



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 06:18 PM GMT

PDB ID : 2HSA  
Title : Crystal structure of 12-oxophytodienoate reductase 3 (OPR3) from tomato  
Authors : Breithaupt, C.; Clausen, T.; Huber, R.  
Deposited on : 2006-07-21  
Resolution : 1.50 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 : unknown  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

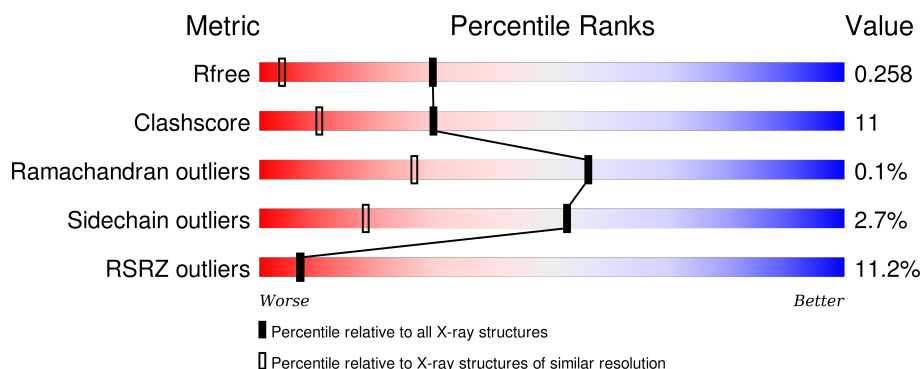
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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	402	
1	B	402	

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	A	603	-	-	X	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6365 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 12-oxophytodienoate reductase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	374	Total	C	N	O	S	10	0	0
			2871	1826	506	529	10			
1	A	376	Total	C	N	O	S	7	0	0
			2918	1853	515	539	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP Q9FEW9
A	-4	HIS	-	EXPRESSION TAG	UNP Q9FEW9
A	-3	HIS	-	EXPRESSION TAG	UNP Q9FEW9
A	-2	HIS	-	EXPRESSION TAG	UNP Q9FEW9
A	-1	HIS	-	EXPRESSION TAG	UNP Q9FEW9
A	0	HIS	-	EXPRESSION TAG	UNP Q9FEW9
B	-5	HIS	-	EXPRESSION TAG	UNP Q9FEW9
B	-4	HIS	-	EXPRESSION TAG	UNP Q9FEW9
B	-3	HIS	-	EXPRESSION TAG	UNP Q9FEW9
B	-2	HIS	-	EXPRESSION TAG	UNP Q9FEW9
B	-1	HIS	-	EXPRESSION TAG	UNP Q9FEW9
B	0	HIS	-	EXPRESSION TAG	UNP Q9FEW9

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).

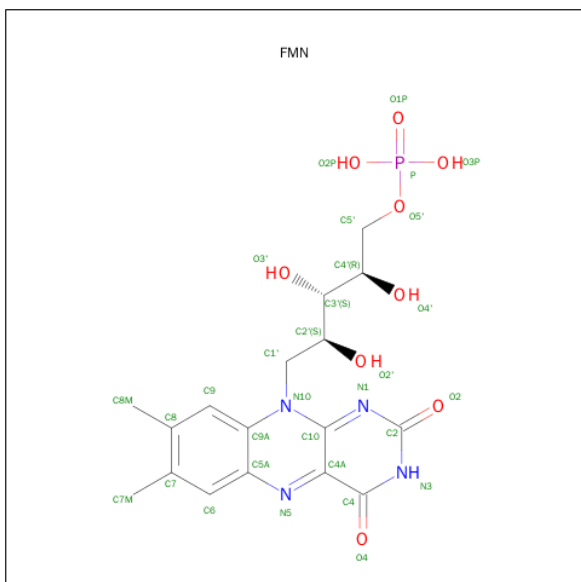


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
4	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	351	Total	O	0	0
			351	351		
5	B	152	Total	O	0	0
			152	152		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.90 Å 89.68 Å 81.38 Å 90.00° 109.46° 90.00°	Depositor
Resolution (Å)	20.00 – 1.50 14.95 – 1.45	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.50) 91.6 (14.95-1.45)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.37 (at 1.45 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.225 , 0.255 0.228 , 0.258	Depositor DCC
$R_{free}$ test set	5720 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.5	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 52.4	EDS
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 126778 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6365	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 5.57% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: FMN, SO4, CL

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	0.54	0/2986	0.71	1/4054 (0.0%)
1	B	0.35	0/2938	0.61	0/3991
All	All	0.45	0/5924	0.66	1/8045 (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	198	ASP	CB-CG-OD1	5.26	123.03	118.30

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	2918	0	2882	45	0
1	B	2871	0	2820	85	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	1	0	0	4	0
4	A	31	0	19	2	0
4	B	31	0	19	1	0
5	A	351	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	152	0	0	7	0
All	All	6365	0	5740	129	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 11.

All (129) 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:B:287:TYR:HA	1:B:289:GLN:HE22	1.18	1.06
1:A:299:GLU:HG2	1:A:303:ARG:HH12	1.25	0.98
1:A:106:GLN:HE22	4:A:401:FMN:HN3	1.15	0.95
1:A:320:GLY:HA3	5:A:834:HOH:O	1.67	0.94
1:A:299:GLU:HG2	1:A:303:ARG:NH1	1.82	0.93
1:A:348:ASN:HD21	1:A:362:ASN:H	1.09	0.93
1:B:239:SER:HB2	1:B:242:ILE:HG13	1.50	0.92
1:A:299:GLU:CG	1:A:303:ARG:HH12	1.86	0.89
1:B:348:ASN:ND2	1:B:362:ASN:H	1.69	0.88
1:B:348:ASN:HD21	1:B:362:ASN:N	1.70	0.88
1:B:348:ASN:HD21	1:B:362:ASN:H	0.91	0.88
1:B:287:TYR:HA	1:B:289:GLN:NE2	1.91	0.85
1:B:368:THR:HG23	5:B:617:HOH:O	1.81	0.80
1:B:39:ASN:ND2	1:B:41:ILE:HD12	1.98	0.79
1:A:242:ILE:HD11	1:A:280:THR:HG22	1.68	0.76
1:B:143:ASP:OD1	1:B:145:THR:HG22	1.87	0.75
1:B:376:VAL:HA	1:B:380:ASP:OD2	1.88	0.74
1:B:239:SER:HB2	1:B:242:ILE:CG1	2.17	0.74
1:A:242:ILE:CD1	1:A:280:THR:HG22	2.19	0.72
1:A:20:LYS:HE3	3:A:603:CL:CL	2.28	0.70
5:B:613:HOH:O	1:A:280:THR:HG21	1.92	0.69
1:B:253:LEU:HD11	1:B:307:THR:HG21	1.73	0.69
1:A:97:HIS:HE1	1:A:180:ASP:OD2	1.76	0.69
1:B:253:LEU:O	1:B:257:LEU:HD13	1.92	0.68
1:B:39:ASN:HB3	5:B:640:HOH:O	1.93	0.68
1:B:39:ASN:HD21	1:B:41:ILE:HD12	1.58	0.67
1:B:38:LEU:HD22	1:B:38:LEU:H	1.61	0.65
1:B:267:GLN:HE21	1:B:274:LEU:H	1.44	0.65
1:A:267:GLN:HE21	1:A:274:LEU:H	1.42	0.64
1:B:97:HIS:HE1	1:B:180:ASP:OD2	1.81	0.63
1:B:141:MET:CE	1:B:141:MET:HA	2.29	0.63
1:B:267:GLN:NE2	1:B:274:LEU:H	1.96	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:LEU:HD12	1:B:308:LEU:CD2	2.30	0.62
1:B:211:LEU:HD13	1:B:258:ALA:HB2	1.80	0.61
1:B:16:TYR:HB2	1:B:26:ARG:NE	2.16	0.60
1:A:348:ASN:HD21	1:A:362:ASN:N	1.90	0.60
1:A:20:LYS:CE	3:A:603:CL:CL	2.87	0.59
1:A:20:LYS:NZ	5:A:795:HOH:O	2.36	0.58
1:A:135:ASN:HD22	1:A:135:ASN:N	1.99	0.58
1:B:257:LEU:HD12	1:B:308:LEU:HD23	1.85	0.58
1:A:267:GLN:NE2	1:A:274:LEU:H	2.01	0.57
1:B:211:LEU:HD21	1:B:255:LEU:HA	1.86	0.57
1:A:183:GLU:OE2	1:A:278:HIS:HD2	1.87	0.56
1:A:281:GLN:N	5:A:834:HOH:O	2.37	0.56
1:B:51:GLU:HG3	1:B:99:LYS:HD2	1.87	0.56
1:B:239:SER:CB	1:B:242:ILE:HG13	2.31	0.56
1:B:289:GLN:H	1:B:289:GLN:CD	2.11	0.55
1:B:318:CYS:SG	1:B:336:ALA:HB2	2.47	0.55
1:B:384:LEU:HA	5:B:638:HOH:O	2.07	0.54
1:A:248:MET:HE3	5:A:898:HOH:O	2.07	0.54
1:A:258:ALA:O	1:A:262:ARG:HG2	2.07	0.53
1:B:141:MET:HE2	1:B:141:MET:HA	1.91	0.53
1:A:165:GLU:HG3	1:A:169:ARG:NH2	2.23	0.53
1:B:183:GLU:OE2	1:B:278:HIS:HD2	1.90	0.53
1:B:289:GLN:HE21	1:B:290:THR:HG23	1.73	0.52
1:B:99:LYS:HB3	1:B:99:LYS:NZ	2.25	0.52
1:B:13:PHE:CZ	1:B:356:LYS:HB2	2.45	0.52
1:A:10:ASN:C	1:A:10:ASN:HD22	2.13	0.52
1:B:112:ARG:HB2	1:B:152:PRO:HG3	1.91	0.52
1:B:309:ARG:HG3	1:B:335:ASP:O	2.10	0.52
1:B:294:ARG:NH1	1:B:298:GLU:OE2	2.42	0.51
1:B:126:ILE:HB	1:B:155:ILE:CG2	2.40	0.51
1:B:97:HIS:HD2	5:B:647:HOH:O	1.93	0.51
1:B:52:GLN:HE21	1:B:53:ARG:HH12	1.59	0.51
1:A:237:ARG:HH21	1:A:278:HIS:CE1	2.29	0.50
1:B:138:ARG:HB2	1:A:295:LEU:O	2.12	0.50
1:A:146:HIS:HE1	5:A:905:HOH:O	1.94	0.50
1:B:54:ALA:HB3	1:B:99:LYS:HD3	1.93	0.50
1:B:162:GLN:HG3	5:B:627:HOH:O	2.10	0.50
1:B:213:ASN:HA	1:B:216:LYS:HD3	1.93	0.50
1:B:281:GLN:HG2	1:B:283:ARG:CZ	2.43	0.49
1:A:135:ASN:H	1:A:135:ASN:ND2	2.10	0.49
1:B:115:HIS:CE1	1:B:117:VAL:HG13	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:LYS:HB3	1:B:99:LYS:HZ3	1.78	0.48
1:B:300:GLU:OE1	1:B:300:GLU:HA	2.13	0.48
1:A:135:ASN:ND2	1:A:135:ASN:N	2.61	0.48
1:B:316:PHE:HE2	1:B:318:CYS:HG	1.60	0.48
1:A:10:ASN:ND2	1:A:12:LEU:H	2.12	0.48
1:A:216:LYS:HB2	1:A:216:LYS:HE3	1.73	0.47
1:A:64:GLY:HA2	1:A:106:GLN:HE21	1.80	0.47
1:B:138:ARG:CD	1:B:148:ILE:HD13	2.44	0.47
1:B:36:ARG:O	1:B:38:LEU:HD22	2.15	0.47
1:A:15:PRO:HG3	5:A:941:HOH:O	2.13	0.47
1:A:280:THR:HG23	5:A:834:HOH:O	2.13	0.47
1:B:38:LEU:HD22	1:B:43:GLN:HG3	1.97	0.46
1:A:20:LYS:NZ	3:A:603:CL:CL	2.85	0.46
1:B:304:LEU:C	1:B:304:LEU:HD13	2.36	0.46
1:B:138:ARG:HD2	1:B:148:ILE:HD13	1.98	0.46
1:B:32:MET:HA	4:B:401:FMN:N5	2.31	0.46
1:B:38:LEU:O	1:B:39:ASN:CG	2.55	0.45
1:B:377:GLY:N	1:B:380:ASP:OD2	2.42	0.45
1:B:71:SER:HB2	1:B:109:HIS:HA	1.98	0.45
1:B:62:THR:HG22	1:B:103:ILE:HD11	1.99	0.45
1:A:116:GLU:CD	1:A:116:GLU:H	2.19	0.45
1:B:366:ARG:HA	1:B:369:PHE:CD1	2.52	0.45
1:A:299:GLU:CD	1:A:303:ARG:HH12	2.20	0.45
1:A:329:GLU:O	1:A:333:GLN:HG3	2.17	0.44
1:B:316:PHE:HE2	1:B:318:CYS:SG	2.41	0.44
1:B:41:ILE:HD13	1:B:84:GLU:OE1	2.17	0.44
1:A:48:GLU:O	1:A:52:GLN:HG3	2.18	0.44
1:B:347:SER:HA	1:B:381:TYR:CG	2.53	0.43
1:B:131:LYS:HA	1:B:132:PRO:HD3	1.78	0.43
1:B:186:GLY:HA2	1:B:192:ILE:HB	2.00	0.43
1:B:242:ILE:HD13	1:B:282:PRO:HA	1.99	0.43
1:B:222:VAL:O	1:B:226:VAL:HG23	2.18	0.43
1:A:32:MET:HA	4:A:401:FMN:N5	2.34	0.43
1:A:97:HIS:HD2	5:A:875:HOH:O	2.02	0.43
1:B:281:GLN:HG2	1:B:283:ARG:NE	2.34	0.43
1:A:182:ILE:HD12	1:A:182:ILE:C	2.40	0.43
1:A:280:THR:CG2	5:A:834:HOH:O	2.67	0.43
1:B:253:LEU:HD11	1:B:307:THR:CG2	2.45	0.42
1:B:149:TYR:HA	1:B:150:PRO:HD3	1.87	0.42
1:A:232:ASP:OD1	3:A:603:CL:CL	2.74	0.42
1:B:354:ARG:NH1	1:B:360:PRO:O	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:LEU:CD1	1:B:258:ALA:HB2	2.48	0.42
1:B:343:ARG:HB3	1:B:364:TYR:CE2	2.55	0.42
1:B:347:SER:HB3	1:B:364:TYR:HB3	2.01	0.42
1:B:175:ILE:HD13	1:B:175:ILE:HA	1.93	0.41
1:B:14:SER:O	1:B:26:ARG:NE	2.47	0.41
1:A:168:ARG:NH1	1:A:228:ALA:HB2	2.35	0.41
1:B:211:LEU:HD11	1:B:254:SER:O	2.21	0.41
1:B:126:ILE:HB	1:B:155:ILE:HG21	2.02	0.41
1:A:219:THR:HG23	1:A:266:ILE:HD11	2.03	0.41
1:B:51:GLU:CG	1:B:99:LYS:HD2	2.50	0.40
1:B:275:ALA:O	1:B:276:TYR:HB3	2.21	0.40
1:B:257:LEU:HD12	1:B:308:LEU:HD21	2.02	0.40
1:B:381:TYR:HA	1:B:382:PRO:HD3	1.81	0.40
1:B:131:LYS:HG3	5:B:749:HOH:O	2.21	0.40
1:B:197:LYS:HD3	1:B:249:ASP:HB2	2.04	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	374/402 (93%)	360 (96%)	14 (4%)	0	100	100
1	B	372/402 (92%)	363 (98%)	8 (2%)	1 (0%)	46	19
All	All	746/804 (93%)	723 (97%)	22 (3%)	1 (0%)	56	26

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	80	ILE

### 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	305/328 (93%)	297 (97%)	8 (3%)	54	19
1	B	295/328 (90%)	287 (97%)	8 (3%)	52	18
All	All	600/656 (92%)	584 (97%)	16 (3%)	52	18

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	83	LYS
1	B	211	LEU
1	B	261	GLU
1	B	278	HIS
1	B	284	TYR
1	B	309	ARG
1	B	345	PHE
1	B	358	ASN
1	A	10	ASN
1	A	135	ASN
1	A	185	HIS
1	A	278	HIS
1	A	298	GLU
1	A	309	ARG
1	A	325	GLU
1	A	345	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	39	ASN
1	B	43	GLN
1	B	52	GLN
1	B	97	HIS
1	B	135	ASN
1	B	267	GLN

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Mol	Chain	Res	Type
1	B	278	HIS
1	B	289	GLN
1	B	333	GLN
1	B	348	ASN
1	B	358	ASN
1	A	10	ASN
1	A	40	ASN
1	A	43	GLN
1	A	97	HIS
1	A	106	GLN
1	A	135	ASN
1	A	146	HIS
1	A	162	GLN
1	A	267	GLN
1	A	278	HIS
1	A	333	GLN
1	A	348	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	FMN	A	401	-	32,33,33	1.48	4 (12%)	34,50,50	2.97	7 (20%)
2	SO4	A	601	-	4,4,4	0.25	0	6,6,6	0.10	0
4	FMN	B	401	-	32,33,33	1.55	6 (18%)	34,50,50	3.16	9 (26%)
2	SO4	B	602	-	4,4,4	0.24	0	6,6,6	0.12	0

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	FMN	A	401	-	-	0/18/18/18	0/3/3/3
2	SO4	A	601	-	-	0/0/0/0	0/0/0/0
4	FMN	B	401	-	-	0/18/18/18	0/3/3/3
2	SO4	B	602	-	-	0/0/0/0	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	401	FMN	C5A-N5	2.12	1.38	1.35
4	A	401	FMN	C9A-N10	2.22	1.42	1.38
4	B	401	FMN	C2-N3	2.33	1.43	1.38
4	A	401	FMN	C4-C4A	2.35	1.46	1.41
4	B	401	FMN	C8-C7	2.74	1.48	1.41
4	B	401	FMN	C6-C5A	2.99	1.46	1.41
4	B	401	FMN	C4-C4A	3.02	1.47	1.41
4	A	401	FMN	C2-N3	3.20	1.44	1.38
4	B	401	FMN	C4A-C10	4.25	1.48	1.40
4	A	401	FMN	C4A-C10	4.26	1.48	1.40

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	FMN	C4A-C4-N3	-6.19	115.44	123.52
4	A	401	FMN	C4A-C4-N3	-6.02	115.65	123.52
4	A	401	FMN	N3-C2-N1	-5.47	118.48	127.69
4	B	401	FMN	N3-C2-N1	-5.37	118.64	127.69
4	B	401	FMN	C4A-C10-N10	-5.26	116.70	120.52
4	B	401	FMN	C4-C4A-C10	-5.22	116.60	119.94
4	A	401	FMN	C4-C4A-C10	-5.18	116.63	119.94
4	A	401	FMN	C4A-C10-N10	-5.07	116.84	120.52
4	B	401	FMN	O2'-C2'-C3'	-2.80	101.74	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	FMN	C6-C5A-C9A	-2.47	116.39	119.11
4	A	401	FMN	C6-C5A-C9A	-2.13	116.76	119.11
4	B	401	FMN	C5A-C9A-N10	-2.02	116.06	117.58
4	A	401	FMN	C1'-C2'-C3'	2.29	116.36	109.82
4	B	401	FMN	C1'-C2'-C3'	3.40	119.54	109.82
4	A	401	FMN	C4-N3-C2	12.08	125.23	115.16
4	B	401	FMN	C4-N3-C2	12.78	125.82	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	FMN	2	0
4	B	401	FMN	1	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	376/402 (93%)	0.35	17 (4%) 37 38	12, 20, 32, 41	9 (2%)
1	B	374/402 (93%)	1.08	67 (17%) 2 2	16, 34, 44, 48	6 (1%)
All	All	750/804 (93%)	0.71	84 (11%) 7 7	12, 26, 41, 48	15 (2%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	318	CYS	11.2
1	A	23	LEU	10.9
1	A	95	VAL	10.3
1	A	280	THR	9.8
1	A	71	SER	8.0
1	B	284	TYR	7.7
1	B	384	LEU	7.4
1	B	289	GLN	6.6
1	B	360	PRO	6.2
1	B	357	LEU	5.7
1	A	286	ALA	5.4
1	A	285	VAL	5.3
1	B	383	PHE	5.2
1	B	376	VAL	5.0
1	B	98	ALA	4.9
1	B	158	TYR	4.6
1	B	306	ARG	4.6
1	A	262	ARG	4.6
1	B	248	MET	4.5
1	B	204	THR	4.2
1	B	251	ASN	4.1
1	B	285	VAL	4.1
1	B	95	VAL	3.9
1	B	120	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	298	GLU	3.8
1	B	121	ALA	3.7
1	A	204	THR	3.6
1	B	122	GLY	3.6
1	B	39	ASN	3.6
1	B	307	THR	3.5
1	B	56	ALA	3.4
1	B	382	PRO	3.4
1	A	287	TYR	3.4
1	B	361	LEU	3.3
1	B	145	THR	3.2
1	B	81	PHE	3.2
1	B	212	ALA	3.2
1	A	269	HIS	3.2
1	A	299	GLU	3.1
1	B	38	LEU	3.0
1	B	157	THR	3.0
1	B	325	GLU	2.9
1	B	368	THR	2.9
1	B	211	LEU	2.9
1	B	268	LEU	2.8
1	B	135	ASN	2.8
1	B	206	GLU	2.8
1	A	346	ILE	2.8
1	B	242	ILE	2.7
1	B	156	GLY	2.6
1	B	83	LYS	2.6
1	B	302	ALA	2.6
1	A	80	ILE	2.6
1	B	356	LYS	2.6
1	B	367	LYS	2.6
1	B	198	ASP	2.6
1	B	286	ALA	2.6
1	B	144	GLY	2.5
1	B	124	ALA	2.5
1	B	250	SER	2.5
1	B	363	LYS	2.5
1	A	135	ASN	2.5
1	B	332	ALA	2.4
1	B	326	LEU	2.4
1	B	335	ASP	2.4
1	B	19	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	160	ILE	2.3
1	B	202	ASP	2.3
1	B	44	ALA	2.2
1	A	385	GLN	2.2
1	B	133	ILE	2.2
1	B	210	SER	2.2
1	B	143	ASP	2.2
1	B	358	ASN	2.2
1	B	359	ALA	2.1
1	B	365	ASN	2.1
1	B	94	ASP	2.1
1	A	296	GLY	2.1
1	B	380	ASP	2.1
1	B	148	ILE	2.1
1	A	121	ALA	2.1
1	B	209	GLY	2.1
1	B	297	SER	2.0
1	B	12	LEU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	CL	A	603	1/1	0.82	0.17	2.64	72,72,72,72	0
2	SO4	B	602	5/5	0.96	0.19	0.64	38,40,40,41	0
4	FMN	B	401	31/31	0.93	0.10	-0.11	20,24,28,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	FMN	A	401	31/31	0.98	0.08	-0.32	10,12,16,18	0
2	SO4	A	601	5/5	0.99	0.10	-0.37	25,25,27,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.