIE	C24-C21-C27	3.59	123.02	119.29
3	B	876	RIE	C24-C21-C27	3.55	122.98	119.29
3	C	876	RIE	C24-C21-C27	3.51	122.94	119.29
3	A	876	RIE	C24-C21-C27	3.45	122.88	119.29
3	C	876	RIE	C15-C18-C27	3.32	122.74	119.29
3	D	876	RIE	C15-C18-C27	3.31	122.73	119.29
3	B	876	RIE	C15-C18-C27	3.22	122.63	119.29
3	A	876	RIE	C15-C18-C27	3.17	122.58	119.29
3	A	876	RIE	C7-C4-N3	3.12	127.38	120.64
3	B	876	RIE	C7-C4-N3	2.99	127.09	120.64
3	D	876	RIE	C7-C4-N3	2.99	127.08	120.64
3	C	876	RIE	C7-C4-N3	2.92	126.94	120.64
3	D	876	RIE	C24-C30-C15	-2.63	119.33	122.90
3	B	876	RIE	C24-C30-C15	-2.60	119.36	122.90
3	C	876	RIE	C24-C30-C15	-2.58	119.39	122.90
3	A	876	RIE	C24-C30-C15	-2.47	119.54	122.90
3	C	876	RIE	C8-C7-C4	-2.17	106.69	112.95
3	C	876	RIE	C10-C11-C35	-2.07	108.67	113.02
3	B	876	RIE	C10-C11-C35	-2.07	108.68	113.02
3	A	876	RIE	C10-C11-C35	-2.03	108.76	113.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

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, 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	420/441 (95%)	0.58	32 (7%) 14 17	14, 23, 49, 69	0
1	B	405/441 (91%)	0.74	41 (10%) 7 10	14, 23, 81, 109	0
1	C	404/441 (91%)	0.65	36 (8%) 10 12	13, 22, 80, 101	0
1	D	394/441 (89%)	0.58	31 (7%) 13 15	13, 22, 45, 94	0
All	All	1623/1764 (92%)	0.64	140 (8%) 11 13	13, 23, 61, 109	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	449	LEU	15.5
1	B	452	LEU	14.9
1	D	484	LEU	13.0
1	B	461	PHE	12.2
1	A	455	ALA	11.3
1	B	450	GLN	10.4
1	B	444	PRO	10.2
1	D	470	LEU	9.7
1	C	484	LEU	9.7
1	B	474	LYS	9.4
1	B	451	ILE	9.3
1	D	469	GLN	9.0
1	B	473	ALA	8.8
1	C	461	PHE	8.7
1	D	472	ASN	8.6
1	A	453	GLY	8.5
1	C	483	THR	8.0
1	C	471	VAL	7.9
1	B	447	GLU	7.6
1	D	458	GLY	7.5
1	B	448	CYS	7.2

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Mol	Chain	Res	Type	RSRZ
1	D	471	VAL	7.1
1	D	486	GLU	7.1
1	D	468	ILE	7.0
1	A	461	PHE	6.9
1	D	461	PHE	6.9
1	C	444	PRO	6.8
1	A	441	GLU	6.8
1	B	445	ASN	6.6
1	B	484	LEU	6.5
1	D	483	THR	6.3
1	C	458	GLY	6.2
1	C	470	LEU	6.2
1	D	485	ILE	6.1
1	A	442	PRO	6.0
1	B	471	VAL	5.9
1	C	462	LEU	5.9
1	A	454	ASN	5.7
1	B	446	GLU	5.6
1	C	450	GLN	5.4
1	C	451	ILE	5.3
1	C	486	GLU	5.2
1	D	462	LEU	5.2
1	C	482	GLU	5.1
1	C	452	LEU	4.9
1	D	487	THR	4.9
1	A	446	GLU	4.8
1	C	445	ASN	4.8
1	D	459	ALA	4.5
1	A	633	LYS	4.3
1	A	450	GLN	4.3
1	C	487	THR	4.3
1	B	470	LEU	4.2
1	D	466	GLU	4.1
1	B	462	LEU	4.1
1	C	468	ILE	4.1
1	A	523	MET	4.1
1	B	485	ILE	4.0
1	C	469	GLN	4.0
1	B	442	PRO	3.9
1	D	786	PRO	3.9
1	B	486	GLU	3.9
1	C	449	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	453	GLY	3.8
1	C	829	ASP	3.8
1	C	448	CYS	3.8
1	A	452	LEU	3.7
1	B	468	ILE	3.7
1	A	456	GLU	3.7
1	A	457	LYS	3.7
1	C	447	GLU	3.6
1	B	523	MET	3.6
1	A	462	LEU	3.6
1	C	467	ILE	3.5
1	B	460	LYS	3.5
1	B	472	ASN	3.5
1	D	630	ARG	3.5
1	C	446	GLU	3.5
1	D	465	ALA	3.5
1	C	460	LYS	3.4
1	A	449	LEU	3.4
1	A	650	ARG	3.4
1	B	633	LYS	3.4
1	A	444	PRO	3.3
1	B	469	GLN	3.3
1	C	463	SER	3.3
1	A	630	ARG	3.3
1	B	459	ALA	3.3
1	B	829	ASP	3.2
1	A	485	ILE	3.2
1	C	630	ARG	3.2
1	B	467	ILE	3.2
1	D	467	ILE	3.1
1	D	463	SER	3.1
1	A	828	LYS	3.0
1	D	633	LYS	3.0
1	D	829	ASP	3.0
1	D	464	ASP	2.9
1	C	459	ALA	2.9
1	A	483	THR	2.9
1	B	466	GLU	2.8
1	B	464	ASP	2.8
1	C	485	ILE	2.8
1	B	787	THR	2.8
1	C	860	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	633	LYS	2.7
1	A	658	ASN	2.7
1	B	441	GLU	2.6
1	A	501	LYS	2.6
1	B	828	LYS	2.6
1	D	828	LYS	2.6
1	B	650	ARG	2.6
1	C	454	ASN	2.6
1	C	628	PHE	2.5
1	A	786	PRO	2.5
1	A	468	ILE	2.5
1	C	786	PRO	2.4
1	B	443	ARG	2.4
1	D	516	ASP	2.4
1	D	523	MET	2.4
1	D	571	ARG	2.3
1	C	828	LYS	2.3
1	C	490	ARG	2.3
1	D	627	ARG	2.3
1	A	486	GLU	2.3
1	A	498	LEU	2.3
1	B	501	LYS	2.2
1	B	465	ALA	2.2
1	B	718	ARG	2.2
1	B	524	GLY	2.2
1	D	482	GLU	2.1
1	A	600	CYS	2.1
1	A	475	HIS	2.1
1	D	620	GLU	2.1
1	A	460	LYS	2.1
1	A	447	GLU	2.1
1	D	658	ASN	2.1
1	B	666	LYS	2.0
1	B	630	ARG	2.0
1	A	787	THR	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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	B	2	5/5	0.22	3.05	58,58,58,58	0
3	RIE	A	876	38/38	0.12	1.93	16,21,23,23	0
2	SO4	A	1	5/5	0.20	1.44	47,47,47,47	0
3	RIE	B	876	38/38	0.10	0.73	16,22,23,24	0
3	RIE	C	876	38/38	0.11	0.62	15,20,22,22	0
3	RIE	D	876	38/38	0.10	0.57	16,20,22,22	0
2	SO4	C	3	5/5	0.14	0.18	42,42,42,42	0
2	SO4	D	4	5/5	0.12	-0.13	45,45,45,45	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.