



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:55 pm GMT

PDB ID : 1YHY  
Title : Crystal structure of Arabidopsis thaliana Acetohydroxyacid synthase In Complex With A Sulfonylurea Herbicide, Metsulfuron methyl  
Authors : McCourt, J.A.; Pang, S.S.; King-Scott, J.; Guddat, L.W.; Duggleby, R.G.  
Deposited on : 2005-01-10  
Resolution : 2.70 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 : trunk28620  
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) : recalc28949

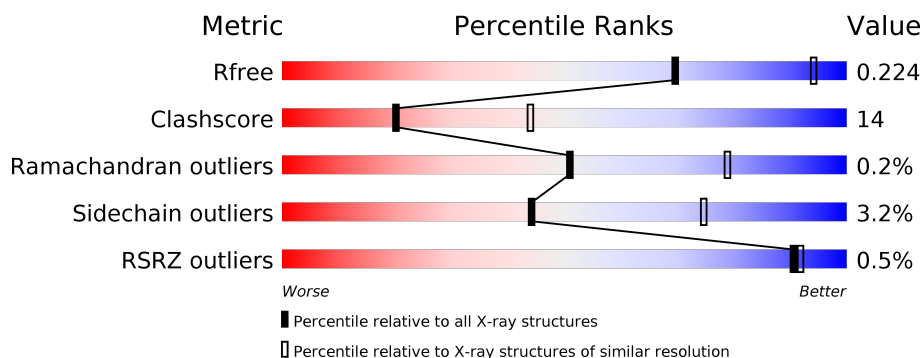
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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. 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	590	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; left: 0; top: -10px; font-size: 8px;">%</div> <div style="position: absolute; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="position: absolute; left: 50%; top: -10px;">74%</div> <div style="position: absolute; left: 90%; top: -10px;">22%</div> <div style="position: absolute; left: 98%; top: -10px;">..</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	1MM	A	695	-	X	-	-
4	NHE	A	696	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4798 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 Acetolactate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	0	0	0
			4419	2803	759	833	24			

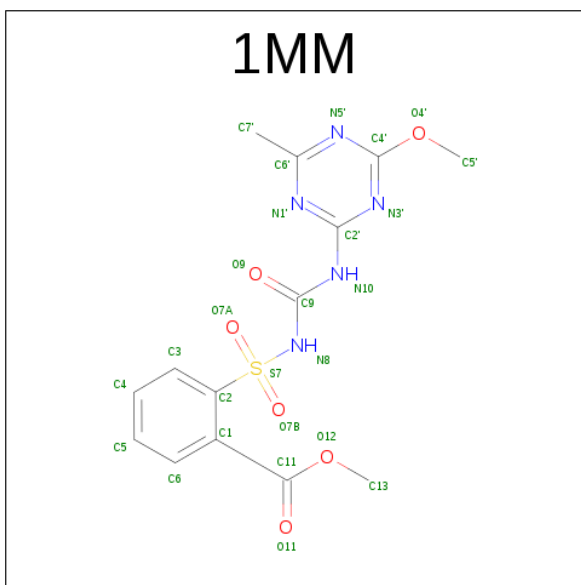
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	340	CSD	CYS	MODIFIED RESIDUE	UNP P17597
A	668	LEU	-	EXPRESSION TAG	UNP P17597
A	669	GLU	-	EXPRESSION TAG	UNP P17597
A	670	HIS	-	EXPRESSION TAG	UNP P17597
A	671	HIS	-	EXPRESSION TAG	UNP P17597
A	672	HIS	-	EXPRESSION TAG	UNP P17597
A	673	HIS	-	EXPRESSION TAG	UNP P17597
A	674	HIS	-	EXPRESSION TAG	UNP P17597
A	675	HIS	-	EXPRESSION TAG	UNP P17597

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

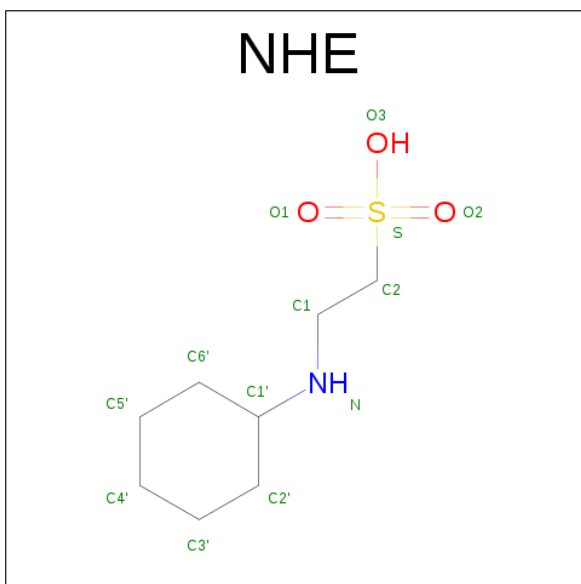
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is METHYL 2-[(4-METHOXY-6-METHYL-1,3,5-TRIAZIN-2-YL)AMINO]CARBONYL}AMINO)SULFONYL]BENZOATE (three-letter code: 1MM) (formula: C<sub>14</sub>H<sub>15</sub>N<sub>5</sub>O<sub>6</sub>S).



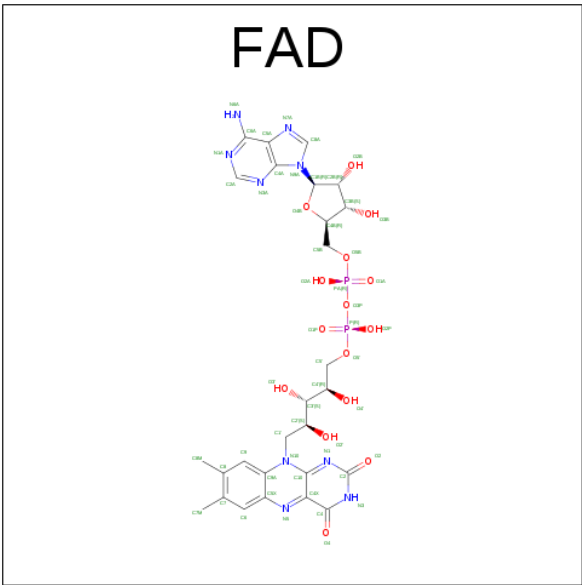
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			26	14	5	6	1		

- Molecule 4 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula:  $C_8H_{17}NO_3S$ ).



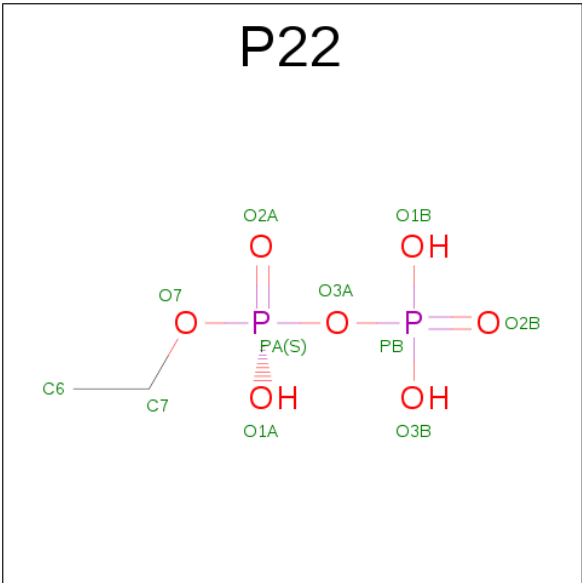
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 6 is ETHYL DIHYDROGEN DIPHOSPHATE (three-letter code: P22) (formula: C<sub>2</sub>H<sub>8</sub>O<sub>7</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	O	P	0	0
			11	2	7	2		

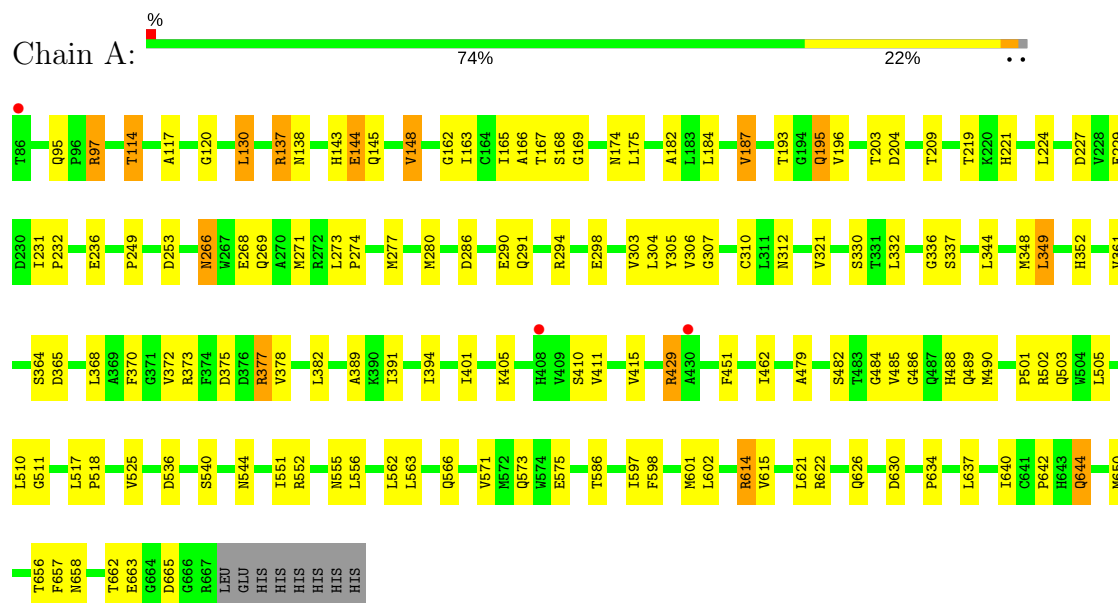
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	275	Total 275	O 275	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 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 ( $RSRZ > 2$ ). 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: Acetolactate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	178.23Å 178.23Å 185.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.70 79.42 – 2.70	Depositor EDS
% Data completeness (in resolution range)	89.8 (50.00-2.70) 89.8 (79.42-2.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 2.69Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.193 , 0.224 0.195 , 0.224	Depositor DCC
$R_{free}$ test set	4341 reflections (10.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.5	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4798	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NHE, MG, CSD, 1MM, P22, FAD

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	0.34	1/4507 (0.0%)	0.59	0/6127

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	336	GLY	C-N	5.01	1.45	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4419	0	4367	125	0
2	A	1	0	0	0	0
3	A	26	0	15	1	0
4	A	13	0	17	1	0
5	A	53	0	31	3	0
6	A	11	0	5	0	0
7	A	275	0	0	10	0
All	All	4798	0	4435	126	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 14.

All (126) 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:195:GLN:HE21	1:A:196:VAL:H	1.07	0.98
1:A:566:GLN:HE22	1:A:598:PHE:H	1.08	0.97
1:A:143:HIS:HD2	1:A:145:GLN:H	1.13	0.97
1:A:195:GLN:HE21	1:A:196:VAL:N	1.63	0.96
1:A:195:GLN:NE2	1:A:196:VAL:H	1.66	0.92
1:A:364:SER:O	1:A:389:ALA:HB2	1.71	0.90
1:A:656:THR:HG22	1:A:658:ASN:H	1.38	0.89
1:A:586:THR:HG23	7:A:4076:HOH:O	1.71	0.88
1:A:117:ALA:H	1:A:138:ASN:HD21	1.29	0.79
1:A:266:ASN:HB3	1:A:269:GLN:HE21	1.49	0.77
1:A:145:GLN:HE21	1:A:544:ASN:HD21	1.29	0.77
1:A:614:ARG:HD2	1:A:640:ILE:HD11	1.70	0.74
1:A:209:THR:HG22	7:A:4193:HOH:O	1.86	0.74
1:A:484:GLY:H	1:A:488:HIS:HE1	1.35	0.73
1:A:373:ARG:HG2	5:A:701:FAD:O1P	1.90	0.72
1:A:332:LEU:CD1	1:A:348:MET:HE1	2.22	0.70
1:A:352:HIS:HB2	1:A:490:MET:CE	2.26	0.66
1:A:566:GLN:NE2	1:A:598:PHE:H	1.90	0.63
1:A:622:ARG:NE	7:A:4003:HOH:O	2.27	0.63
1:A:566:GLN:HE22	1:A:598:PHE:N	1.88	0.63
1:A:304:LEU:HD23	1:A:368:LEU:HB2	1.80	0.63
1:A:552:ARG:O	1:A:552:ARG:HD3	1.98	0.62
1:A:332:LEU:HD12	1:A:348:MET:HE1	1.82	0.62
1:A:182:ALA:HA	1:A:187:VAL:HG13	1.81	0.62
1:A:184:LEU:HD12	1:A:510:LEU:HB2	1.81	0.61
1:A:375:ASP:OD2	1:A:377:ARG:HB2	2.01	0.60
1:A:114:THR:HG21	1:A:525:VAL:HG11	1.83	0.60
1:A:321:VAL:HG12	1:A:344:LEU:HD13	1.83	0.60
1:A:169:GLY:HA2	1:A:209:THR:HG23	1.83	0.59
1:A:144:GLU:HG3	1:A:174:ASN:HB2	1.84	0.59
1:A:332:LEU:HD13	1:A:348:MET:HE1	1.87	0.57
1:A:540:SER:HB3	7:A:4132:HOH:O	2.04	0.57
1:A:277:MET:HA	1:A:280:MET:HG3	1.87	0.57
1:A:562:LEU:HD21	1:A:601:MET:HG3	1.85	0.57
1:A:462:ILE:HG23	1:A:621:LEU:HD22	1.86	0.56
1:A:266:ASN:ND2	1:A:268:GLU:H	2.03	0.56
1:A:117:ALA:HB2	1:A:165:ILE:HB	1.87	0.56
1:A:352:HIS:HB2	1:A:490:MET:HE3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ARG:O	1:A:298:GLU:HG3	2.06	0.55
1:A:365:ASP:C	1:A:389:ALA:HB1	2.27	0.55
1:A:231:ILE:HB	1:A:232:PRO:HD3	1.88	0.55
1:A:571:VAL:O	1:A:575:GLU:HG3	2.06	0.55
1:A:555:ASN:ND2	7:A:4210:HOH:O	2.39	0.55
1:A:484:GLY:N	1:A:488:HIS:HE1	2.04	0.55
1:A:143:HIS:CD2	1:A:145:GLN:H	2.06	0.54
1:A:120:GLY:HA3	1:A:167:THR:HB	1.90	0.54
1:A:337:SER:HA	1:A:501:PRO:HG3	1.88	0.54
1:A:370:PHE:HB3	1:A:415:VAL:HG21	1.89	0.53
1:A:137:ARG:HD2	7:A:4109:HOH:O	2.07	0.53
1:A:502:ARG:HG2	1:A:502:ARG:HH11	1.74	0.53
1:A:332:LEU:HA	1:A:348:MET:HE2	1.90	0.53
1:A:401:ILE:HG21	1:A:410:SER:HB2	1.91	0.52
1:A:321:VAL:CG1	1:A:344:LEU:HD13	2.40	0.52
1:A:163:ILE:HD12	1:A:163:ILE:N	2.25	0.52
1:A:489:GLN:HE22	5:A:701:FAD:HM83	1.75	0.51
1:A:117:ALA:H	1:A:138:ASN:ND2	2.02	0.51
1:A:642:PRO:HB2	1:A:644:GLN:HE21	1.76	0.51
1:A:266:ASN:HD21	1:A:268:GLU:HB2	1.74	0.51
1:A:286:ASP:O	1:A:290:GLU:HG3	2.11	0.51
1:A:391:ILE:HB	7:A:4004:HOH:O	2.10	0.51
1:A:615:VAL:CG2	1:A:637:LEU:HD11	2.42	0.50
1:A:167:THR:HG22	7:A:4159:HOH:O	2.11	0.50
1:A:221:HIS:ND1	4:A:696:NHE:H6'1	2.27	0.50
1:A:394:ILE:HG12	1:A:411:VAL:HB	1.94	0.49
1:A:501:PRO:HA	7:A:4022:HOH:O	2.13	0.49
1:A:307:GLY:HA3	1:A:372:VAL:HG12	1.95	0.49
1:A:227:ASP:OD1	1:A:229:GLU:HB2	2.12	0.49
1:A:306:VAL:HG13	1:A:310:CYS:SG	2.52	0.49
1:A:597:ILE:HD13	1:A:640:ILE:HD11	1.94	0.48
1:A:486:GLY:H	1:A:489:GLN:HE21	1.60	0.48
1:A:597:ILE:HD13	1:A:640:ILE:CD1	2.44	0.48
1:A:120:GLY:HA3	1:A:167:THR:CB	2.44	0.47
1:A:517:LEU:HB3	1:A:518:PRO:HD3	1.95	0.47
1:A:195:GLN:HG3	1:A:253:ASP:OD2	2.14	0.47
1:A:484:GLY:H	1:A:488:HIS:CE1	2.25	0.47
1:A:195:GLN:NE2	1:A:196:VAL:HG22	2.29	0.47
1:A:662:THR:O	1:A:663:GLU:HG2	2.14	0.47
1:A:148:VAL:HG22	1:A:175:LEU:CD2	2.44	0.47
1:A:352:HIS:CB	1:A:490:MET:HE3	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:THR:C	1:A:663:GLU:HG2	2.34	0.47
1:A:656:THR:CG2	1:A:657:PHE:N	2.77	0.47
1:A:117:ALA:CB	1:A:165:ILE:HB	2.45	0.47
1:A:556:LEU:O	1:A:634:PRO:HG3	2.15	0.47
1:A:203:THR:O	1:A:204:ASP:HB2	2.14	0.47
1:A:644:GLN:O	1:A:665:ASP:HB2	2.14	0.47
1:A:656:THR:HG22	1:A:657:PHE:N	2.29	0.47
1:A:162:GLY:C	1:A:163:ILE:HD12	2.36	0.46
1:A:488:HIS:HB2	1:A:563:LEU:HD12	1.97	0.46
1:A:517:LEU:HD11	1:A:551:ILE:CD1	2.45	0.46
1:A:305:TYR:CE2	1:A:372:VAL:HG21	2.51	0.46
1:A:332:LEU:HA	1:A:348:MET:CE	2.46	0.45
1:A:219:THR:HA	1:A:249:PRO:HG2	1.98	0.45
1:A:349:LEU:HD13	1:A:378:VAL:HG13	1.99	0.45
1:A:502:ARG:NH1	1:A:502:ARG:HG2	2.30	0.45
3:A:695:1MM:H5'2	5:A:701:FAD:HM72	1.98	0.45
1:A:485:VAL:HG21	1:A:511:GLY:C	2.37	0.45
1:A:95:GLN:O	1:A:97:ARG:NH1	2.49	0.45
1:A:566:GLN:NE2	1:A:597:ILE:HA	2.32	0.45
1:A:224:LEU:HA	1:A:253:ASP:HB3	1.99	0.44
1:A:236:GLU:HG2	1:A:271:MET:SD	2.58	0.44
1:A:349:LEU:HD23	1:A:361:VAL:HG21	1.99	0.44
1:A:144:GLU:HG2	1:A:144:GLU:H	1.45	0.44
1:A:195:GLN:HG2	1:A:253:ASP:OD1	2.17	0.44
1:A:382:LEU:HD22	1:A:405:LYS:HG2	1.99	0.44
1:A:195:GLN:HE21	1:A:195:GLN:CA	2.28	0.43
1:A:312:ASN:HD21	1:A:502:ARG:HH21	1.66	0.43
1:A:330:SER:O	1:A:348:MET:HA	2.18	0.43
1:A:349:LEU:H	1:A:349:LEU:HD12	1.82	0.43
1:A:552:ARG:C	1:A:552:ARG:HD3	2.35	0.43
1:A:166:ALA:O	1:A:193:THR:HA	2.19	0.43
1:A:479:ALA:O	1:A:503:GLN:HG2	2.19	0.42
1:A:602:LEU:HD11	1:A:614:ARG:HB2	2.01	0.42
1:A:303:VAL:CG2	1:A:364:SER:HB3	2.49	0.42
1:A:168:SER:HB2	7:A:4137:HOH:O	2.19	0.42
1:A:130:LEU:HD12	1:A:130:LEU:HA	1.93	0.41
1:A:195:GLN:CA	1:A:195:GLN:NE2	2.84	0.41
1:A:377:ARG:N	1:A:377:ARG:HD2	2.32	0.41
1:A:451:PHE:CD1	1:A:451:PHE:N	2.88	0.41
1:A:485:VAL:HA	1:A:489:GLN:NE2	2.36	0.41
1:A:144:GLU:HG3	1:A:174:ASN:CB	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:GLN:O	1:A:294:ARG:HB3	2.21	0.41
1:A:482:SER:HA	1:A:505:LEU:O	2.20	0.41
1:A:626:GLN:HG3	1:A:630:ASP:OD2	2.21	0.41
1:A:573:GLN:HE21	1:A:650:MET:CE	2.34	0.41
1:A:195:GLN:HE21	1:A:195:GLN:C	2.22	0.40
1:A:273:LEU:N	1:A:274:PRO:CD	2.84	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	579/590 (98%)	560 (97%)	18 (3%)	1 (0%)	51 79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	429	ARG

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	468/486 (96%)	453 (97%)	15 (3%)	44 75

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ARG
1	A	114	THR
1	A	130	LEU
1	A	137	ARG
1	A	144	GLU
1	A	148	VAL
1	A	187	VAL
1	A	195	GLN
1	A	266	ASN
1	A	349	LEU
1	A	377	ARG
1	A	429	ARG
1	A	536	ASP
1	A	614	ARG
1	A	644	GLN

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	138	ASN
1	A	143	HIS
1	A	145	GLN
1	A	174	ASN
1	A	195	GLN
1	A	261	GLN
1	A	266	ASN
1	A	269	GLN
1	A	291	GLN
1	A	312	ASN
1	A	363	HIS
1	A	488	HIS
1	A	489	GLN
1	A	566	GLN
1	A	643	HIS
1	A	644	GLN
1	A	658	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	CSD	A	340	1	4,7,8	0.89	0	2,8,10	5.56	1 (50%)

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	CSD	A	340	1	-	0/2/6/8	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( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	340	CSD	OD1-SG-CB	7.70	120.04	105.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	$\# Z  > 2$
3	1MM	A	695	-	27,27,27	4.23	20 (74%)	36,38,38	3.98	17 (47%)
4	NHE	A	696	-	13,13,13	3.25	6 (46%)	15,17,17	2.74	5 (33%)
5	FAD	A	701	-	51,58,58	2.77	26 (50%)	54,89,89	2.14	11 (20%)
6	P22	A	702	2	9,10,10	1.57	3 (33%)	9,15,15	1.73	2 (22%)

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
3	1MM	A	695	-	-	0/23/23/23	0/2/2/2
4	NHE	A	696	-	-	0/7/15/15	0/1/1/1
5	FAD	A	701	-	-	0/28/50/50	0/6/6/6
6	P22	A	702	2	-	0/10/10/10	0/0/0/0

All (55) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	695	1MM	C2'-N10	-4.74	1.33	1.38
5	A	701	FAD	C5'-C4'	-3.02	1.47	1.51
3	A	695	1MM	C9-N10	-2.80	1.31	1.37
5	A	701	FAD	P-O2P	-2.52	1.42	1.55
3	A	695	1MM	C9-N8	-2.47	1.35	1.39
4	A	696	NHE	C3'-C2'	-2.34	1.47	1.53
5	A	701	FAD	C8A-N7A	-2.28	1.30	1.34
5	A	701	FAD	O2B-C2B	-2.27	1.37	1.43
5	A	701	FAD	PA-O2A	-2.22	1.44	1.55
5	A	701	FAD	PA-O5B	-2.12	1.50	1.59
6	A	702	P22	PA-O1A	-2.11	1.44	1.55
6	A	702	P22	PA-O2A	-2.10	1.43	1.50
6	A	702	P22	PB-O1B	-2.03	1.46	1.54
5	A	701	FAD	C6A-N1A	2.01	1.46	1.37
5	A	701	FAD	C9-C8	2.02	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	695	1MM	O9-C9	2.02	1.27	1.23
4	A	696	NHE	C6'-C1'	2.06	1.57	1.51
5	A	701	FAD	C5X-N5	2.09	1.38	1.35
3	A	695	1MM	C1-C11	2.20	1.55	1.50
5	A	701	FAD	C8-C7	2.43	1.47	1.41
3	A	695	1MM	C2'-N3'	2.51	1.43	1.34
3	A	695	1MM	S7-N8	2.52	1.69	1.64
3	A	695	1MM	C5-C4	2.60	1.44	1.38
5	A	701	FAD	C9A-C5X	2.61	1.47	1.42
5	A	701	FAD	C6A-C5A	2.62	1.56	1.42
5	A	701	FAD	C3B-C4B	2.79	1.60	1.53
4	A	696	NHE	C2'-C1'	2.91	1.59	1.51
3	A	695	1MM	C2'-N1'	2.91	1.44	1.34
5	A	701	FAD	C1'-N10	3.14	1.51	1.48
5	A	701	FAD	C4X-C10	3.26	1.46	1.41
5	A	701	FAD	C9A-N10	3.27	1.43	1.38
3	A	695	1MM	C2-S7	3.29	1.82	1.77
5	A	701	FAD	C4-C4X	3.30	1.47	1.41
3	A	695	1MM	C5-C6	3.31	1.45	1.38
5	A	701	FAD	C4X-N5	3.67	1.38	1.33
5	A	701	FAD	C5A-C4A	3.98	1.49	1.40
5	A	701	FAD	O4'-C4'	4.07	1.52	1.43
5	A	701	FAD	C10-N1	4.42	1.39	1.33
5	A	701	FAD	O3'-C3'	4.49	1.53	1.43
3	A	695	1MM	O12-C11	4.69	1.44	1.33
3	A	695	1MM	C6-C1	4.69	1.47	1.39
5	A	701	FAD	C2A-N3A	4.70	1.40	1.32
3	A	695	1MM	C4-C3	5.09	1.48	1.38
5	A	701	FAD	C4-N3	5.14	1.42	1.33
3	A	695	1MM	C6'-N5'	5.19	1.43	1.34
4	A	696	NHE	O3-S	5.52	1.66	1.47
3	A	695	1MM	C4'-N3'	5.71	1.41	1.33
4	A	696	NHE	O2-S	6.02	1.62	1.45
5	A	701	FAD	C2A-N1A	6.33	1.45	1.33
4	A	696	NHE	O1-S	6.34	1.63	1.45
3	A	695	1MM	C1-C2	6.44	1.47	1.40
3	A	695	1MM	C6'-N1'	6.50	1.46	1.34
5	A	701	FAD	C4A-N3A	8.61	1.48	1.35
3	A	695	1MM	C4'-N5'	8.88	1.46	1.33
3	A	695	1MM	C3-C2	9.30	1.49	1.39

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	695	1MM	C3-C2-S7	-10.22	104.79	117.34
3	A	695	1MM	C2-C1-C11	-6.33	115.36	124.19
5	A	701	FAD	N3A-C2A-N1A	-5.93	123.69	128.86
3	A	695	1MM	N3'-C4'-N5'	-4.90	120.95	127.80
3	A	695	1MM	N3'-C2'-N1'	-4.86	118.88	126.23
5	A	701	FAD	C4X-C4-N3	-4.79	116.66	123.48
3	A	695	1MM	N8-C9-N10	-3.93	108.91	114.75
3	A	695	1MM	N5'-C6'-N1'	-3.67	118.18	125.60
3	A	695	1MM	O12-C11-C1	-3.48	106.48	112.30
5	A	701	FAD	C4X-C10-N10	-3.17	118.32	120.52
4	A	696	NHE	C5'-C6'-C1'	-2.99	106.71	111.11
3	A	695	1MM	O7B-S7-O7A	-2.72	116.07	119.55
5	A	701	FAD	C4-C4X-C10	-2.65	117.82	119.96
4	A	696	NHE	O3-S-O1	-2.45	105.75	111.37
5	A	701	FAD	O3'-C3'-C4'	-2.13	103.54	108.82
5	A	701	FAD	C1'-C2'-C3'	2.03	115.62	109.82
6	A	702	P22	O3B-PB-O1B	2.05	115.88	107.61
3	A	695	1MM	C4'-N5'-C6'	2.06	119.75	114.30
5	A	701	FAD	C5B-C4B-C3B	2.46	124.65	115.29
3	A	695	1MM	O7A-S7-C2	2.82	112.25	107.60
4	A	696	NHE	C2-C1-N	2.89	119.61	111.21
5	A	701	FAD	O2B-C2B-C3B	2.90	121.11	111.83
5	A	701	FAD	O2B-C2B-C1B	2.98	120.92	111.61
4	A	696	NHE	O2-S-C2	3.05	109.41	106.79
3	A	695	1MM	C7'-C6'-N1'	3.38	122.74	117.20
3	A	695	1MM	C6-C1-C11	3.70	126.33	118.67
3	A	695	1MM	O12-C11-O11	3.74	131.07	123.44
3	A	695	1MM	O9-C9-N10	3.83	130.10	123.58
6	A	702	P22	O7-C7-C6	4.10	137.31	111.19
3	A	695	1MM	O7B-S7-C2	4.52	115.07	107.60
5	A	701	FAD	C1B-N9A-C4A	5.97	136.95	126.64
5	A	701	FAD	C4-N3-C2	7.70	121.89	115.16
4	A	696	NHE	O1-S-C2	8.20	113.84	106.79
3	A	695	1MM	C4'-N3'-C2'	10.02	120.61	112.83
3	A	695	1MM	C5'-O4'-C4'	11.23	136.81	117.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	695	1MM	1	0
4	A	696	NHE	1	0
5	A	701	FAD	3	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	581/590 (98%)	-0.34	3 (0%) 90 92	24, 40, 64, 83	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	86	THR	5.3
1	A	430	ALA	2.4
1	A	408	HIS	2.3

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

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	CSD	A	340	8/9	0.85	0.36	-	51,53,54,55	0

### 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	NHE	A	696	13/13	0.97	0.20	2.99	37,39,41,44	0
3	1MM	A	695	26/26	0.98	0.17	1.99	36,38,42,44	0
5	FAD	A	701	53/53	0.98	0.15	0.79	22,33,36,42	0
6	P22	A	702	11/11	0.97	0.14	0.20	54,54,56,57	0
2	MG	A	699	1/1	0.99	0.06	-5.51	48,48,48,48	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.