



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:46 PM GMT

PDB ID : 1YKJ  
Title : A45G p-hydroxybenzoate hydroxylase with p-hydroxybenzoate bound  
Authors : Cole, L.J.; Gatti, D.L.; Entsch, B.; Ballou, D.P.  
Deposited on : 2005-01-18  
Resolution : 2.00 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

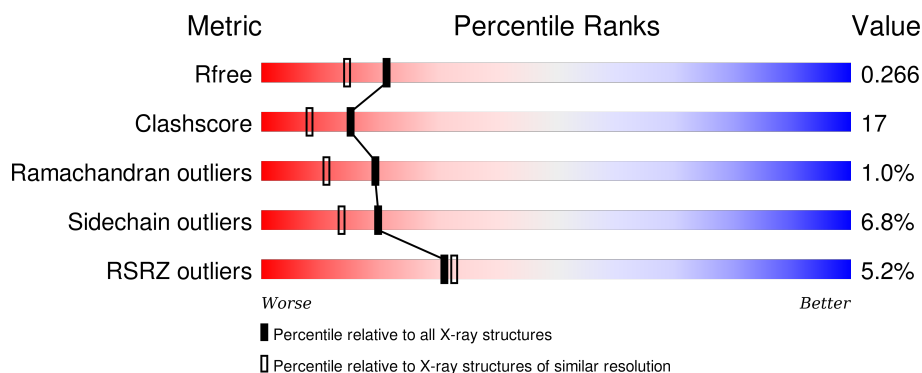
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	394	<div> <div>7%</div> <div>69%</div> <div>27%</div> <div>• •</div> </div>
1	B	394	<div> <div>4%</div> <div>73%</div> <div>23%</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	SO4	A	709	-	-	-	X
2	SO4	B	702	-	-	X	-
2	SO4	B	707	-	-	-	X
5	PSL	B	714	-	-	-	X
5	PSL	B	715	-	-	-	X

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6958 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 P-hydroxybenzoate hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	394	Total	C	N	O	S	0	0	0
			3124	1974	563	576	11			
1	B	392	Total	C	N	O	S	0	0	0
			3088	1954	552	572	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1045	GLY	ALA	ENGINEERED	UNP P20586
B	2045	GLY	ALA	ENGINEERED	UNP P20586

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



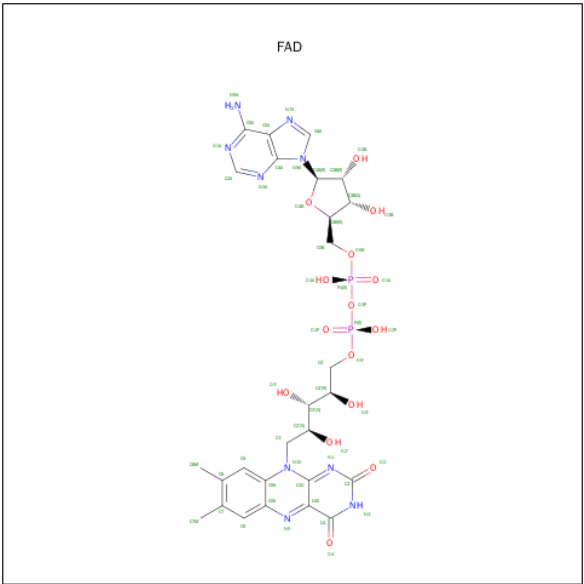
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

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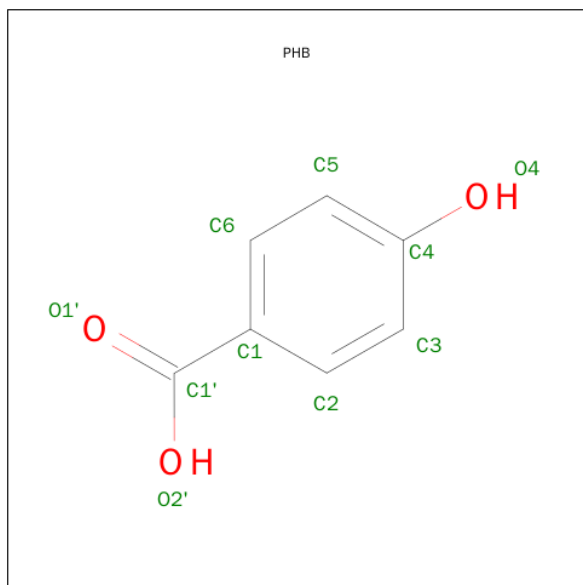
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total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

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



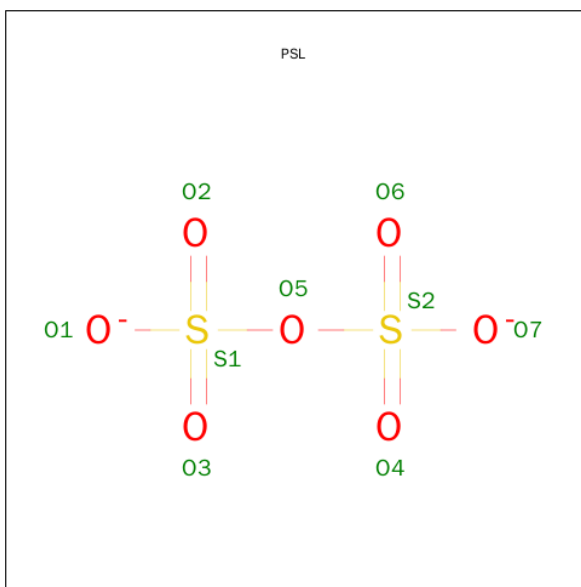
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is P-HYDROXYBENZOIC ACID (three-letter code: PHB) (formula:  $C_7H_6O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	7	3		
4	B	1	Total	C	O	0	0
			10	7	3		

- Molecule 5 is PYROSULFATE (three-letter code: PSL) (formula:  $O_7S_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			9	7	2		
5	B	1	Total	O	S	0	0
			9	7	2		

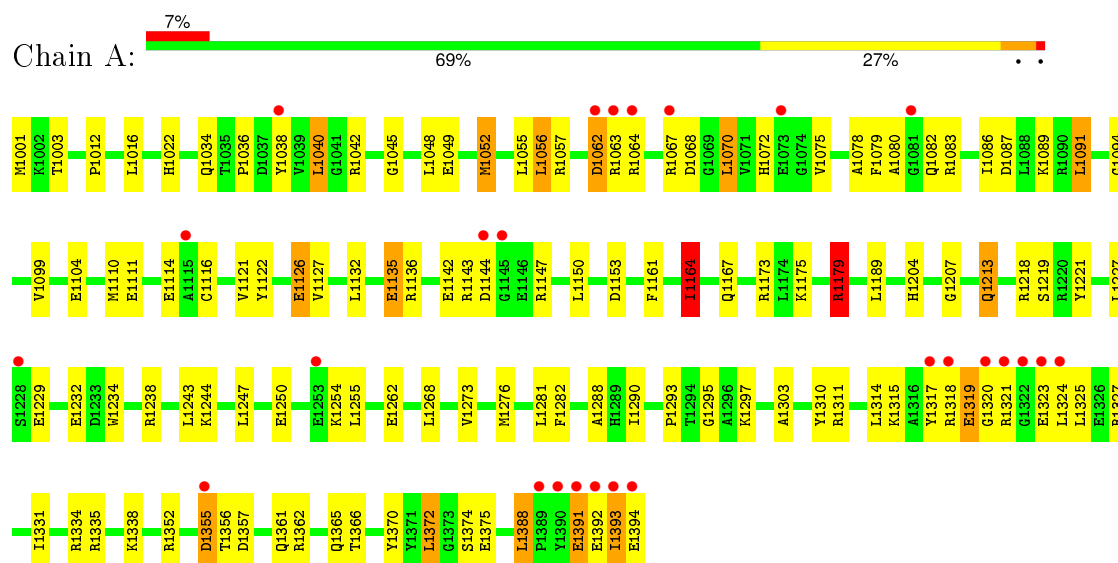
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	232	Total	O	0	0
			232	232		
6	B	310	Total	O	0	0
			310	310		

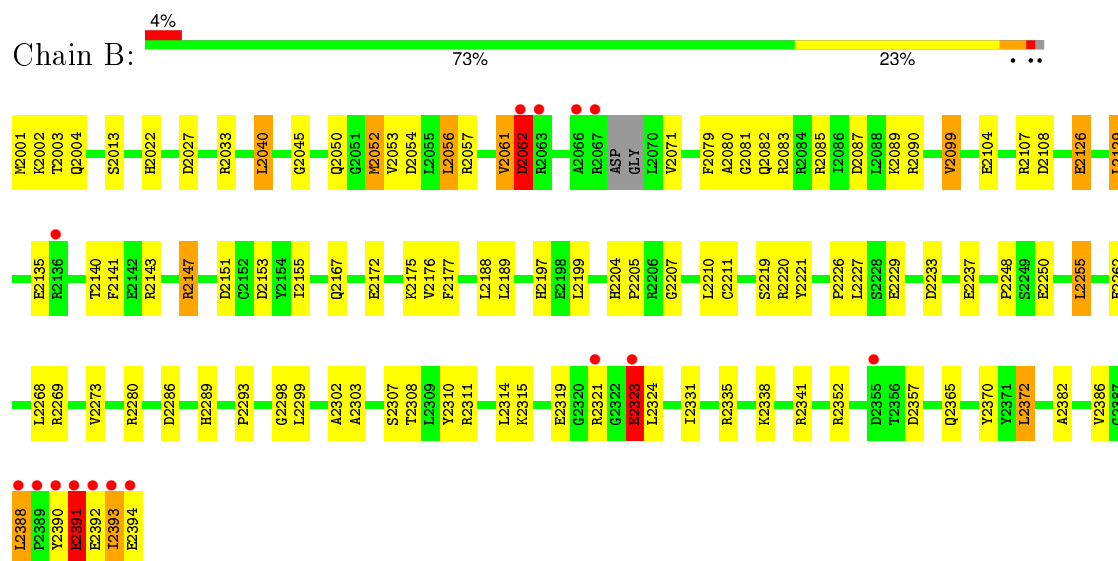
### 3 Residue-property plots

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: P-hydroxybenzoate hydroxylase



#### • Molecule 1: P-hydroxybenzoate hydroxylase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.86 Å   85.90 Å   146.07 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	31.51 – 2.00 31.59 – 1.74	Depositor EDS
% Data completeness (in resolution range)	99.7 (31.51-2.00) 83.9 (31.59-1.74)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 1.74 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.201   ,   0.265 0.202   ,   0.266	Depositor DCC
$R_{free}$ test set	6131 reflections (10.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 66.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	6 of 76003 reflections (0.008%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6958	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.18 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.8410e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PHB, FAD, PSL, 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	0.71	0/3189	0.84	2/4314 (0.0%)
1	B	0.78	0/3152	0.92	3/4267 (0.1%)
All	All	0.75	0/6341	0.88	5/8581 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2147	ARG	NE-CZ-NH2	12.15	126.38	120.30
1	B	2147	ARG	NE-CZ-NH1	-7.37	116.61	120.30
1	A	1179	ARG	NE-CZ-NH1	-7.00	116.80	120.30
1	B	2255	LEU	CA-CB-CG	6.30	129.80	115.30
1	A	1164	ILE	CG1-CB-CG2	-5.54	99.22	111.40

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	3124	0	3115	121	1
1	B	3088	0	3058	103	1
2	A	25	0	0	2	0
2	B	35	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	53	0	31	6	0
3	B	53	0	31	2	0
4	A	10	0	5	0	0
4	B	10	0	5	0	0
5	B	18	0	0	1	0
6	A	232	0	0	21	0
6	B	310	0	0	21	0
All	All	6958	0	6245	221	1

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 17.

All (221) 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:1016:LEU:HD21	1:A:1055:LEU:HD23	1.35	1.08
1:B:2061:VAL:HG13	1:B:2062:ASP:H	1.16	1.07
1:B:2140:THR:HB	1:B:2147:ARG:HD2	1.45	0.98
1:B:2061:VAL:HG13	1:B:2062:ASP:N	1.80	0.97
1:B:2237:GLU:HB2	6:B:3294:HOH:O	1.66	0.95
1:A:1063:ARG:HH12	1:A:1067:ARG:HH12	1.17	0.92
1:A:1207:GLY:HA2	1:A:1352:ARG:HG2	1.56	0.86
1:A:1175:LYS:HD3	6:A:3551:HOH:O	1.78	0.83
1:B:2391:GLU:HG3	1:B:2392:GLU:N	1.93	0.83
1:B:2393:ILE:HG22	1:B:2394:GLU:H	1.43	0.83
1:A:1393:ILE:HD11	6:A:3291:HOH:O	1.80	0.82
1:A:1327:ARG:HG2	1:A:1327:ARG:HH21	1.42	0.82
1:B:2175:LYS:HD2	1:B:2177:PHE:CZ	2.15	0.81
1:A:1126:GLU:HB2	1:A:1147:ARG:HH22	1.47	0.80
1:A:1063:ARG:HH22	1:A:1067:ARG:CZ	1.97	0.77
1:A:1319:GLU:HB3	1:A:1321:ARG:HG2	1.68	0.76
1:A:1079:PHE:O	1:A:1082:GLN:HG2	1.87	0.75
1:B:2308:THR:HG23	1:B:2393:ILE:HG23	1.68	0.75
1:A:1318:ARG:O	1:A:1319:GLU:HG3	1.87	0.73
1:B:2370:TYR:HB2	6:B:3396:HOH:O	1.90	0.72
1:A:1142:GLU:HG3	1:A:1147:ARG:HD2	1.71	0.72
1:A:1063:ARG:HH22	1:A:1067:ARG:NH2	1.88	0.72
1:B:2061:VAL:CG1	1:B:2062:ASP:N	2.51	0.71
1:B:2393:ILE:HG22	1:B:2394:GLU:N	2.05	0.71
1:B:2310:TYR:HD2	1:B:2311:ARG:NH2	1.90	0.70
1:B:2175:LYS:HE3	6:B:3269:HOH:O	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2207:GLY:HA2	1:B:2352:ARG:HG2	1.74	0.69
1:B:2079:PHE:CE2	1:B:2372:LEU:HD23	2.28	0.69
1:A:1331:ILE:HD13	1:A:1393:ILE:HA	1.75	0.69
1:A:1042:ARG:NH1	3:A:1395:FAD:H3B	2.08	0.69
1:B:2323:GLU:N	1:B:2323:GLU:CD	2.46	0.69
1:A:1127:VAL:HG23	6:A:3062:HOH:O	1.91	0.69
1:B:2061:VAL:HG21	1:B:2108:ASP:HB3	1.74	0.68
1:A:1042:ARG:NH1	3:A:1395:FAD:O3B	2.26	0.68
1:A:1244:LYS:NZ	6:A:3557:HOH:O	2.24	0.68
1:A:1232:GLU:CD	1:A:1232:GLU:H	1.97	0.68
1:B:2083:ARG:HD3	6:B:3155:HOH:O	1.94	0.67
1:B:2391:GLU:HB3	6:B:3259:HOH:O	1.94	0.67
1:A:1042:ARG:HH12	3:A:1395:FAD:C3B	2.07	0.67
1:B:2189:LEU:HD12	1:B:2219:SER:O	1.95	0.66
1:B:2323:GLU:CD	1:B:2323:GLU:H	1.99	0.66
1:A:1042:ARG:NH1	3:A:1395:FAD:C3B	2.58	0.66
1:A:1338:LYS:HD3	1:A:1388:LEU:HD23	1.78	0.66
1:A:1063:ARG:NH1	1:A:1067:ARG:HH12	1.93	0.65
1:B:2061:VAL:CG2	1:B:2108:ASP:HB3	2.27	0.64
1:B:2079:PHE:O	1:B:2082:GLN:HG2	1.97	0.64
1:A:1135:GLU:H	1:A:1135:GLU:CD	2.00	0.64
1:B:2226:PRO:HG2	1:B:2229:GLU:HG2	1.80	0.63
1:A:1366:THR:HG23	6:A:3290:HOH:O	1.98	0.62
1:A:1052:MET:HE3	1:A:1303:ALA:HB2	1.82	0.61
1:A:1392:GLU:O	1:A:1393:ILE:HB	2.00	0.61
1:B:2197:HIS:ND1	6:B:3412:HOH:O	2.31	0.61
1:B:2081:GLY:C	6:B:3421:HOH:O	2.39	0.61
1:A:1315:LYS:O	1:A:1319:GLU:HB2	2.01	0.61
1:B:2321:ARG:HH11	1:B:2324:LEU:HD21	1.65	0.61
1:A:1179:ARG:NH1	1:B:2357:ASP:OD1	2.30	0.61
1:B:2090:ARG:HG3	6:B:3323:HOH:O	2.00	0.60
1:B:2315:LYS:HG3	1:B:2394:GLU:OE2	2.00	0.60
1:B:2001:MET:N	6:B:3262:HOH:O	2.35	0.59
1:B:2321:ARG:HB3	1:B:2323:GLU:OE2	2.01	0.59
1:B:2033:ARG:NH2	5:B:715:PSL:O2	2.36	0.59
1:B:2393:ILE:CG2	1:B:2394:GLU:H	2.13	0.58
1:B:2079:PHE:HE2	1:B:2372:LEU:HD23	1.67	0.58
1:A:1063:ARG:HH22	1:A:1067:ARG:NH1	2.00	0.58
1:A:1319:GLU:CB	1:A:1321:ARG:HG2	2.32	0.58
1:A:1072:HIS:CE1	1:A:1213:GLN:OE1	2.57	0.58
1:A:1075:VAL:HG12	1:A:1086:ILE:HB	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2002:LYS:HD2	1:B:2151:ASP:HB2	1.86	0.57
1:A:1391:GLU:HG2	1:A:1392:GLU:H	1.70	0.57
1:A:1045:GLY:HA3	3:A:1395:FAD:N5	2.20	0.57
1:A:1057:ARG:HA	1:A:1062:ASP:HB3	1.88	0.56
1:A:1391:GLU:CG	1:A:1392:GLU:H	2.18	0.56
1:A:1164:ILE:HG13	1:A:1164:ILE:O	2.05	0.56
1:A:1268:LEU:HG	1:A:1293:PRO:HD2	1.86	0.56
1:B:2143:ARG:HA	6:B:3380:HOH:O	2.04	0.55
1:B:2071:VAL:HG22	1:B:2099:VAL:HG12	1.89	0.55
1:A:1327:ARG:CG	1:A:1327:ARG:HH21	2.17	0.55
1:A:1334:ARG:HE	1:A:1391:GLU:CD	2.10	0.55
1:B:2226:PRO:HG2	1:B:2229:GLU:CG	2.36	0.55
1:A:1334:ARG:NE	1:A:1391:GLU:OE1	2.39	0.55
1:A:1001:MET:N	6:A:3284:HOH:O	2.40	0.54
1:A:1089:LYS:HG2	1:A:1094:GLY:HA2	1.88	0.54
1:B:2054:ASP:CG	1:B:2057:ARG:HH11	2.10	0.54
1:B:2331:ILE:HG21	1:B:2393:ILE:HA	1.90	0.54
1:B:2054:ASP:OD2	1:B:2057:ARG:NH1	2.39	0.54
1:B:2061:VAL:CG1	1:B:2062:ASP:H	1.90	0.54
1:A:1335:ARG:NH2	6:A:3275:HOH:O	2.41	0.54
1:A:1179:ARG:HA	1:A:1179:ARG:HE	1.73	0.53
1:B:2382:ALA:O	1:B:2386:VAL:HG22	2.08	0.53
1:B:2002:LYS:HG3	1:B:2003:THR:N	2.23	0.53
1:A:1189:LEU:HD12	1:A:1219:SER:O	2.08	0.53
1:B:2129:LEU:HG	1:B:2155:ILE:HD13	1.90	0.53
1:A:1366:THR:HG22	1:B:2341:ARG:HD3	1.90	0.53
1:B:2204:HIS:CG	1:B:2205:PRO:HD2	2.44	0.53
1:A:1042:ARG:NH2	2:A:708:SO4:O2	2.41	0.53
1:A:1048:LEU:HD22	1:A:1052:MET:HG2	1.91	0.53
1:B:2135:GLU:HB3	6:B:3541:HOH:O	2.09	0.52
1:B:2140:THR:HB	1:B:2147:ARG:CD	2.29	0.52
1:A:1064:ARG:NH1	1:A:1111:GLU:OE2	2.42	0.52
1:B:2176:VAL:HG22	1:B:2273:VAL:HG12	1.91	0.52
1:A:1003:THR:HG22	1:A:1150:LEU:HD11	1.91	0.52
1:A:1040:LEU:HD13	1:A:1110:MET:SD	2.49	0.52
1:A:1052:MET:HE3	1:A:1303:ALA:CB	2.39	0.52
1:B:2310:TYR:CD2	1:B:2311:ARG:NH2	2.74	0.51
1:A:1311:ARG:HG3	1:A:1311:ARG:HH21	1.75	0.51
1:B:2126:GLU:HB3	1:B:2147:ARG:HH12	1.75	0.51
1:B:2056:LEU:O	1:B:2061:VAL:HG12	2.10	0.51
1:A:1034:GLN:HG3	1:A:1038:TYR:CD1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2079:PHE:CE2	1:B:2372:LEU:CD2	2.93	0.51
1:A:1262:GLU:OE1	2:A:709:SO4:O4	2.29	0.51
1:A:1331:ILE:HD11	1:A:1394:GLU:H	1.76	0.51
1:A:1321:ARG:HH21	1:A:1321:ARG:HG3	1.75	0.51
1:B:2233:ASP:OD2	6:B:3016:HOH:O	2.18	0.50
1:B:2172:GLU:HB2	6:B:3095:HOH:O	2.11	0.50
1:B:2140:THR:CB	1:B:2147:ARG:HH21	2.24	0.50
1:A:1079:PHE:CE2	1:A:1372:LEU:HD23	2.46	0.50
1:A:1063:ARG:HH12	1:A:1067:ARG:NH1	1.98	0.50
1:B:2319:GLU:O	1:B:2321:ARG:HG3	2.12	0.50
1:A:1243:LEU:O	1:A:1247:LEU:HG	2.12	0.50
1:B:2087:ASP:OD1	1:B:2090:ARG:NH1	2.45	0.50
1:A:1089:LYS:CG	1:A:1094:GLY:HA2	2.41	0.49
1:A:1229:GLU:HA	6:A:3384:HOH:O	2.11	0.49
1:B:2268:LEU:HG	1:B:2293:PRO:HD2	1.93	0.49
1:B:2391:GLU:HG3	1:B:2392:GLU:H	1.77	0.48
1:A:1318:ARG:O	1:A:1319:GLU:CG	2.60	0.48
1:B:2085:ARG:NH2	1:B:2087:ASP:OD2	2.46	0.48
1:B:2107:ARG:HD2	6:B:3271:HOH:O	2.11	0.48
1:A:1234:TRP:CZ3	1:A:1238:ARG:HG2	2.48	0.48
1:A:1121:VAL:CG1	1:A:1143:ARG:HD2	2.43	0.48
1:B:2393:ILE:CG2	1:B:2394:GLU:N	2.74	0.48
1:A:1167:GLN:OE1	1:A:1167:GLN:HA	2.14	0.48
1:A:1335:ARG:HG3	6:A:3558:HOH:O	2.14	0.47
1:A:1034:GLN:HB3	1:A:1038:TYR:HB3	1.95	0.47
1:A:1126:GLU:HB2	1:A:1147:ARG:NH2	2.23	0.47
1:A:1121:VAL:HG13	1:A:1143:ARG:HD2	1.96	0.47
1:A:1132:LEU:HD22	1:A:1281:LEU:HB2	1.97	0.47
1:B:2153:ASP:O	1:B:2280:ARG:NH2	2.43	0.47
1:B:2022:HIS:HA	6:B:3367:HOH:O	2.14	0.47
1:A:1063:ARG:NH2	1:A:1067:ARG:NH2	2.60	0.47
1:A:1063:ARG:HH21	1:A:1063:ARG:HG2	1.78	0.47
1:A:1153:ASP:HB2	1:A:1317:TYR:OH	2.14	0.47
1:A:1204:HIS:O	1:A:1352:ARG:HD3	2.15	0.46
1:B:2167:GLN:HA	1:B:2167:GLN:NE2	2.30	0.46
1:B:2126:GLU:HB3	1:B:2147:ARG:NH1	2.29	0.46
1:A:1179:ARG:HA	1:A:1179:ARG:NE	2.30	0.46
1:A:1310:TYR:HD2	1:A:1311:ARG:NH2	2.13	0.46
1:B:2052:MET:HG2	1:B:2303:ALA:CB	2.45	0.46
1:A:1250:GLU:OE2	1:A:1250:GLU:N	2.42	0.46
1:A:1070:LEU:N	1:A:1070:LEU:CD1	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2220:ARG:NH2	1:B:2262:GLU:OE2	2.49	0.46
1:A:1099:VAL:HG11	1:A:1213:GLN:HG2	1.98	0.45
1:A:1067:ARG:HG2	1:A:1068:ASP:OD2	2.15	0.45
1:B:2321:ARG:C	1:B:2323:GLU:OE2	2.55	0.45
1:A:1143:ARG:O	1:A:1144:ASP:OD1	2.34	0.45
1:B:2061:VAL:HG23	6:B:3123:HOH:O	2.16	0.45
1:A:1040:LEU:CD1	1:A:1110:MET:SD	3.05	0.45
1:B:2175:LYS:HG2	6:B:3343:HOH:O	2.16	0.45
1:B:2061:VAL:HG22	1:B:2062:ASP:N	2.31	0.45
1:A:1355:ASP:N	6:A:3224:HOH:O	2.45	0.45
1:A:1083:ARG:HD3	6:A:3547:HOH:O	2.17	0.45
1:B:2204:HIS:ND1	1:B:2205:PRO:HD2	2.31	0.45
1:B:2335:ARG:NH2	6:B:3208:HOH:O	2.42	0.45
1:B:2286:ASP:HA	1:B:2289:HIS:O	2.17	0.45
1:A:1049:GLU:HB2	6:A:3231:HOH:O	2.16	0.45
1:B:2061:VAL:O	1:B:2062:ASP:C	2.55	0.44
1:A:1078:ALA:HA	1:A:1082:GLN:O	2.17	0.44
1:A:1391:GLU:CG	1:A:1392:GLU:N	2.80	0.44
1:A:1327:ARG:NH2	1:A:1327:ARG:HG2	2.19	0.44
1:A:1136:ARG:HB2	6:A:3405:HOH:O	2.17	0.44
1:B:2040:LEU:HA	1:B:2040:LEU:HD12	1.86	0.44
1:A:1243:LEU:HG	1:A:1247:LEU:HD11	2.00	0.44
1:A:1219:SER:HB3	1:A:1221:TYR:CE2	2.52	0.44
1:B:2298:GLY:HA3	3:B:2395:FAD:H1'2	2.00	0.44
1:A:1362:ARG:HG3	1:B:2177:PHE:CE1	2.52	0.44
1:B:2090:ARG:HB2	6:B:3323:HOH:O	2.18	0.43
1:B:2204:HIS:CE1	1:B:2205:PRO:HD2	2.52	0.43
1:A:1276:MET:HG2	1:A:1288:ALA:HB1	2.00	0.43
1:A:1392:GLU:O	1:A:1393:ILE:CB	2.66	0.43
1:B:2188:LEU:C	1:B:2188:LEU:HD23	2.38	0.43
1:B:2079:PHE:O	1:B:2080:ALA:C	2.57	0.43
1:A:1175:LYS:HD2	6:A:3228:HOH:O	2.19	0.43
1:A:1365:GLN:NE2	6:A:3267:HOH:O	2.51	0.43
1:A:1370:TYR:HB2	6:A:3559:HOH:O	2.18	0.43
1:A:1012:PRO:HD2	3:A:1395:FAD:O1P	2.19	0.42
1:B:2104:GLU:N	1:B:2104:GLU:OE1	2.51	0.42
1:A:1218:ARG:HD2	6:A:3116:HOH:O	2.19	0.42
1:B:2338:LYS:HD3	1:B:2388:LEU:HD23	2.00	0.42
1:A:1175:LYS:CD	6:A:3551:HOH:O	2.51	0.42
1:A:1250:GLU:CD	1:A:1250:GLU:H	2.17	0.42
1:A:1022:HIS:NE2	1:A:1116:CYS:SG	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2085:ARG:NH2	2:B:702:SO4:O2	2.44	0.42
1:A:1070:LEU:HB3	6:A:3401:HOH:O	2.19	0.42
1:B:2299:LEU:HA	1:B:2299:LEU:HD12	1.85	0.42
1:A:1016:LEU:HD21	1:A:1055:LEU:CD2	2.26	0.42
1:A:1052:MET:HE1	1:A:1056:LEU:HD13	2.02	0.42
1:A:1144:ASP:O	1:A:1144:ASP:OD1	2.38	0.42
1:A:1161:PHE:HB2	1:A:1290:ILE:HD11	2.02	0.42
1:A:1036:PRO:HD3	1:A:1122:TYR:CG	2.53	0.42
1:B:2219:SER:HB3	1:B:2221:TYR:CE2	2.55	0.41
1:A:1070:LEU:HB2	1:A:1099:VAL:HB	2.02	0.41
1:A:1104:GLU:OE1	1:A:1104:GLU:N	2.44	0.41
1:A:1282:PHE:CZ	1:A:1325:LEU:HB3	2.55	0.41
1:A:1079:PHE:O	1:A:1080:ALA:C	2.59	0.41
1:B:2269:ARG:NH1	6:B:3553:HOH:O	2.52	0.41
1:A:1375:GLU:HG3	6:A:3482:HOH:O	2.20	0.41
1:B:2013:SER:OG	1:B:2302:ALA:HB1	2.21	0.41
1:B:2089:LYS:HB2	2:B:702:SO4:O1	2.21	0.41
1:A:1295:GLY:O	1:A:1297:LYS:HG2	2.20	0.41
1:A:1070:LEU:HD12	1:A:1070:LEU:N	2.35	0.41
1:B:2099:VAL:HG23	6:B:3419:HOH:O	2.21	0.41
1:A:1356:THR:HG22	1:A:1361:GLN:HG3	2.03	0.41
1:B:2004:GLN:HB2	1:B:2027:ASP:O	2.21	0.41
1:B:2045:GLY:HA3	3:B:2395:FAD:N5	2.36	0.41
1:A:1320:GLY:HA3	6:A:3105:HOH:O	2.20	0.41
1:B:2392:GLU:HG3	1:B:2393:ILE:N	2.36	0.40
1:B:2210:LEU:HD12	1:B:2211:CYS:N	2.36	0.40
1:B:2323:GLU:N	1:B:2323:GLU:OE2	2.54	0.40
1:B:2141:PHE:O	1:B:2147:ARG:HD3	2.21	0.40
1:B:2050:GLN:OE1	1:B:2053:VAL:HB	2.22	0.40
1:B:2175:LYS:HD2	1:B:2177:PHE:HZ	1.79	0.40
1:A:1087:ASP:O	1:A:1091:LEU:HD22	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1357:ASP:OD1	1:B:2172:GLU:OE2[2_765]	2.16	0.04



## 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	392/394 (100%)	374 (95%)	15 (4%)	3 (1%)	24	15
1	B	388/394 (98%)	372 (96%)	11 (3%)	5 (1%)	15	7
All	All	780/788 (99%)	746 (96%)	26 (3%)	8 (1%)	19	11

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2393	ILE
1	A	1319	GLU
1	A	1393	ILE
1	B	2062	ASP
1	A	1391	GLU
1	B	2061	VAL
1	B	2391	GLU
1	B	2323	GLU

### 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	325/325 (100%)	301 (93%)	24 (7%)	17	11
1	B	319/325 (98%)	299 (94%)	20 (6%)	22	16
All	All	644/650 (99%)	600 (93%)	44 (7%)	20	13

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1040	LEU
1	A	1052	MET
1	A	1056	LEU
1	A	1062	ASP
1	A	1070	LEU
1	A	1091	LEU
1	A	1114	GLU
1	A	1126	GLU
1	A	1135	GLU
1	A	1164	ILE
1	A	1173	ARG
1	A	1179	ARG
1	A	1213	GLN
1	A	1227	LEU
1	A	1254	LYS
1	A	1255	LEU
1	A	1273	VAL
1	A	1314	LEU
1	A	1323	GLU
1	A	1324	LEU
1	A	1355	ASP
1	A	1372	LEU
1	A	1374	SER
1	A	1388	LEU
1	B	2040	LEU
1	B	2052	MET
1	B	2056	LEU
1	B	2062	ASP
1	B	2099	VAL
1	B	2126	GLU
1	B	2129	LEU
1	B	2199	LEU
1	B	2227	LEU
1	B	2248	PRO
1	B	2250	GLU
1	B	2255	LEU
1	B	2307	SER
1	B	2314	LEU
1	B	2323	GLU
1	B	2365	GLN
1	B	2372	LEU
1	B	2388	LEU
1	B	2390	TYR

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Mol	Chain	Res	Type
1	B	2391	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1072	HIS
1	B	2034	GLN
1	B	2162	HIS
1	B	2167	GLN
1	B	2213	GLN
1	B	2361	GLN
1	B	2365	GLN

### 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](#)

18 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	$\# Z  > 2$
3	FAD	A	1395	-	48,58,58	1.74	12 (25%)	54,89,89	2.62	16 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PHB	A	1396	-	7,10,10	1.73	2 (28%)	10,13,13	1.41	2 (20%)
2	SO4	A	701	-	4,4,4	0.14	0	6,6,6	0.23	0
2	SO4	A	704	-	4,4,4	0.13	0	6,6,6	0.10	0
2	SO4	A	705	-	4,4,4	0.27	0	6,6,6	0.08	0
2	SO4	A	708	-	4,4,4	0.43	0	6,6,6	0.35	0
2	SO4	A	709	-	4,4,4	0.31	0	6,6,6	0.41	0
3	FAD	B	2395	-	48,58,58	2.07	16 (33%)	54,89,89	2.83	16 (29%)
4	PHB	B	2396	-	7,10,10	1.31	0	10,13,13	1.47	2 (20%)
2	SO4	B	702	-	4,4,4	0.38	0	6,6,6	0.39	0
2	SO4	B	703	-	4,4,4	0.18	0	6,6,6	0.10	0
2	SO4	B	706	-	4,4,4	0.24	0	6,6,6	0.24	0
2	SO4	B	707	-	4,4,4	0.59	0	6,6,6	0.27	0
2	SO4	B	711	-	4,4,4	0.06	0	6,6,6	0.19	0
2	SO4	B	712	-	4,4,4	0.16	0	6,6,6	0.09	0
2	SO4	B	713	-	4,4,4	0.11	0	6,6,6	0.11	0
5	PSL	B	714	-	6,8,8	0.70	0	6,13,13	0.87	0
5	PSL	B	715	-	6,8,8	0.53	0	6,13,13	1.41	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
3	FAD	A	1395	-	-	0/30/50/50	0/6/6/6
4	PHB	A	1396	-	-	0/0/4/4	0/1/1/1
2	SO4	A	701	-	-	0/0/0/0	0/0/0/0
2	SO4	A	704	-	-	0/0/0/0	0/0/0/0
2	SO4	A	705	-	-	0/0/0/0	0/0/0/0
2	SO4	A	708	-	-	0/0/0/0	0/0/0/0
2	SO4	A	709	-	-	0/0/0/0	0/0/0/0
3	FAD	B	2395	-	-	0/30/50/50	0/6/6/6
4	PHB	B	2396	-	-	0/0/4/4	0/1/1/1
2	SO4	B	702	-	-	0/0/0/0	0/0/0/0
2	SO4	B	703	-	-	0/0/0/0	0/0/0/0
2	SO4	B	706	-	-	0/0/0/0	0/0/0/0
2	SO4	B	707	-	-	0/0/0/0	0/0/0/0
2	SO4	B	711	-	-	0/0/0/0	0/0/0/0
2	SO4	B	712	-	-	0/0/0/0	0/0/0/0
2	SO4	B	713	-	-	0/0/0/0	0/0/0/0
5	PSL	B	714	-	-	0/4/6/6	0/0/0/0
5	PSL	B	715	-	-	0/4/6/6	0/0/0/0

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2395	FAD	C6-C5X	-3.74	1.36	1.41
3	A	1395	FAD	C1'-N10	-3.02	1.45	1.48
3	B	2395	FAD	C5'-C4'	-3.01	1.47	1.51
3	B	2395	FAD	P-O2P	-2.63	1.43	1.54
3	B	2395	FAD	C8M-C8	-2.54	1.45	1.51
3	A	1395	FAD	C4A-N3A	-2.45	1.31	1.35
3	A	1395	FAD	C9A-C5X	-2.37	1.37	1.42
3	B	2395	FAD	O4'-C4'	-2.02	1.38	1.43
3	B	2395	FAD	C5B-C4B	2.01	1.58	1.51
4	A	1396	PHB	C6-C1	2.11	1.43	1.39
3	B	2395	FAD	C9-C9A	2.14	1.45	1.40
3	B	2395	FAD	C4-C4X	2.18	1.45	1.41
3	A	1395	FAD	C8M-C8	2.37	1.55	1.51
3	A	1395	FAD	O3B-C3B	2.40	1.48	1.43
3	B	2395	FAD	O5B-C5B	2.41	1.54	1.44
3	A	1395	FAD	C2'-C3'	2.49	1.58	1.53
3	A	1395	FAD	C5B-C4B	2.54	1.59	1.51
3	A	1395	FAD	C7M-C7	2.59	1.56	1.51
4	A	1396	PHB	C6-C5	2.60	1.43	1.38
3	A	1395	FAD	C4-N3	3.06	1.38	1.33
3	A	1395	FAD	C4'-C3'	3.10	1.59	1.53
3	A	1395	FAD	C5'-C4'	3.20	1.56	1.51
3	B	2395	FAD	C2A-N3A	3.48	1.38	1.32
3	B	2395	FAD	C4'-C3'	3.64	1.60	1.53
3	B	2395	FAD	C2'-C3'	3.72	1.61	1.53
3	B	2395	FAD	O4B-C1B	3.72	1.45	1.41
3	B	2395	FAD	C4X-N5	4.12	1.39	1.33
3	B	2395	FAD	C10-N10	4.16	1.44	1.39
3	A	1395	FAD	C5X-N5	4.74	1.42	1.35
3	B	2395	FAD	C4-N3	5.25	1.42	1.33

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1395	FAD	C4X-C10-N10	-6.61	116.62	120.52
3	B	2395	FAD	C4X-C4-N3	-6.50	114.70	123.59
3	B	2395	FAD	C4X-C10-N10	-6.19	116.87	120.52
3	B	2395	FAD	N3A-C2A-N1A	-5.50	124.68	128.89
3	A	1395	FAD	C4X-N5-C5X	-5.13	110.87	116.76
3	B	2395	FAD	C4X-N5-C5X	-5.07	110.94	116.76
3	A	1395	FAD	C4-C4X-C10	-4.65	116.97	119.94
3	A	1395	FAD	C5X-C9A-N10	-4.36	114.30	117.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2395	FAD	C6-C5X-N5	-4.11	113.68	118.96
3	A	1395	FAD	O4B-C1B-N9A	-4.02	99.69	108.10
3	B	2395	FAD	C4-C4X-C10	-3.93	117.43	119.94
3	A	1395	FAD	C6-C5X-N5	-3.60	114.33	118.96
3	A	1395	FAD	C4X-C4-N3	-3.49	118.82	123.59
4	B	2396	PHB	C5-C4-C3	-2.85	115.73	119.79
3	A	1395	FAD	C1'-C2'-C3'	-2.83	101.72	109.82
4	A	1396	PHB	C5-C6-C1	-2.60	117.34	121.14
3	B	2395	FAD	O4B-C1B-N9A	-2.54	102.78	108.10
3	A	1395	FAD	C4-C4X-N5	-2.52	115.67	118.72
3	B	2395	FAD	O5B-C5B-C4B	-2.38	100.36	109.12
3	B	2395	FAD	C4B-O4B-C1B	-2.25	107.25	109.72
5	B	715	PSL	O6-S2-O4	-2.24	102.71	112.46
4	A	1396	PHB	C2-C1-C1'	-2.11	117.62	120.45
3	A	1395	FAD	O3P-P-O5'	-2.06	97.47	102.94
3	A	1395	FAD	O2A-PA-O1A	2.05	123.61	112.53
3	B	2395	FAD	N6A-C6A-N1A	2.05	123.60	119.20
3	B	2395	FAD	C4A-C5A-N7A	2.20	111.50	109.48
3	B	2395	FAD	O4B-C4B-C3B	2.32	109.83	105.15
3	A	1395	FAD	C7M-C7-C8	2.35	125.90	120.73
3	B	2395	FAD	O2A-PA-O1A	2.38	125.42	112.53
4	B	2396	PHB	C2-C3-C4	2.52	122.78	119.87
3	B	2395	FAD	O2P-P-O1P	2.61	126.70	112.53
3	A	1395	FAD	N3A-C2A-N1A	3.06	131.24	128.89
3	A	1395	FAD	C2B-C1B-N9A	3.34	119.39	114.29
3	A	1395	FAD	C9A-C5X-N5	3.92	128.15	122.36
3	B	2395	FAD	C9A-C5X-N5	4.08	128.38	122.36
3	A	1395	FAD	C4-N3-C2	11.03	124.78	115.25
3	B	2395	FAD	C4-N3-C2	13.10	126.57	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1395	FAD	6	0
2	A	708	SO4	1	0
2	A	709	SO4	1	0
3	B	2395	FAD	2	0
2	B	702	SO4	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	715	PSL	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	394/394 (100%)	0.16	26 (6%)	22 22	23, 36, 69, 114	1 (0%)
1	B	392/394 (99%)	-0.00	15 (3%)	44 45	18, 29, 60, 121	1 (0%)
All	All	786/788 (99%)	0.08	41 (5%)	31 33	18, 33, 66, 121	2 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2393	ILE	11.3
1	B	2391	GLU	9.8
1	A	1392	GLU	8.9
1	B	2392	GLU	7.9
1	A	1393	ILE	7.7
1	B	2390	TYR	7.7
1	B	2389	PRO	7.5
1	B	2394	GLU	7.0
1	A	1389	PRO	6.8
1	A	1390	TYR	5.9
1	A	1321	ARG	5.3
1	A	1324	LEU	5.2
1	A	1391	GLU	5.2
1	A	1394	GLU	4.6
1	B	2321	ARG	4.5
1	A	1355	ASP	3.9
1	A	1322	GLY	3.8
1	B	2388	LEU	3.4
1	A	1318	ARG	3.3
1	A	1253	GLU	3.2
1	A	1038	TYR	3.2
1	A	1062	ASP	3.1
1	B	2066	ALA	3.0
1	A	1067	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	2323	GLU	3.0
1	A	1064	ARG	2.9
1	A	1144	ASP	2.8
1	A	1073	GLU	2.8
1	A	1081	GLY	2.7
1	B	2062	ASP	2.7
1	A	1323	GLU	2.5
1	B	2136	ARG	2.5
1	B	2355	ASP	2.3
1	A	1320	GLY	2.3
1	A	1115	ALA	2.3
1	A	1228	SER	2.3
1	A	1063	ARG	2.3
1	A	1317	TYR	2.2
1	B	2063	ARG	2.2
1	B	2067	ARG	2.1
1	A	1145	GLY	2.1

## 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( $\text{\AA}^2$ )	Q<0.9
5	PSL	B	715	9/9	0.90	0.23	7.29	21,32,37,42	9
2	SO4	B	707	5/5	0.96	0.25	4.13	20,21,23,23	5
5	PSL	B	714	9/9	0.91	0.26	2.89	30,37,46,46	9
2	SO4	A	709	5/5	0.97	0.21	2.45	18,20,23,29	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	PHB	B	2396	10/10	0.96	0.15	0.34	21,22,27,28	0
2	SO4	A	704	5/5	0.95	0.16	0.14	52,52,55,57	5
2	SO4	A	701	5/5	0.97	0.11	0.04	32,36,39,40	5
4	PHB	A	1396	10/10	0.95	0.13	-0.10	22,25,32,33	0
2	SO4	B	706	5/5	0.93	0.12	-0.21	27,29,32,37	5
3	FAD	B	2395	53/53	0.98	0.10	-0.43	12,20,26,27	0
3	FAD	A	1395	53/53	0.97	0.10	-0.65	19,29,38,43	0
2	SO4	B	702	5/5	0.98	0.09	-0.67	28,28,29,29	5
2	SO4	A	705	5/5	0.91	0.12	-0.74	46,48,52,54	5
2	SO4	B	712	5/5	0.79	0.35	-	82,83,83,83	5
2	SO4	B	703	5/5	0.97	0.09	-	32,37,40,40	5
2	SO4	A	708	5/5	0.91	0.15	-	27,33,38,43	5
2	SO4	B	713	5/5	0.87	0.24	-	70,71,73,73	5
2	SO4	B	711	5/5	0.94	0.22	-	46,46,49,54	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.