



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 03:36 PM GMT

PDB ID : 3B9J
Title : Structure of Xanthine Oxidase with 2-hydroxy-6-methylpurine
Authors : Paufl, J.M.; Zhang, J.; Bell, C.E.; Hille, R.
Deposited on : 2007-11-05
Resolution : 2.30 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

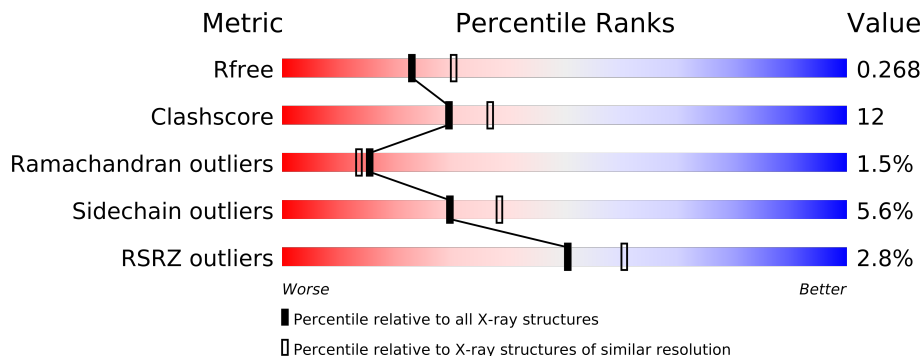
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.30 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	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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 ≥ 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	219	
1	I	219	
2	B	350	
2	J	350	
3	C	763	
3	K	763	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	CA	C	1	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 19847 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 xanthine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	0	0
			1239	778	222	227	12			
1	I	162	Total	C	N	O	S	0	0	0
			1215	764	214	225	12			

- Molecule 2 is a protein called xanthine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	305	Total	C	N	O	S	0	0	0
			2381	1533	400	435	13			
2	J	305	Total	C	N	O	S	0	0	0
			2356	1516	393	434	13			

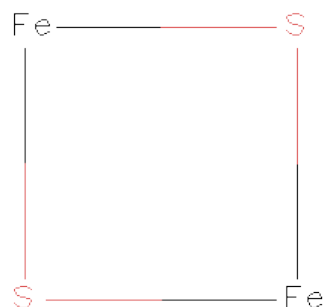
- Molecule 3 is a protein called xanthine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	758	Total	C	N	O	S	0	0	0
			5835	3688	1005	1107	35			
3	K	747	Total	C	N	O	S	0	0	0
			5759	3645	987	1093	34			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

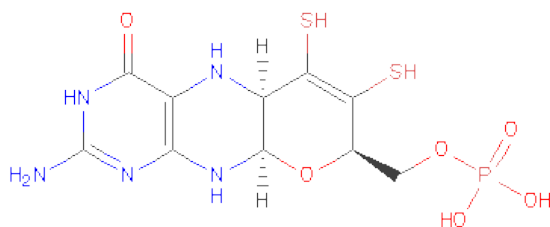
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Ca	0	0
			1	1		

- Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



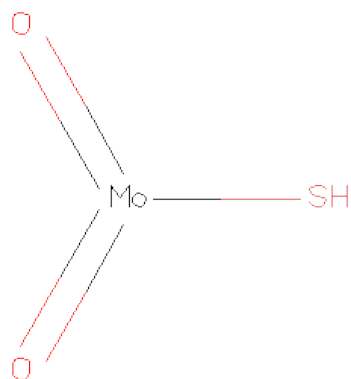
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Fe	S	0	0
			4	2	2		
5	A	1	Total	Fe	S	0	0
			4	2	2		
5	I	1	Total	Fe	S	0	0
			4	2	2		
5	I	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 6 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: MTE) (formula: C₁₀H₁₄N₅O₆PS₂).



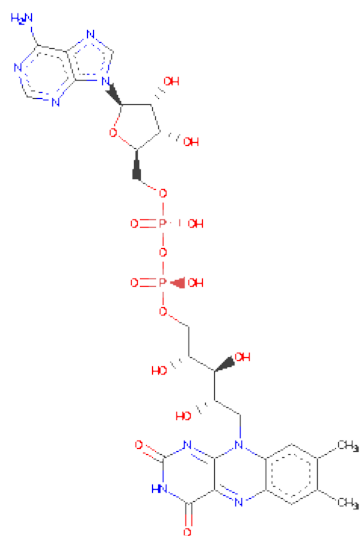
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	C	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
6	K	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 7 is DIOXOTHIOMOLYBDENUM(VI)ION (three-letter code: MOS) (formula: HMoO_2S).



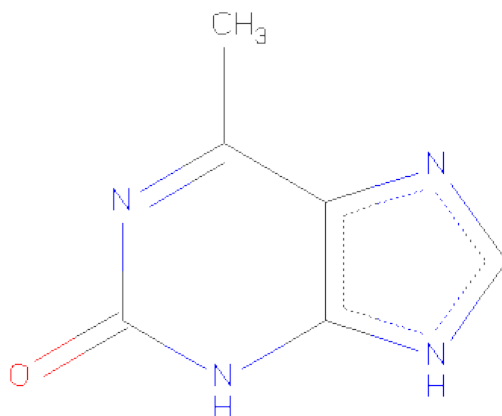
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	Mo	O	S	0	0
			4	1	2	1		
7	K	1	Total	Mo	O	S	0	0
			4	1	2	1		

- Molecule 8 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).



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

- Molecule 9 is 6-METHYL-3,9-DIHYDRO-2H-PURIN-2-ONE (three-letter code: 290) (formula: C₆H₆N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	N	O	0	0
			11	6	4	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	K	1	Total	C	N	O	0	0
			11	6	4	1		

- Molecule 10 is water.

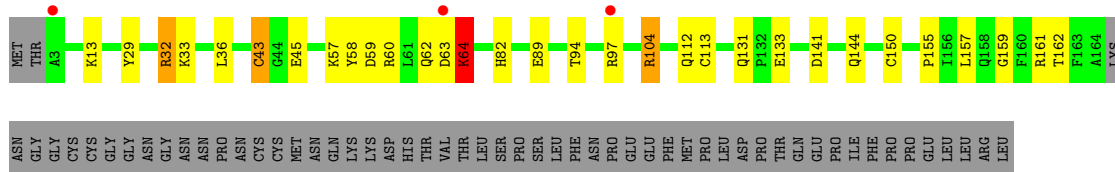
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	68	Total	O	0	0
			68	68		
10	B	87	Total	O	0	0
			87	87		
10	C	247	Total	O	0	0
			247	247		
10	I	73	Total	O	0	0
			73	73		
10	J	90	Total	O	0	0
			90	90		
10	K	296	Total	O	0	0
			296	296		

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.

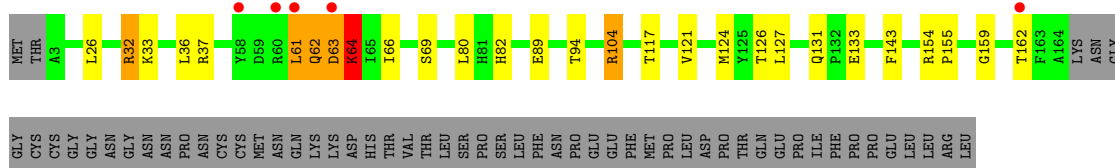
- Molecule 1: xanthine oxidase

Chain A: 



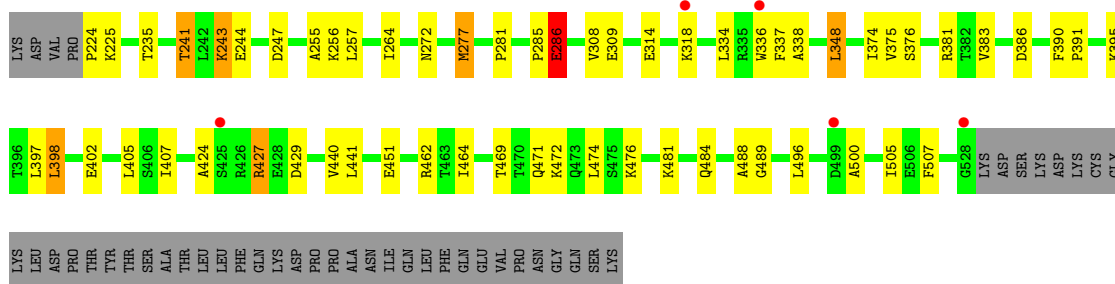
- Molecule 1: xanthine oxidase

Chain I: 



- Molecule 2: xanthine oxidase

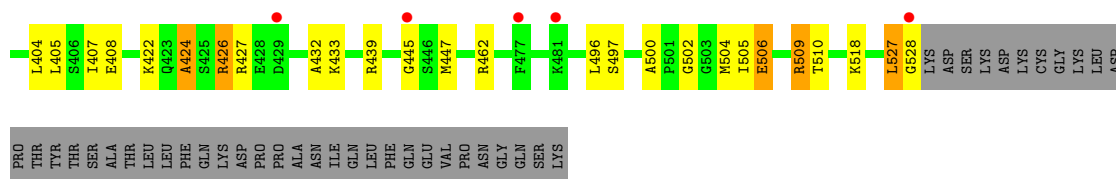
Chain B: 



- Molecule 2: xanthine oxidase

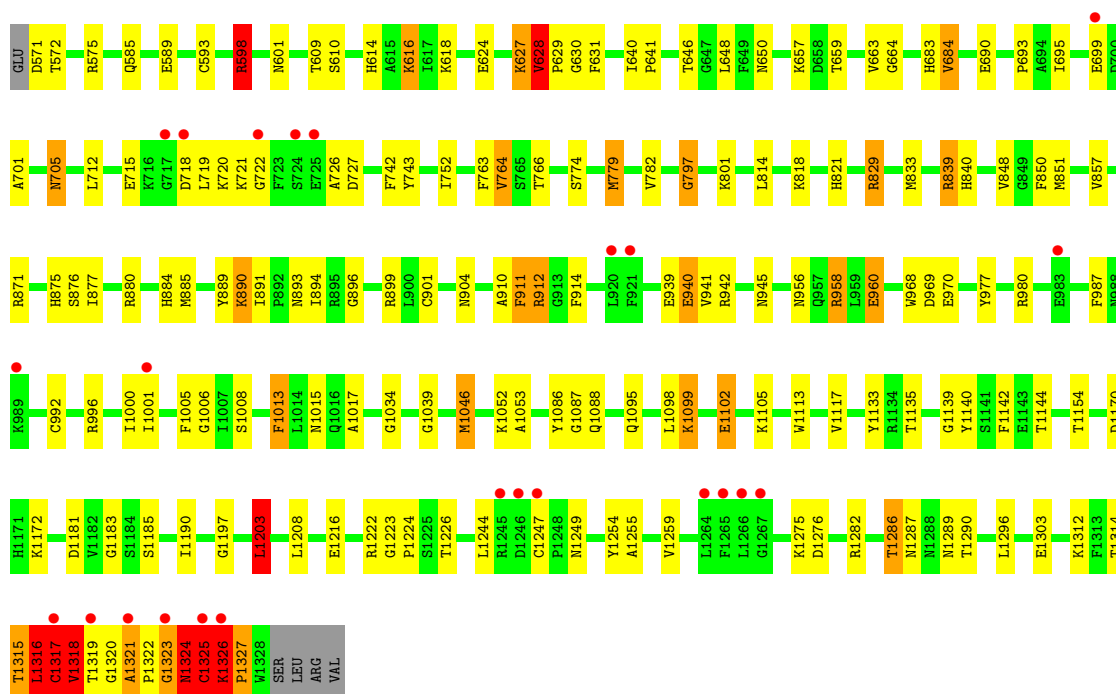
Chain J: 





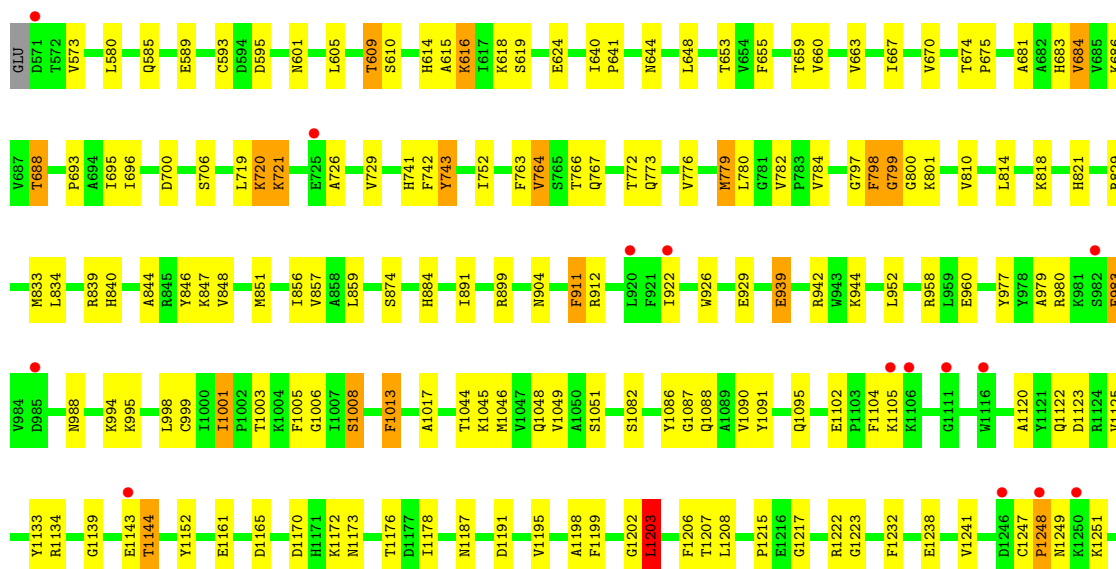
• Molecule 3: xanthine oxidase

Chain C:



• Molecule 3: xanthine oxidase

Chain K:





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	133.19Å 73.79Å 146.50Å 90.00° 98.87° 90.00°	Depositor
Resolution (Å)	144.34 – 2.30 33.59 – 2.23	Depositor EDS
% Data completeness (in resolution range)	96.2 (144.34-2.30) 94.6 (33.59-2.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.194 , 0.263 0.202 , 0.268	Depositor DCC
R_{free} test set	6568 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.786	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 25.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 130252 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19847	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: MOS, CA, FES, FAD, 290, MTE

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	0.84	0/1261	0.90	4/1702 (0.2%)
1	I	0.78	0/1237	0.85	2/1672 (0.1%)
2	B	0.77	0/2430	0.80	2/3282 (0.1%)
2	J	0.72	1/2403 (0.0%)	0.78	2/3248 (0.1%)
3	C	0.83	4/5963 (0.1%)	0.93	16/8078 (0.2%)
3	K	0.78	1/5885 (0.0%)	0.85	8/7971 (0.1%)
All	All	0.79	6/19179 (0.0%)	0.86	34/25953 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	I	0	1
3	C	3	10
3	K	0	5
All	All	3	17

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	593	CYS	CB-SG	-6.74	1.70	1.82
3	K	593	CYS	CB-SG	-6.64	1.71	1.82
3	C	992	CYS	CB-SG	-6.30	1.71	1.82
2	J	314	GLU	CG-CD	5.70	1.60	1.51
3	C	699	GLU	CG-CD	5.22	1.59	1.51

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	839	ARG	NE-CZ-NH2	-10.28	115.16	120.30
1	I	32	ARG	NE-CZ-NH2	-10.17	115.21	120.30
1	A	32	ARG	NE-CZ-NH2	-10.06	115.27	120.30
3	C	1326	LYS	N-CA-C	9.29	136.07	111.00
1	I	32	ARG	NE-CZ-NH1	9.20	124.90	120.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	1315	THR	CA
3	C	1319	THR	CA
3	C	1326	LYS	CA

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	64	LYS	Peptide
3	C	1314	THR	Peptide
3	C	627	LYS	Peptide
3	C	628	VAL	Peptide
3	C	630	GLY	Peptide

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	1239	0	1245	26	0
1	I	1215	0	1201	19	0
2	B	2381	0	2437	58	0
2	J	2356	0	2394	48	0
3	C	5835	0	5747	162	0
3	K	5759	0	5679	156	0
4	C	1	0	0	0	0
5	A	8	0	0	0	0
5	I	8	0	0	0	0
6	C	24	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	K	24	0	10	2	0
7	C	4	0	0	7	0
7	K	4	0	0	8	0
8	B	53	0	31	2	0
8	J	53	0	31	3	0
9	C	11	0	6	4	0
9	K	11	0	6	5	0
10	A	68	0	0	7	0
10	B	87	0	0	6	0
10	C	247	0	0	22	0
10	I	73	0	0	2	0
10	J	90	0	0	5	0
10	K	296	0	0	15	0
All	All	19847	0	18797	461	0

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 12.

The worst 5 of 461 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:K:1334:MOS:O1	9:K:1335:290:C8	1.75	1.32
3:K:833:MET:HE3	3:K:1222:ARG:C	1.51	1.31
3:K:1046:MET:HE1	3:K:1086:TYR:C	1.65	1.16
7:K:1334:MOS:O1	9:K:1335:290:H8	1.30	1.15
3:C:683:HIS:HB2	10:C:1420:HOH:O	1.46	1.12

There are no symmetry-related clashes.

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	160/219 (73%)	151 (94%)	7 (4%)	2 (1%)	18 17
1	I	160/219 (73%)	150 (94%)	7 (4%)	3 (2%)	12 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	303/350 (87%)	286 (94%)	16 (5%)	1 (0%)	50	60
2	J	303/350 (87%)	286 (94%)	12 (4%)	5 (2%)	14	11
3	C	756/763 (99%)	710 (94%)	30 (4%)	16 (2%)	11	8
3	K	743/763 (97%)	704 (95%)	29 (4%)	10 (1%)	18	17
All	All	2425/2664 (91%)	2287 (94%)	101 (4%)	37 (2%)	15	13

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	LYS
2	B	286	GLU
3	C	1316	LEU
3	C	1317	CYS
3	C	1323	GLY

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	135/187 (72%)	128 (95%)	7 (5%)	32	42
1	I	130/187 (70%)	125 (96%)	5 (4%)	44	59
2	B	259/302 (86%)	248 (96%)	11 (4%)	40	53
2	J	254/302 (84%)	240 (94%)	14 (6%)	30	39
3	C	630/639 (99%)	589 (94%)	41 (6%)	24	30
3	K	623/639 (98%)	588 (94%)	35 (6%)	30	38
All	All	2031/2256 (90%)	1918 (94%)	113 (6%)	30	38

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	1276	ASP
1	I	104	ARG
3	K	1134	ARG
3	C	1286	THR

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Mol	Chain	Res	Type
3	C	1316	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	1212	HIS
1	I	82	HIS
3	K	1033	HIS
3	C	1284	GLN
3	C	1287	ASN

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 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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	$\# Z > 2$
5	FES	A	601	1	0,4,4	0.00	-	0,4,4	0.00	-
5	FES	A	602	1	0,4,4	0.00	-	0,4,4	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	FAD	B	606	-	58,58,58	1.10	3 (5%)	85,89,89	2.26	19 (22%)
6	MTE	C	1333	7	26,26,26	1.65	3 (11%)	34,40,40	2.10	10 (29%)
7	MOS	C	1334	6	0,3,3	0.00	-	0,3,3	0.00	-
9	290	C	1335	-	12,12,12	1.91	2 (16%)	13,17,17	3.50	5 (38%)
5	FES	I	601	1	0,4,4	0.00	-	0,4,4	0.00	-
5	FES	I	602	1	0,4,4	0.00	-	0,4,4	0.00	-
8	FAD	J	606	-	58,58,58	1.08	5 (8%)	85,89,89	2.06	14 (16%)
6	MTE	K	1333	7	26,26,26	1.30	3 (11%)	34,40,40	2.13	11 (32%)
7	MOS	K	1334	6	0,3,3	0.00	-	0,3,3	0.00	-
9	290	K	1335	-	12,12,12	1.96	4 (33%)	13,17,17	3.19	5 (38%)

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
5	FES	A	601	1	-	0/0/4/4	0/0/1/1
5	FES	A	602	1	-	0/0/4/4	0/0/1/1
8	FAD	B	606	-	-	0/34/50/50	0/1/6/6
6	MTE	C	1333	7	-	0/6/34/34	0/0/3/3
7	MOS	C	1334	6	-	0/0/0/0	0/0/0/0
9	290	C	1335	-	-	0/0/0/0	0/0/2/2
5	FES	I	601	1	-	0/0/4/4	0/0/1/1
5	FES	I	602	1	-	0/0/4/4	0/0/1/1
8	FAD	J	606	-	-	0/34/50/50	0/1/6/6
6	MTE	K	1333	7	-	0/6/34/34	0/0/3/3
7	MOS	K	1334	6	-	0/0/0/0	0/0/0/0
9	290	K	1335	-	-	0/0/0/0	0/0/2/2

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	1335	290	C6-C5	4.67	1.48	1.43
6	C	1333	MTE	C4-C9	4.57	1.49	1.41
9	K	1335	290	C6-C5	4.36	1.47	1.43
6	C	1333	MTE	C9-C10	4.31	1.47	1.41
6	K	1333	MTE	C9-C10	4.02	1.47	1.41

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	606	FAD	N3A-C2A-N1A	-13.88	117.10	128.71
8	J	606	FAD	N3A-C2A-N1A	-12.42	118.32	128.71
9	C	1335	290	C2-N1-C6	6.91	122.62	115.49
8	B	606	FAD	C2-N1-C10	6.70	121.73	114.98
9	K	1335	290	C2-N1-C6	6.52	122.21	115.49

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, 95th 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 ²)	Q<0.9
1	A	162/219 (73%)	-0.24	3 (1%) 64 73	13, 21, 37, 50	0
1	I	162/219 (73%)	-0.03	5 (3%) 47 56	17, 27, 44, 54	0
2	B	305/350 (87%)	0.01	5 (1%) 68 77	15, 28, 39, 43	0
2	J	305/350 (87%)	0.23	11 (3%) 41 51	22, 34, 44, 47	0
3	C	758/763 (99%)	0.10	24 (3%) 45 55	13, 25, 39, 51	0
3	K	747/763 (97%)	0.02	19 (2%) 54 65	12, 25, 40, 55	0
All	All	2439/2664 (91%)	0.05	67 (2%) 50 62	12, 26, 41, 55	0

The worst 5 of 67 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	1325	CYS	6.6
3	K	1248	PRO	5.3
2	J	429	ASP	3.9
2	J	378	GLY	3.7
3	K	1111	GLY	3.7

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, 95th 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 ²)	Q<0.9
4	CA	C	1	1/1	0.23	2.37	49,49,49,49	0
9	290	C	1335	11/11	0.16	0.98	30,31,32,32	0
8	FAD	J	606	53/53	0.13	-0.32	19,25,30,37	0
8	FAD	B	606	53/53	0.12	-0.42	13,22,25,27	0
5	FES	A	602	4/4	0.10	-0.55	13,14,16,18	0
9	290	K	1335	11/11	0.12	-0.60	19,21,22,23	0
5	FES	A	601	4/4	0.09	-0.74	13,16,18,18	0
5	FES	I	602	4/4	0.10	-1.05	19,19,19,20	0
5	FES	I	601	4/4	0.08	-1.29	19,19,20,21	0
6	MTE	K	1333	24/24	0.10	-1.54	27,29,32,35	0
7	MOS	K	1334	4/4	0.12	-1.80	40,44,45,46	0
6	MTE	C	1333	24/24	0.09	-1.98	20,24,29,32	0
7	MOS	C	1334	4/4	0.09	-2.87	42,45,48,49	0

6.5 Other polymers ⓘ

There are no such residues in this entry.