



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 12:06 PM GMT

PDB ID : 1VCF  
Title : Crystal Structure of IPP isomerase at I422  
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Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2004-03-08  
Resolution : 2.60 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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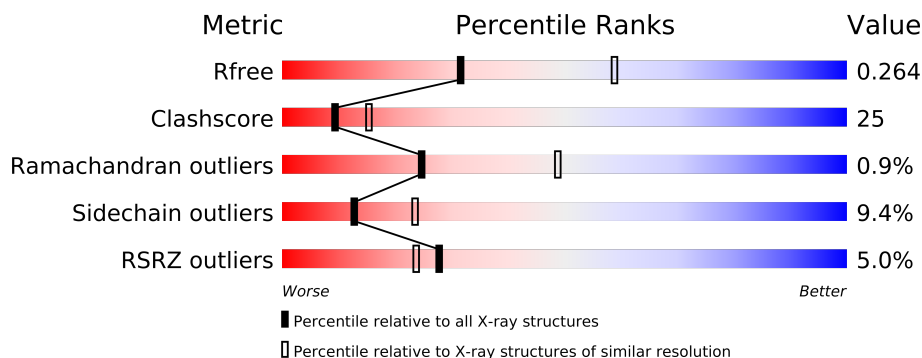
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.60 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))
$R_{free}$	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	332	
1	B	332	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4569 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called isopentenyl-diphosphatedelta-isomerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	Se	0	0	0
			2264	1441	409	408	1	5			
1	B	298	Total	C	N	O	S	Se	0	0	0
			2242	1424	407	405	1	5			

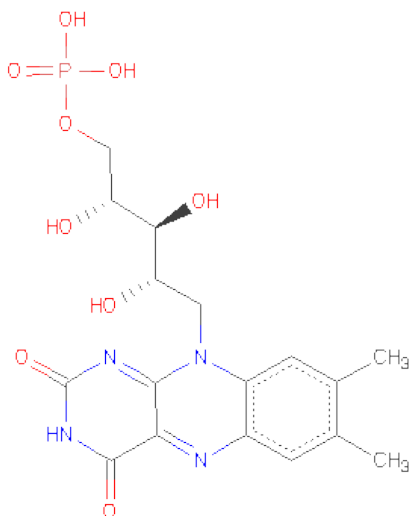
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
A	66	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
A	91	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
A	92	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
A	143	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
A	185	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
B	66	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
B	91	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
B	92	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
B	143	MSE	MET	MODIFIED RESIDUE	UNP Q746I8
B	185	MSE	MET	MODIFIED RESIDUE	UNP Q746I8

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

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

- Molecule 3 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).



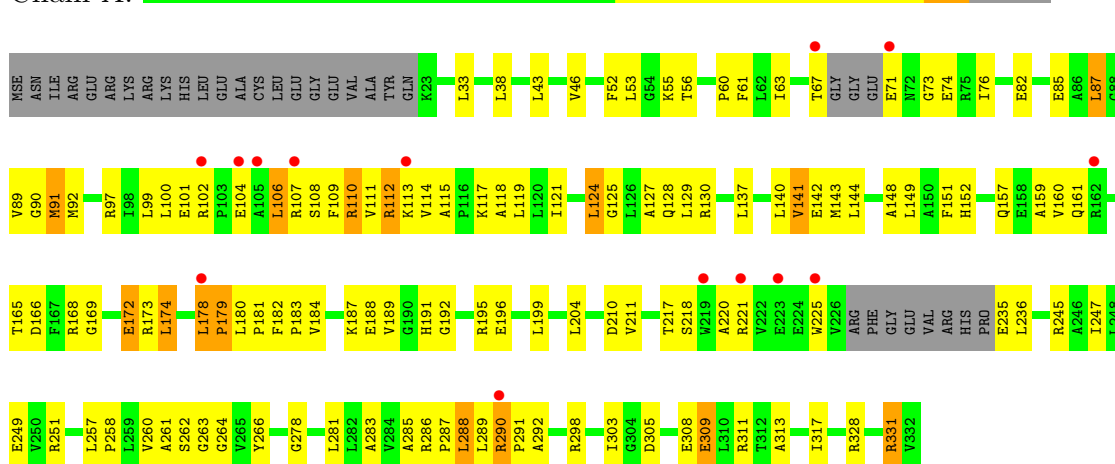
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 17	N 4	O 9	P 1	0	0
3	B	1	Total 31	C 17	N 4	O 9	P 1	0	0

### 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 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.

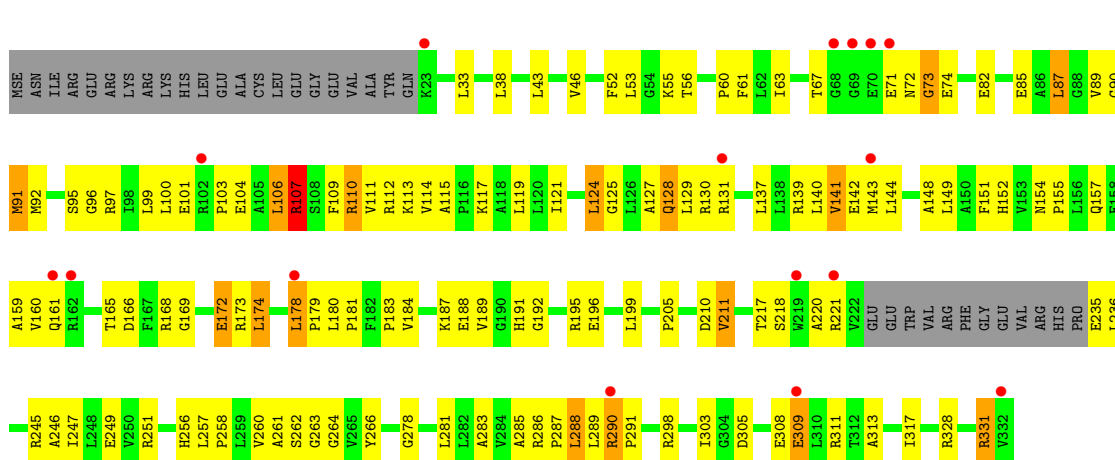
- Molecule 1: isopentenyl-diphosphatedelta-isomerase

Chain A:



- Molecule 1: isopentenyl-diphosphatedelta-isomerase

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	144.43Å 144.43Å 169.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.94 – 2.60 19.94 – 2.60	Depositor EDS
% Data completeness (in resolution range)	92.3 (19.94-2.60) 92.3 (19.94-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.55 (at 2.59Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.242 , 0.260 0.246 , 0.264	Depositor DCC
$R_{free}$ test set	1237 reflections (4.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.1	Xtriage
Anisotropy	0.920	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 33.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 25755 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4569	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, CD

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	0.46	0/2292	0.75	7/3095 (0.2%)
1	B	0.47	0/2269	0.75	6/3063 (0.2%)
All	All	0.47	0/4561	0.75	13/6158 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	ARG	NE-CZ-NH1	-6.69	116.95	120.30
1	B	110	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	A	112	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	A	110	ARG	NE-CZ-NH2	6.66	123.63	120.30
1	A	112	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	B	107	ARG	NE-CZ-NH2	-6.50	117.05	120.30
1	B	110	ARG	NE-CZ-NH2	-6.50	117.05	120.30
1	A	107	ARG	NE-CZ-NH1	-6.37	117.12	120.30
1	B	107	ARG	NE-CZ-NH1	5.85	123.23	120.30
1	A	107	ARG	NE-CZ-NH2	5.77	123.18	120.30
1	B	112	ARG	NE-CZ-NH1	-5.62	117.49	120.30
1	A	298	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	B	298	ARG	NE-CZ-NH1	-5.25	117.67	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2264	0	2358	113	0
1	B	2242	0	2340	117	2
2	A	1	0	0	0	0
3	A	31	0	19	3	0
3	B	31	0	19	3	0
All	All	4569	0	4736	230	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 25.

All (230) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:85:GLU:HG3	1:B:115:ALA:HA	1.28	1.12
1:A:85:GLU:HG3	1:A:115:ALA:HA	1.30	1.07
1:A:188:GLU:HG3	1:A:189:VAL:H	1.21	1.04
1:B:188:GLU:HG3	1:B:189:VAL:H	1.20	1.04
1:B:188:GLU:HG3	1:B:189:VAL:N	1.85	0.92
1:A:188:GLU:HG3	1:A:189:VAL:N	1.87	0.90
1:B:33:LEU:HB3	1:B:317:ILE:HD11	1.56	0.88
1:A:218:SER:HB3	1:A:221:ARG:HD3	1.56	0.87
1:B:218:SER:HB3	1:B:221:ARG:HD3	1.57	0.84
1:A:33:LEU:HB3	1:A:317:ILE:HD11	1.61	0.82
1:B:43:LEU:O	1:B:46:VAL:HG12	1.80	0.80
1:B:245:ARG:HH22	1:B:331:ARG:HH22	1.30	0.79
1:B:188:GLU:CG	1:B:189:VAL:H	1.95	0.78
1:B:290:ARG:HD2	1:B:290:ARG:H	1.47	0.78
1:A:290:ARG:H	1:A:290:ARG:HD2	1.47	0.78
1:B:106:LEU:HD12	1:B:110:ARG:HH11	1.48	0.77
1:A:245:ARG:HH22	1:A:331:ARG:HH22	1.31	0.77
1:A:97:ARG:HH11	1:A:125:GLY:H	1.30	0.77
1:B:97:ARG:HH11	1:B:125:GLY:H	1.31	0.76
1:A:188:GLU:CG	1:A:189:VAL:H	1.97	0.76
1:B:317:ILE:HG22	1:B:328:ARG:HD3	1.67	0.75
1:A:43:LEU:O	1:A:46:VAL:HG12	1.85	0.75
1:A:221:ARG:HB2	1:A:221:ARG:NH1	2.03	0.74
1:B:221:ARG:HB2	1:B:221:ARG:NH1	2.03	0.74
1:B:221:ARG:HB2	1:B:221:ARG:HH11	1.52	0.73
1:B:85:GLU:HG3	1:B:115:ALA:CA	2.14	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:174:LEU:HD22	1:A:178:LEU:HG	1.71	0.72
1:A:286:ARG:HB3	1:A:287:PRO:HD3	1.70	0.72
1:A:85:GLU:HG3	1:A:115:ALA:CA	2.15	0.72
1:A:317:ILE:HG22	1:A:328:ARG:HD3	1.70	0.72
1:A:97:ARG:HH12	1:A:152:HIS:CE1	2.08	0.72
1:A:130:ARG:HB3	1:A:173:ARG:NH1	2.05	0.71
1:A:188:GLU:HG2	1:A:192:GLY:N	2.06	0.70
1:A:221:ARG:HB2	1:A:221:ARG:HH11	1.55	0.70
1:A:251:ARG:NH2	1:A:257:LEU:O	2.24	0.70
1:A:264:GLY:HA2	1:A:266:TYR:CZ	2.27	0.70
1:A:218:SER:H	1:A:221:ARG:NH1	1.88	0.69
1:B:286:ARG:HH11	1:B:286:ARG:HG2	1.59	0.68
1:B:97:ARG:HH12	1:B:152:HIS:CE1	2.11	0.68
1:B:196:GLU:HA	1:B:199:LEU:HD12	1.75	0.68
1:B:130:ARG:HB3	1:B:173:ARG:NH1	2.09	0.67
1:A:286:ARG:HH11	1:A:286:ARG:HG2	1.58	0.67
1:A:157:GLN:HE21	1:A:161:GLN:HE22	1.44	0.66
1:A:196:GLU:HA	1:A:199:LEU:HD12	1.76	0.66
1:B:187:LYS:HB3	1:B:210:ASP:HB3	1.76	0.66
1:B:251:ARG:NH2	1:B:257:LEU:O	2.28	0.65
1:B:262:SER:HB3	1:B:283:ALA:HB3	1.78	0.65
1:B:218:SER:H	1:B:221:ARG:NH1	1.94	0.65
1:B:188:GLU:HG2	1:B:192:GLY:N	2.12	0.65
1:B:286:ARG:HB3	1:B:287:PRO:HD3	1.77	0.65
1:B:180:LEU:HD12	1:B:184:VAL:HG21	1.79	0.65
1:A:85:GLU:OE1	1:A:117:LYS:N	2.26	0.64
1:A:178:LEU:O	1:A:180:LEU:N	2.30	0.64
1:B:178:LEU:O	1:B:180:LEU:N	2.31	0.64
1:B:61:PHE:O	1:B:89:VAL:HG13	1.98	0.64
1:A:180:LEU:HD12	1:A:184:VAL:HG21	1.80	0.64
1:B:157:GLN:HE21	1:B:161:GLN:HE22	1.45	0.64
1:B:290:ARG:N	1:B:290:ARG:HD2	2.13	0.63
1:A:290:ARG:N	1:A:290:ARG:HD2	2.14	0.63
1:B:85:GLU:OE1	1:B:117:LYS:N	2.29	0.62
1:A:257:LEU:HD12	1:A:258:PRO:HD2	1.81	0.62
1:A:148:ALA:HB2	1:A:183:PRO:HG2	1.81	0.61
1:B:257:LEU:HD12	1:B:258:PRO:HD2	1.83	0.61
1:A:245:ARG:NH2	1:A:331:ARG:HH22	1.99	0.61
1:A:187:LYS:HB3	1:A:210:ASP:HB3	1.81	0.61
1:B:174:LEU:HD22	1:B:178:LEU:HG	1.83	0.60
1:A:217:THR:HG21	1:A:286:ARG:HG2	1.84	0.60
1:A:188:GLU:HG2	1:A:192:GLY:H	1.66	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:217:THR:HG21	1:B:286:ARG:HG2	1.85	0.59
1:B:157:GLN:HG3	1:B:161:GLN:NE2	2.17	0.59
1:A:61:PHE:O	1:A:89:VAL:HG13	2.03	0.59
1:B:187:LYS:CB	1:B:210:ASP:HB3	2.33	0.58
1:B:264:GLY:HA2	1:B:266:TYR:CZ	2.38	0.58
1:A:262:SER:HB3	1:A:283:ALA:HB3	1.85	0.58
1:B:97:ARG:HH11	1:B:125:GLY:N	2.00	0.57
1:A:288:LEU:HD21	1:A:303:ILE:HD11	1.87	0.57
1:A:157:GLN:HG3	1:A:161:GLN:NE2	2.19	0.57
1:A:187:LYS:CB	1:A:210:ASP:HB3	2.36	0.56
1:B:124:LEU:O	1:B:151:PHE:HA	2.05	0.56
1:A:97:ARG:HH11	1:A:125:GLY:N	2.01	0.56
1:A:313:ALA:O	1:A:317:ILE:HG12	2.07	0.55
1:A:266:TYR:CD2	1:A:287:PRO:HG2	2.42	0.55
1:B:266:TYR:CD2	1:B:287:PRO:HG2	2.41	0.55
1:A:97:ARG:NH1	1:A:152:HIS:CE1	2.75	0.55
1:B:82:GLU:HB2	1:B:114:VAL:HG21	1.87	0.55
1:B:188:GLU:CG	1:B:189:VAL:N	2.58	0.54
1:B:61:PHE:HD2	1:B:89:VAL:HG11	1.72	0.54
1:B:148:ALA:HB2	1:B:183:PRO:HG2	1.88	0.54
1:B:245:ARG:NH2	1:B:331:ARG:HH22	2.01	0.53
1:B:263:GLY:HA2	3:B:502:FMN:O2P	2.08	0.53
1:A:129:LEU:O	1:A:173:ARG:HD3	2.09	0.53
1:A:61:PHE:HD2	1:A:89:VAL:HG11	1.72	0.53
1:B:180:LEU:HB3	1:B:181:PRO:HD2	1.91	0.53
1:B:188:GLU:HG2	1:B:192:GLY:H	1.74	0.53
1:A:285:ALA:HB3	3:A:501:FMN:O5'	2.09	0.52
1:A:99:LEU:HD21	1:A:106:LEU:HA	1.91	0.52
1:B:172:GLU:CD	1:B:172:GLU:H	2.12	0.52
1:A:172:GLU:CD	1:A:172:GLU:H	2.13	0.52
1:A:55:LYS:HD3	1:A:56:THR:H	1.75	0.52
1:B:217:THR:HG21	1:B:286:ARG:HH11	1.75	0.51
1:A:82:GLU:HB2	1:A:114:VAL:HG21	1.91	0.51
1:A:106:LEU:HD12	1:A:110:ARG:HH11	1.75	0.51
1:B:308:GLU:OE2	1:B:311:ARG:HD2	2.10	0.51
1:B:288:LEU:HD21	1:B:303:ILE:HD11	1.93	0.51
1:A:286:ARG:HD2	1:A:289:LEU:HD12	1.92	0.51
1:A:124:LEU:O	1:A:151:PHE:HA	2.11	0.51
1:A:85:GLU:CG	1:A:115:ALA:HA	2.21	0.51
1:B:313:ALA:O	1:B:317:ILE:HG12	2.11	0.51
1:B:169:GLY:HA2	1:B:172:GLU:CG	2.40	0.50
1:A:195:ARG:HB3	1:A:249:GLU:HB3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:99:LEU:HD11	1:B:144:LEU:HD21	1.92	0.50
1:B:99:LEU:HD21	1:B:106:LEU:HA	1.92	0.50
1:A:217:THR:HG21	1:A:286:ARG:HH11	1.75	0.50
1:B:85:GLU:CG	1:B:115:ALA:HA	2.21	0.50
1:B:251:ARG:NH1	1:B:278:GLY:O	2.41	0.50
1:B:63:ILE:HB	1:B:91:MSE:HG3	1.93	0.50
1:B:195:ARG:HB3	1:B:249:GLU:HB3	1.94	0.50
1:A:218:SER:H	1:A:221:ARG:HH11	1.58	0.50
1:B:89:VAL:CG1	1:B:90:GLY:N	2.74	0.50
1:A:235:GLU:HG3	1:A:236:LEU:HD22	1.94	0.49
1:A:286:ARG:NH1	1:A:286:ARG:HG2	2.25	0.49
1:B:317:ILE:CG2	1:B:328:ARG:HD3	2.39	0.49
1:A:127:ALA:O	1:A:130:ARG:HG2	2.13	0.49
1:B:285:ALA:HB3	3:B:502:FMN:O5'	2.11	0.49
1:B:106:LEU:HD21	1:B:143:MSE:HB3	1.95	0.49
1:B:97:ARG:NH1	1:B:152:HIS:CE1	2.79	0.48
1:A:61:PHE:CE2	1:A:303:ILE:HD12	2.49	0.48
1:A:140:LEU:HA	1:A:143:MSE:HE3	1.95	0.48
1:A:97:ARG:NH1	1:A:125:GLY:H	2.05	0.48
1:A:180:LEU:HB3	1:A:181:PRO:HD2	1.96	0.48
1:A:264:GLY:HA2	1:A:266:TYR:CE1	2.49	0.48
1:B:286:ARG:HD2	1:B:289:LEU:HD12	1.95	0.48
1:A:63:ILE:HB	1:A:91:MSE:HG3	1.96	0.48
1:B:129:LEU:O	1:B:173:ARG:HD3	2.14	0.48
1:A:106:LEU:HD21	1:A:143:MSE:HB3	1.97	0.47
1:B:305:ASP:O	1:B:309:GLU:HB2	2.14	0.47
1:A:178:LEU:HA	1:A:178:LEU:HD23	1.64	0.47
1:A:188:GLU:OE1	1:A:191:HIS:HB2	2.14	0.47
1:A:92:MSE:HG2	1:A:121:ILE:HD12	1.96	0.47
1:B:92:MSE:HG2	1:B:121:ILE:HD12	1.96	0.47
1:B:169:GLY:HA2	1:B:172:GLU:HG2	1.96	0.47
1:B:104:GLU:C	1:B:106:LEU:H	2.17	0.47
1:B:60:PRO:HA	1:B:281:LEU:HD13	1.97	0.47
1:A:245:ARG:NH2	1:A:331:ARG:NH2	2.62	0.47
1:B:99:LEU:CD1	1:B:144:LEU:HD21	2.45	0.47
1:A:181:PRO:HG2	1:A:182:PHE:CD2	2.50	0.47
1:A:245:ARG:HH22	1:A:331:ARG:NH2	2.07	0.46
1:B:286:ARG:NH1	1:B:286:ARG:HG2	2.26	0.46
1:B:178:LEU:HD23	1:B:178:LEU:HA	1.65	0.46
1:A:99:LEU:HD11	1:A:144:LEU:HD21	1.96	0.46
1:A:308:GLU:OE2	1:A:311:ARG:HD2	2.15	0.46
1:B:61:PHE:CE2	1:B:303:ILE:HD12	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:235:GLU:HG3	1:B:236:LEU:HD22	1.98	0.46
1:B:290:ARG:HB2	1:B:291:PRO:CD	2.46	0.46
1:A:263:GLY:HA2	3:A:501:FMN:O2P	2.15	0.46
1:B:245:ARG:HH22	1:B:331:ARG:NH2	2.06	0.46
1:A:169:GLY:HA2	1:A:172:GLU:HG2	1.97	0.46
1:A:247:ILE:HD11	1:A:261:ALA:HB1	1.98	0.46
1:A:305:ASP:O	1:A:309:GLU:HB2	2.16	0.46
1:A:67:THR:H	3:A:501:FMN:H6	1.80	0.45
1:A:60:PRO:HA	1:A:281:LEU:HD13	1.98	0.45
1:B:169:GLY:O	1:B:172:GLU:HG2	2.16	0.45
1:B:128:GLN:HA	1:B:131:ARG:NH1	2.32	0.45
1:B:290:ARG:HG2	1:B:290:ARG:HH11	1.82	0.45
1:A:317:ILE:CG2	1:A:328:ARG:HD3	2.43	0.45
1:B:137:LEU:O	1:B:141:VAL:HG13	2.16	0.45
1:B:245:ARG:NH2	1:B:331:ARG:NH2	2.64	0.45
1:B:96:GLY:O	1:B:99:LEU:HB2	2.17	0.45
1:A:89:VAL:CG1	1:A:90:GLY:N	2.80	0.45
1:A:137:LEU:O	1:A:141:VAL:HG13	2.16	0.45
1:A:74:GLU:HB2	1:A:108:SER:HA	1.98	0.44
1:B:166:ASP:OD1	1:B:168:ARG:HD3	2.17	0.44
1:A:104:GLU:C	1:A:106:LEU:H	2.20	0.44
1:B:218:SER:H	1:B:221:ARG:HH11	1.64	0.44
1:B:139:ARG:O	1:B:143:MSE:HG3	2.18	0.44
1:A:166:ASP:OD1	1:A:168:ARG:HD3	2.17	0.44
1:B:159:ALA:HA	1:B:165:THR:HG22	2.00	0.44
1:B:140:LEU:HA	1:B:143:MSE:HE3	1.99	0.44
1:B:67:THR:H	3:B:502:FMN:H6	1.83	0.44
1:A:174:LEU:HD13	1:A:204:LEU:HD23	1.99	0.43
1:A:290:ARG:HH11	1:A:290:ARG:HG2	1.83	0.43
1:A:290:ARG:HB2	1:A:291:PRO:CD	2.47	0.43
1:A:181:PRO:HG2	1:A:182:PHE:CE2	2.53	0.43
1:B:97:ARG:NH1	1:B:125:GLY:N	2.66	0.43
1:B:82:GLU:HB2	1:B:114:VAL:CG2	2.48	0.43
1:B:74:GLU:OE2	1:B:107:ARG:HD3	2.18	0.43
1:A:251:ARG:NH1	1:A:278:GLY:O	2.47	0.43
1:B:157:GLN:HB2	1:B:220:ALA:HB2	1.99	0.43
1:A:169:GLY:HA2	1:A:172:GLU:CG	2.49	0.43
1:A:101:GLU:HG3	1:A:102:ARG:HD2	2.01	0.43
1:A:71:GLU:N	1:A:71:GLU:OE1	2.51	0.43
1:B:188:GLU:OE1	1:B:191:HIS:HB2	2.19	0.43
1:A:157:GLN:HB2	1:A:220:ALA:HB2	1.99	0.42
1:B:109:PHE:O	1:B:110:ARG:C	2.57	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:210:ASP:HA	1:A:260:VAL:HB	2.00	0.42
1:A:109:PHE:O	1:A:110:ARG:C	2.58	0.42
1:A:159:ALA:HA	1:A:165:THR:HG22	2.01	0.42
1:A:99:LEU:CD1	1:A:144:LEU:HD21	2.49	0.42
1:B:154:ASN:O	1:B:155:PRO:C	2.57	0.42
1:B:72:ASN:O	1:B:73:GLY:C	2.58	0.42
1:A:97:ARG:NH1	1:A:125:GLY:N	2.67	0.42
1:B:55:LYS:HD3	1:B:56:THR:H	1.84	0.42
1:A:76:ILE:HG23	1:A:292:ALA:HB1	2.02	0.42
1:B:101:GLU:O	1:B:103:PRO:HD3	2.19	0.42
1:A:100:LEU:N	1:A:100:LEU:HD22	2.35	0.42
1:B:317:ILE:HG23	1:B:328:ARG:HB3	2.01	0.41
1:B:210:ASP:HA	1:B:260:VAL:HB	2.01	0.41
1:B:46:VAL:HG11	1:B:311:ARG:HG3	2.02	0.41
1:A:99:LEU:CD2	1:A:106:LEU:HA	2.50	0.41
1:A:52:PHE:CE2	1:A:53:LEU:HD22	2.54	0.41
1:B:127:ALA:O	1:B:130:ARG:HG2	2.21	0.41
1:A:112:ARG:NH2	1:A:118:ALA:O	2.44	0.41
1:A:218:SER:CB	1:A:221:ARG:HD3	2.39	0.41
1:A:188:GLU:CG	1:A:189:VAL:N	2.61	0.41
1:B:264:GLY:HA2	1:B:266:TYR:CE1	2.56	0.41
1:B:52:PHE:CE2	1:B:53:LEU:HD22	2.55	0.41
1:B:247:ILE:HD11	1:B:261:ALA:HB1	2.02	0.41
1:B:71:GLU:OE1	1:B:71:GLU:N	2.53	0.41
1:B:95:SER:OG	1:B:97:ARG:HB2	2.21	0.40
1:B:87:LEU:HD23	1:B:303:ILE:HB	2.03	0.40
1:B:100:LEU:HD22	1:B:100:LEU:N	2.36	0.40
1:B:99:LEU:CD2	1:B:106:LEU:HA	2.52	0.40
1:A:148:ALA:CB	1:A:183:PRO:HG2	2.49	0.40
1:A:87:LEU:HD23	1:A:303:ILE:HB	2.02	0.40
1:A:178:LEU:O	1:A:179:PRO:C	2.58	0.40
1:B:178:LEU:O	1:B:179:PRO:C	2.59	0.40
1:B:211:VAL:HG22	1:B:246:ALA:HB1	2.03	0.40
1:A:317:ILE:HG23	1:A:328:ARG:HB3	2.02	0.40
1:B:178:LEU:HD13	1:B:205:PRO:CD	2.52	0.40
1:B:106:LEU:HD12	1:B:110:ARG:NH1	2.24	0.40

All (2) 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	Distance(Å)	Clash(Å)
1:B:256:HIS:CE1	1:B:256:HIS:CE1[8_666]	1.93	0.27

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:235:GLU:OE2	1:B:309:GLU:OE2[4_665]	2.19	0.01

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	293/332 (88%)	273 (93%)	17 (6%)	3 (1%)	22	45
1	B	294/332 (89%)	271 (92%)	21 (7%)	2 (1%)	30	58
All	All	587/664 (88%)	544 (93%)	38 (6%)	5 (1%)	25	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	GLY
1	A	178	LEU
1	B	73	GLY
1	B	178	LEU
1	A	179	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	225/246 (92%)	204 (91%)	21 (9%)	13	24
1	B	222/246 (90%)	201 (90%)	21 (10%)	12	23
All	All	447/492 (91%)	405 (91%)	42 (9%)	13	23

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	LEU
1	A	87	LEU
1	A	91	MSE
1	A	106	LEU
1	A	111	VAL
1	A	113	LYS
1	A	119	LEU
1	A	124	LEU
1	A	128	GLN
1	A	141	VAL
1	A	142	GLU
1	A	149	LEU
1	A	160	VAL
1	A	172	GLU
1	A	174	LEU
1	A	211	VAL
1	A	225	TRP
1	A	288	LEU
1	A	290	ARG
1	A	309	GLU
1	A	331	ARG
1	B	38	LEU
1	B	87	LEU
1	B	91	MSE
1	B	106	LEU
1	B	107	ARG
1	B	111	VAL
1	B	113	LYS
1	B	119	LEU
1	B	124	LEU
1	B	128	GLN
1	B	141	VAL
1	B	142	GLU
1	B	149	LEU
1	B	160	VAL
1	B	172	GLU
1	B	174	LEU
1	B	211	VAL
1	B	288	LEU
1	B	290	ARG
1	B	309	GLU
1	B	331	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	152	HIS
1	A	161	GLN
1	B	128	GLN
1	B	161	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	FMN	A	501	-	33,33,33	2.56	10 (30%)	46,50,50	3.78	20 (43%)
3	FMN	B	502	-	33,33,33	2.58	10 (30%)	46,50,50	3.78	19 (41%)

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	FMN	A	501	-	-	0/18/18/18	0/0/3/3
3	FMN	B	502	-	-	0/18/18/18	0/0/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	FMN	C4A-C10	7.75	1.54	1.40
3	A	501	FMN	C4A-C10	7.69	1.54	1.40
3	B	502	FMN	C2-N3	5.79	1.48	1.37
3	A	501	FMN	C2-N3	5.26	1.47	1.37
3	A	501	FMN	C5A-N5	5.01	1.43	1.35
3	B	502	FMN	C5A-N5	5.00	1.43	1.35
3	A	501	FMN	C9-C9A	4.78	1.50	1.40
3	B	502	FMN	C9-C9A	4.61	1.49	1.40
3	B	502	FMN	C4-N3	4.00	1.43	1.37
3	A	501	FMN	C4-N3	3.81	1.43	1.37
3	A	501	FMN	C5'-C4'	3.49	1.57	1.51
3	A	501	FMN	C9A-C5A	3.48	1.49	1.42
3	B	502	FMN	C9A-C5A	3.43	1.49	1.42
3	A	501	FMN	C6-C7	3.17	1.46	1.37
3	B	502	FMN	C5'-C4'	2.91	1.56	1.51
3	B	502	FMN	C6-C7	2.90	1.45	1.37
3	B	502	FMN	C4A-N5	-2.77	1.30	1.36
3	A	501	FMN	C4A-N5	-2.55	1.30	1.36
3	A	501	FMN	C8-C7	2.27	1.47	1.40
3	B	502	FMN	C8-C7	2.04	1.46	1.40

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	FMN	C1'-N10-C9A	9.47	128.08	118.87
3	A	501	FMN	C2-N1-C10	9.46	124.51	114.98
3	A	501	FMN	O3P-P-O5'	-9.45	80.56	106.65
3	B	502	FMN	C2-N1-C10	9.40	124.45	114.98
3	A	501	FMN	C1'-N10-C9A	9.19	127.81	118.87
3	B	502	FMN	O3P-P-O5'	-9.00	81.80	106.65
3	B	502	FMN	O3P-P-O1P	-8.76	81.82	110.44
3	A	501	FMN	O3P-P-O1P	-8.67	82.12	110.44
3	B	502	FMN	C5A-C9A-N10	7.64	124.33	116.80
3	A	501	FMN	C5A-C9A-N10	7.64	124.32	116.80
3	B	502	FMN	C9A-N10-C10	-6.41	115.48	121.77
3	A	501	FMN	C9A-N10-C10	-6.36	115.52	121.77
3	B	502	FMN	O3P-P-O2P	-5.23	87.22	107.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	FMN	O3P-P-O2P	-5.14	87.61	107.61
3	A	501	FMN	O5'-P-O1P	4.93	121.17	106.71
3	B	502	FMN	C7M-C7-C6	-4.87	108.63	120.38
3	A	501	FMN	C7M-C7-C6	-4.86	108.67	120.38
3	B	502	FMN	O5'-P-O1P	4.85	120.93	106.71
3	A	501	FMN	C4A-C10-N1	-4.67	118.06	122.73
3	B	502	FMN	C4A-C10-N1	-4.44	118.30	122.73
3	B	502	FMN	C7M-C7-C8	4.44	130.99	120.74
3	A	501	FMN	C7M-C7-C8	4.41	130.93	120.74
3	A	501	FMN	O2P-P-O5'	3.70	116.87	106.65
3	B	502	FMN	O2P-P-O5'	3.59	116.54	106.65
3	B	502	FMN	C9A-C5A-N5	-3.55	116.92	122.37
3	B	502	FMN	C6-C5A-N5	3.48	123.03	118.97
3	B	502	FMN	C4A-N5-C5A	3.46	120.57	116.69
3	A	501	FMN	C9A-C5A-N5	-3.45	117.08	122.37
3	A	501	FMN	C6-C5A-N5	3.34	122.86	118.97
3	A	501	FMN	C4A-N5-C5A	3.33	120.43	116.69
3	A	501	FMN	C5'-C4'-C3'	3.22	118.14	112.06
3	B	502	FMN	C5'-C4'-C3'	3.15	118.00	112.06
3	B	502	FMN	O2P-P-O1P	2.56	118.81	110.44
3	B	502	FMN	C4-C4A-C10	2.37	120.77	116.95
3	A	501	FMN	O2P-P-O1P	2.32	118.01	110.44
3	B	502	FMN	O3'-C3'-C4'	-2.31	102.89	108.74
3	A	501	FMN	C4-C4A-C10	2.23	120.56	116.95
3	A	501	FMN	O3'-C3'-C4'	-2.20	103.18	108.74
3	A	501	FMN	C2'-C1'-N10	2.10	115.24	112.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	299/332 (90%)	-0.05	14 (4%) 30 27	34, 49, 91, 106	0
1	B	298/332 (89%)	-0.03	16 (5%) 25 21	31, 49, 89, 106	0
All	All	597/664 (89%)	-0.04	30 (5%) 28 24	31, 49, 90, 106	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	162	ARG	4.3
1	A	162	ARG	3.5
1	A	219	TRP	3.3
1	A	102	ARG	3.3
1	B	68	GLY	3.3
1	A	225	TRP	3.1
1	B	70	GLU	3.1
1	A	223	GLU	3.0
1	B	161	GLN	3.0
1	A	104	GLU	2.9
1	B	131	ARG	2.8
1	B	143	MSE	2.7
1	B	102	ARG	2.7
1	B	221	ARG	2.7
1	B	332	VAL	2.6
1	B	178	LEU	2.6
1	B	69	GLY	2.5
1	A	71	GLU	2.5
1	B	71	GLU	2.4
1	A	178	LEU	2.4
1	B	290	ARG	2.3
1	A	113	LYS	2.3
1	B	219	TRP	2.3
1	A	221	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	23	LYS	2.2
1	A	105	ALA	2.1
1	A	290	ARG	2.1
1	A	107	ARG	2.0
1	A	67	THR	2.0
1	B	309	GLU	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	FMN	A	501	31/31	0.21	0.61	60,68,70,71	0
3	FMN	B	502	31/31	0.19	0.24	58,67,69,70	0
2	CD	A	601	1/1	0.08	-1.88	64,64,64,64	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.