



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2017 – 02:47 PM EDT

PDB ID : 1EBV  
Title : OVINE PGHS-1 COMPLEXED WITH SALICYL HYDROXAMIC ACID  
Authors : Loll, P.J.; Sharkey, C.T.; O'Connor, S.J.; Fitzgerald, D.J.  
Deposited on : unknown  
Resolution : 3.20 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](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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
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) : rb-20030345

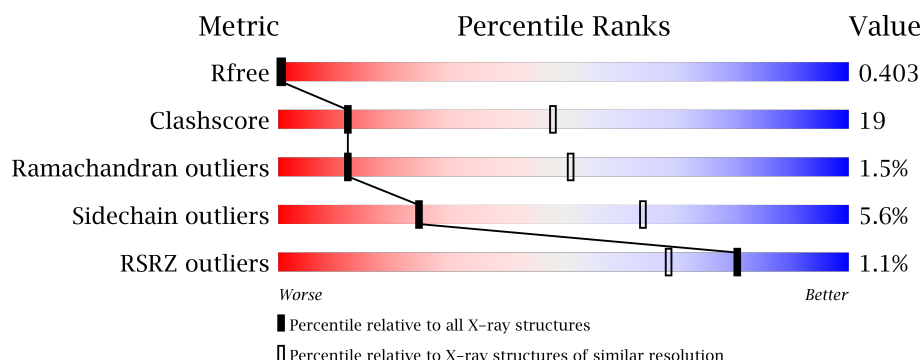
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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	551	<div> <div></div> <div>62%</div> <div>34%</div> <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
2	NAG	A	661	-	-	-	X
2	NAG	A	681	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SCL	A	700	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4594 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.

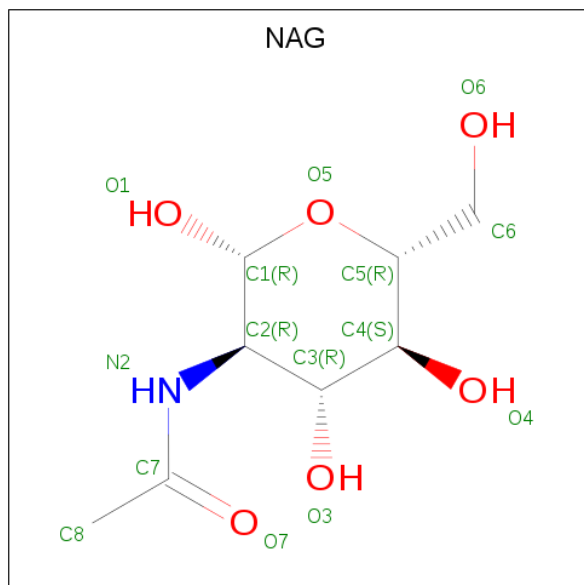
- Molecule 1 is a protein called PROSTAGLANDIN H2 SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	551	Total	C	N	O	S	0	0	0
			4481	2905	758	790	28			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	LEU	MET	CONFLICT	UNP P05979
A	530	OAS	SER	MODIFIED RESIDUE	UNP P05979

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



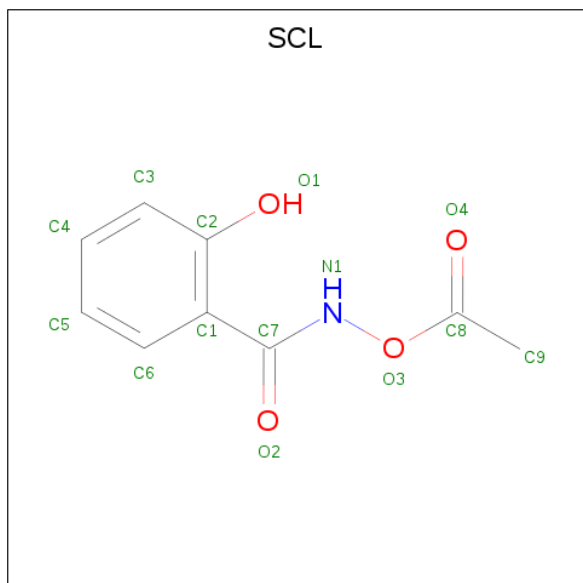
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ACETIC ACID SALICYLOYL-AMINO-ESTER (three-letter code: SCL) (formula:  $C_9H_9NO_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	9	1	4		

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).

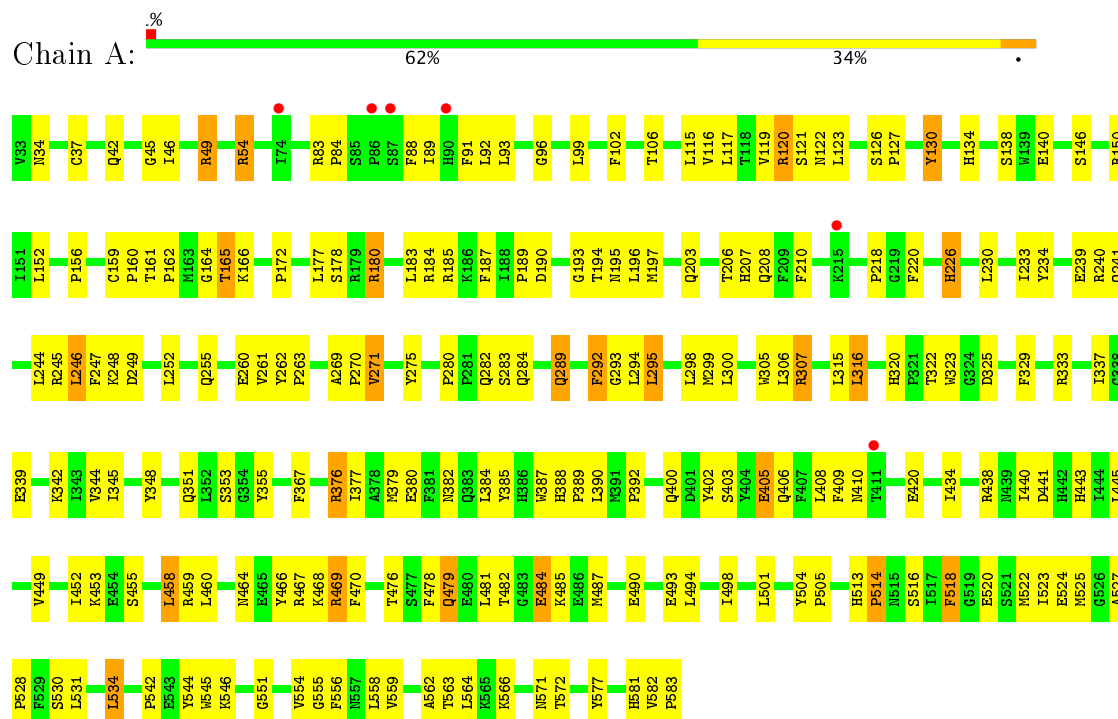


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

### 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 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 ( $\text{RSRZ} > 2$ ). 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: PROTAGLANDIN H2 SYNTHASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.87Å 207.46Å 221.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.50 – 3.20 23.56 – 3.10	Depositor EDS
% Data completeness (in resolution range)	81.8 (23.50-3.20) 67.7 (23.56-3.10)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.33 (at 3.10Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, $R_{free}$	0.218 , 0.248 0.400 , 0.403	Depositor DCC
$R_{free}$ test set	2502 reflections (8.72%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , -15.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.47	EDS
Total number of atoms	4594	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, OAS, NAG, SCL

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	0.40	0/4609	0.64	1/6253 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	252	LEU	CA-CB-CG	5.41	127.73	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4481	0	4385	171	0
2	A	56	0	51	3	0
3	A	14	0	9	5	0
4	A	43	0	30	3	0
All	All	4594	0	4475	172	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (172) 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:A:185:ARG:HE	1:A:438:ARG:HD3	1.29	0.97
1:A:294:LEU:HD22	1:A:409:PHE:CE2	2.13	0.84
1:A:563:THR:HG22	1:A:566:LYS:HD3	1.60	0.83
1:A:530:OAS:OAC	3:A:700:SCL:H5	1.78	0.83
1:A:185:ARG:HH21	1:A:438:ARG:HH11	1.26	0.83
1:A:172:PRO:HB2	1:A:177:LEU:HD22	1.61	0.81
1:A:513:HIS:HB3	1:A:514:PRO:HD2	1.59	0.81
1:A:150:ARG:HB3	1:A:379:MET:HE3	1.61	0.81
1:A:294:LEU:HD22	1:A:409:PHE:HE2	1.46	0.79
1:A:523:ILE:HA	3:A:700:SCL:O1	1.83	0.79
1:A:150:ARG:HD3	1:A:152:LEU:O	1.91	0.71
1:A:241:GLN:NE2	1:A:245:ARG:HH11	1.87	0.71
1:A:577:TYR:CE2	1:A:583:PRO:HD3	2.26	0.71
1:A:84:PRO:HG2	1:A:89:ILE:HD11	1.74	0.70
1:A:513:HIS:HB3	1:A:514:PRO:CD	2.22	0.70
1:A:185:ARG:HH21	1:A:438:ARG:NH1	1.90	0.69
1:A:563:THR:HG23	1:A:566:LYS:H	1.58	0.67
1:A:367:PHE:CD2	1:A:542:PRO:HG3	2.31	0.66
1:A:339:GLU:HG2	1:A:562:ALA:HB2	1.78	0.65
1:A:504:TYR:HB3	1:A:505:PRO:HD3	1.79	0.64
1:A:240:ARG:HG3	1:A:271:VAL:CG2	2.28	0.64
1:A:34:ASN:HB3	1:A:37:CYS:SG	2.37	0.64
1:A:226:HIS:CE1	1:A:376:ARG:HD2	2.33	0.64
1:A:208:GLN:NE2	1:A:230:LEU:H	1.96	0.63
1:A:280:PRO:HG2	1:A:283:SER:OG	1.99	0.63
1:A:241:GLN:HE21	1:A:245:ARG:HH11	1.46	0.62
1:A:582:VAL:HG23	1:A:583:PRO:HD2	1.81	0.62
1:A:130:TYR:HB3	1:A:134:HIS:O	1.99	0.62
1:A:449:VAL:O	1:A:453:LYS:HG3	1.99	0.61
1:A:54:ARG:HB2	1:A:54:ARG:HH11	1.64	0.61
1:A:226:HIS:HB3	1:A:377:ILE:H	1.66	0.61
1:A:93:LEU:HD13	1:A:355:TYR:CE1	2.35	0.61
1:A:115:LEU:O	1:A:119:VAL:HG23	2.01	0.60
1:A:380:GLU:HG3	1:A:460:LEU:HD11	1.83	0.60
1:A:458:LEU:HB3	1:A:460:LEU:HD23	1.83	0.60
1:A:255:GLN:HG2	1:A:263:PRO:O	2.02	0.60
1:A:134:HIS:HD2	1:A:138:SER:OG	1.84	0.60
1:A:294:LEU:O	1:A:295:LEU:HG	2.02	0.59
1:A:234:TYR:CE2	1:A:333:ARG:HG3	2.37	0.59
1:A:208:GLN:HE21	1:A:230:LEU:H	1.50	0.59
1:A:384:LEU:HD23	1:A:384:LEU:C	2.23	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:ARG:HG2	1:A:459:ARG:HH21	1.67	0.59
1:A:126:SER:HA	1:A:127:PRO:C	2.22	0.59
1:A:184:ARG:HA	1:A:438:ARG:O	2.02	0.59
1:A:193:GLY:O	1:A:582:VAL:HG12	2.03	0.59
1:A:554:VAL:HG23	1:A:555:GLY:H	1.67	0.58
1:A:88:PHE:O	1:A:91:PHE:HB3	2.03	0.58
1:A:245:ARG:HD2	1:A:329:PHE:CZ	2.39	0.58
1:A:527:ALA:HB3	1:A:528:PRO:HD3	1.87	0.57
1:A:207:HIS:HB3	1:A:289:GLN:HE21	1.70	0.56
1:A:581:HIS:ND1	1:A:582:VAL:O	2.36	0.56
1:A:248:LYS:HG2	1:A:249:ASP:OD1	2.05	0.55
1:A:403:SER:OG	1:A:406:GLN:HG3	2.06	0.55
1:A:441:ASP:OD2	1:A:443:HIS:HB2	2.05	0.55
1:A:481:LEU:HD22	1:A:501:LEU:HD22	1.88	0.55
1:A:479:GLN:HG3	1:A:485:LYS:HZ1	1.71	0.55
1:A:367:PHE:CE2	1:A:542:PRO:HG3	2.42	0.54
1:A:582:VAL:CG2	1:A:583:PRO:HD2	2.36	0.54
1:A:195:ASN:OD1	1:A:197:MET:HB3	2.08	0.54
1:A:46:ILE:HD12	1:A:46:ILE:N	2.23	0.53
1:A:152:LEU:HD21	1:A:469:ARG:CG	2.39	0.53
1:A:389:PRO:HG3	1:A:440:ILE:HG12	1.91	0.53
1:A:577:TYR:HE2	1:A:583:PRO:HD3	1.73	0.53
1:A:342:LYS:HD2	1:A:559:VAL:O	2.08	0.53
1:A:260:GLU:HB2	1:A:262:TYR:HE1	1.73	0.52
1:A:306:LEU:HD23	1:A:306:LEU:C	2.30	0.52
1:A:282:GLN:N	1:A:282:GLN:OE1	2.40	0.52
1:A:420:GLU:HG3	1:A:572:THR:HB	1.92	0.51
1:A:159:CYS:HB3	1:A:164:GLY:O	2.10	0.51
1:A:307:ARG:HG2	1:A:571:ASN:HB3	1.91	0.51
1:A:513:HIS:HB2	1:A:516:SER:OG	2.11	0.51
1:A:239:GLU:H	1:A:239:GLU:CD	2.14	0.51
1:A:246:LEU:O	1:A:247:PHE:HB2	2.10	0.50
1:A:233:ILE:HD13	1:A:305:TRP:HB3	1.92	0.50
1:A:261:VAL:O	1:A:307:ARG:NH1	2.44	0.50
1:A:410:ASN:ND2	2:A:681:NAG:H82	2.26	0.50
1:A:464:ASN:O	1:A:467:ARG:HB2	2.11	0.50
1:A:527:ALA:HB1	3:A:700:SCL:O4	2.11	0.50
1:A:230:LEU:HD13	1:A:337:ILE:HG12	1.94	0.50
1:A:180:ARG:HD3	1:A:490:GLU:OE2	2.12	0.50
1:A:390:LEU:HD21	1:A:434:ILE:HD11	1.93	0.50
1:A:165:THR:HG22	1:A:166:LYS:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:ARG:NH2	1:A:459:ARG:HG2	2.25	0.49
1:A:156:PRO:HB2	1:A:159:CYS:SG	2.52	0.49
1:A:185:ARG:NH2	1:A:438:ARG:NH1	2.59	0.49
1:A:460:LEU:HD13	1:A:466:TYR:OH	2.12	0.49
1:A:478:PHE:CZ	1:A:498:ILE:HA	2.48	0.49
1:A:183:LEU:HD23	1:A:184:ARG:N	2.27	0.48
1:A:293:GLY:HA2	1:A:299:MET:CE	2.43	0.48
1:A:518:PHE:CD1	1:A:522:MET:HG2	2.47	0.48
1:A:387:TRP:HB2	4:A:601:HEM:HAC	1.96	0.48
1:A:513:HIS:O	1:A:514:PRO:C	2.52	0.48
1:A:306:LEU:HD23	1:A:306:LEU:O	2.14	0.48
1:A:185:ARG:NH2	1:A:438:ARG:HH11	2.03	0.48
1:A:152:LEU:HD21	1:A:469:ARG:HG2	1.96	0.47
1:A:344:VAL:HA	1:A:348:TYR:HB3	1.96	0.47
1:A:523:ILE:HA	3:A:700:SCL:HO1	1.78	0.47
1:A:180:ARG:O	1:A:438:ARG:NH1	2.48	0.47
1:A:282:GLN:H	1:A:282:GLN:CD	2.15	0.47
1:A:389:PRO:HG3	1:A:440:ILE:CG1	2.44	0.47
1:A:203:GLN:HA	4:A:601:HEM:HBC2	1.96	0.47
1:A:388:HIS:N	1:A:389:PRO:CD	2.77	0.47
1:A:121:SER:O	1:A:123:LEU:N	2.48	0.47
1:A:353:SER:HB2	1:A:355:TYR:CD2	2.50	0.47
1:A:544:TYR:O	1:A:546:LYS:N	2.46	0.47
1:A:320:HIS:HE1	1:A:551:GLY:O	1.98	0.46
1:A:120:ARG:NH2	1:A:524:GLU:OE1	2.46	0.46
1:A:420:GLU:CG	1:A:572:THR:HB	2.45	0.46
1:A:208:GLN:HE22	1:A:230:LEU:HD12	1.81	0.46
1:A:45:GLY:C	1:A:46:ILE:HD12	2.36	0.46
1:A:478:PHE:O	1:A:482:THR:HG23	2.16	0.46
1:A:102:PHE:O	1:A:106:THR:HG23	2.15	0.46
1:A:206:THR:HB	1:A:210:PHE:HD2	1.80	0.46
1:A:333:ARG:O	1:A:337:ILE:HG13	2.16	0.46
1:A:403:SER:OG	1:A:405:GLU:HG2	2.16	0.46
1:A:555:GLY:O	1:A:558:LEU:HB2	2.15	0.46
1:A:315:LEU:HD23	1:A:315:LEU:HA	1.80	0.45
1:A:247:PHE:HA	1:A:325:ASP:OD2	2.16	0.45
1:A:384:LEU:HD23	1:A:384:LEU:O	2.16	0.45
1:A:42:GLN:HE22	1:A:468:LYS:NZ	2.15	0.45
1:A:484:GLU:OE2	1:A:487:MET:HB2	2.17	0.45
1:A:123:LEU:O	1:A:469:ARG:NH2	2.49	0.45
1:A:269:ALA:O	1:A:271:VAL:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:GLN:CG	1:A:485:LYS:HZ1	2.30	0.45
1:A:355:TYR:CE1	3:A:700:SCL:H92	2.51	0.45
1:A:534:LEU:HA	1:A:534:LEU:HD12	1.86	0.45
1:A:563:THR:HG22	1:A:566:LYS:HB2	1.98	0.45
1:A:402:TYR:OH	2:A:681:NAG:H61	2.16	0.44
1:A:91:PHE:HD2	1:A:92:LEU:HD12	1.82	0.44
1:A:190:ASP:OD2	1:A:194:THR:OG1	2.28	0.44
1:A:196:LEU:HD11	1:A:392:PRO:HG3	1.99	0.44
1:A:563:THR:HG22	1:A:566:LYS:CD	2.39	0.44
1:A:54:ARG:CB	1:A:54:ARG:HH11	2.29	0.44
1:A:116:VAL:O	1:A:120:ARG:HB2	2.17	0.44
1:A:46:ILE:CD1	1:A:46:ILE:N	2.80	0.44
1:A:470:PHE:CD2	1:A:525:MET:HG2	2.52	0.43
1:A:177:LEU:HD12	1:A:177:LEU:HA	1.82	0.43
1:A:410:ASN:HD22	2:A:681:NAG:H82	1.82	0.43
1:A:160:PRO:HD2	1:A:164:GLY:O	2.18	0.43
1:A:345:ILE:CD1	1:A:534:LEU:HD23	2.48	0.43
1:A:83:ARG:HA	1:A:84:PRO:HD2	1.90	0.43
1:A:88:PHE:CZ	1:A:92:LEU:HD11	2.53	0.43
1:A:292:PHE:HA	1:A:298:LEU:HD23	2.01	0.43
1:A:452:ILE:O	1:A:455:SER:HB3	2.18	0.43
1:A:554:VAL:HG23	1:A:555:GLY:N	2.31	0.43
1:A:49:ARG:CG	1:A:49:ARG:HH11	2.32	0.43
1:A:210:PHE:CE1	1:A:382:ASN:HA	2.54	0.42
1:A:531:LEU:HD23	1:A:531:LEU:HA	1.84	0.42
1:A:185:ARG:NE	1:A:438:ARG:HD3	2.12	0.42
1:A:140:GLU:O	1:A:140:GLU:HG3	2.19	0.42
1:A:218:PRO:HB2	1:A:458:LEU:CD1	2.49	0.42
1:A:513:HIS:HE1	1:A:520:GLU:HA	1.85	0.41
1:A:493:GLU:HG3	1:A:494:LEU:N	2.34	0.41
1:A:146:SER:O	1:A:220:PHE:HA	2.19	0.41
1:A:481:LEU:HD22	1:A:501:LEU:CD2	2.50	0.41
1:A:260:GLU:HB2	1:A:262:TYR:CE1	2.53	0.41
1:A:400:GLN:CA	1:A:400:GLN:HE21	2.32	0.41
1:A:178:SER:HB3	1:A:445:LEU:HD11	2.01	0.41
4:A:601:HEM:HMB1	4:A:601:HEM:HBB2	2.02	0.41
1:A:206:THR:HB	1:A:210:PHE:CD2	2.56	0.41
1:A:479:GLN:CB	1:A:485:LYS:NZ	2.84	0.41
1:A:187:PHE:HE1	1:A:189:PRO:HB3	1.86	0.41
1:A:240:ARG:HG3	1:A:271:VAL:HG22	2.02	0.41
1:A:316:LEU:HA	1:A:316:LEU:HD12	1.91	0.41

*Continued on next page...*

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLY:O	1:A:99:LEU:HB3	2.21	0.41
1:A:49:ARG:HG3	1:A:49:ARG:HH11	1.86	0.41
1:A:161:THR:HB	1:A:162:PRO:CD	2.51	0.41
1:A:348:TYR:O	1:A:351:GLN:HB3	2.21	0.40
1:A:294:LEU:HD22	1:A:409:PHE:CD2	2.55	0.40
1:A:275:TYR:CE2	1:A:284:GLN:HB3	2.57	0.40
1:A:320:HIS:HB3	1:A:323:TRP:CD1	2.57	0.40
1:A:92:LEU:HD12	1:A:92:LEU:N	2.36	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	548/551 (100%)	485 (88%)	55 (10%)	8 (2%)	12	51

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	226	HIS
1	A	408	LEU
1	A	122	ASN
1	A	292	PHE
1	A	545	TRP
1	A	270	PRO
1	A	295	LEU
1	A	514	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	485/485 (100%)	458 (94%)	27 (6%)	25	64

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ARG
1	A	54	ARG
1	A	117	LEU
1	A	120	ARG
1	A	130	TYR
1	A	165	THR
1	A	180	ARG
1	A	244	LEU
1	A	246	LEU
1	A	271	VAL
1	A	289	GLN
1	A	300	LEU
1	A	307	ARG
1	A	316	LEU
1	A	322	THR
1	A	376	ARG
1	A	385	TYR
1	A	405	GLU
1	A	458	LEU
1	A	469	ARG
1	A	476	THR
1	A	479	GLN
1	A	484	GLU
1	A	518	PHE
1	A	534	LEU
1	A	556	PHE
1	A	564	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	56	GLN
1	A	95	HIS
1	A	134	HIS
1	A	170	GLN
1	A	203	GLN
1	A	207	HIS
1	A	208	GLN
1	A	237	ASN
1	A	241	GLN
1	A	320	HIS
1	A	375	ASN
1	A	400	GLN
1	A	443	HIS
1	A	479	GLN
1	A	513	HIS
1	A	515	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	OAS	A	530	1	8,8,9	0.76	0	6,9,11	1.35	1 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OAS	A	530	1	-	0/5/7/9	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	530	OAS	CB-OG-C1A	2.25	122.90	117.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	530	OAS	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

6 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
4	HEM	A	601	1	28,50,50	1.77	8 (28%)	17,82,82	2.26	8 (47%)
2	NAG	A	661	1	14,14,15	0.54	0	15,19,21	0.81	1 (6%)
2	NAG	A	671	1,2	14,14,15	0.51	0	15,19,21	0.81	0
2	NAG	A	672	2	14,14,15	0.45	0	15,19,21	0.88	0
2	NAG	A	681	1	14,14,15	0.48	0	15,19,21	1.00	1 (6%)
3	SCL	A	700	-	13,14,14	1.43	3 (23%)	16,18,18	1.05	1 (6%)

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	HEM	A	601	1	-	0/6/54/54	0/0/8/8
2	NAG	A	661	1	-	0/6/23/26	0/1/1/1
2	NAG	A	671	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	672	2	-	0/6/23/26	0/1/1/1
2	NAG	A	681	1	-	0/6/23/26	0/1/1/1
3	SCL	A	700	-	-	0/9/9/9	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	HEM	C3B-CAB	-3.73	1.40	1.47
4	A	601	HEM	C3C-CAC	-3.11	1.41	1.47
4	A	601	HEM	C3C-C2C	-2.20	1.37	1.40
3	A	700	SCL	C3-C2	2.02	1.43	1.39
4	A	601	HEM	C1D-ND	2.29	1.41	1.36
3	A	700	SCL	C6-C1	2.30	1.43	1.39
4	A	601	HEM	CBC-CAC	2.37	1.45	1.28
4	A	601	HEM	CBB-CAB	2.49	1.46	1.28
3	A	700	SCL	C5-C6	2.51	1.43	1.38
4	A	601	HEM	C1C-NC	2.67	1.39	1.36
4	A	601	HEM	C4C-NC	3.69	1.41	1.36

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	601	HEM	C1D-C2D-C3D	-3.73	104.40	107.00
4	A	601	HEM	C4C-C3C-C2C	-3.30	104.59	106.90
2	A	681	NAG	C2-N2-C7	-2.37	119.49	122.94
2	A	661	NAG	C2-N2-C7	-2.02	119.99	122.94
4	A	601	HEM	CMA-C3A-C4A	-2.02	125.36	128.46
4	A	601	HEM	CAD-CBD-CGD	2.04	116.15	112.66
3	A	700	SCL	C1-C7-N1	2.09	118.85	114.81
4	A	601	HEM	C3B-C4B-NB	2.24	112.10	109.21
4	A	601	HEM	CMB-C2B-C3B	2.71	129.92	124.89
4	A	601	HEM	C4A-C3A-C2A	3.61	109.50	107.00
4	A	601	HEM	CBA-CAA-C2A	3.89	119.92	112.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	HEM	3	0
2	A	681	NAG	3	0
3	A	700	SCL	5	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	550/551 (99%)	0.17	6 (1%)	80 68	1, 11, 32, 53	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	74	ILE	3.1
1	A	90	HIS	2.7
1	A	86	PRO	2.6
1	A	411	THR	2.3
1	A	87	SER	2.1
1	A	215	LYS	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
1	OAS	A	530	9/10	0.91	0.24	-	2,6,14,15	0

### 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, 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
3	SCL	A	700	14/14	0.68	0.39	3.62	51,53,56,57	0
2	NAG	A	661	14/15	0.69	0.35	3.45	34,36,38,39	0
2	NAG	A	681	14/15	0.81	0.34	3.12	18,22,24,24	0
4	HEM	A	601	43/43	0.91	0.29	1.34	13,19,35,41	0
2	NAG	A	671	14/15	0.78	0.30	-	5,6,10,13	0
2	NAG	A	672	14/15	0.74	0.44	-	16,18,20,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.