



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:57 AM GMT

PDB ID : 1FPX
Title : CRYSTAL STRUCTURE ANALYSIS OF SELENOMETHIONINE SUBSTITUTED ISOFLAVONE O-METHYLTRANSFERASE
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Deposited on : 2000-08-31
Resolution : 1.65 Å(reported)

This is a full wwPDB validation 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>

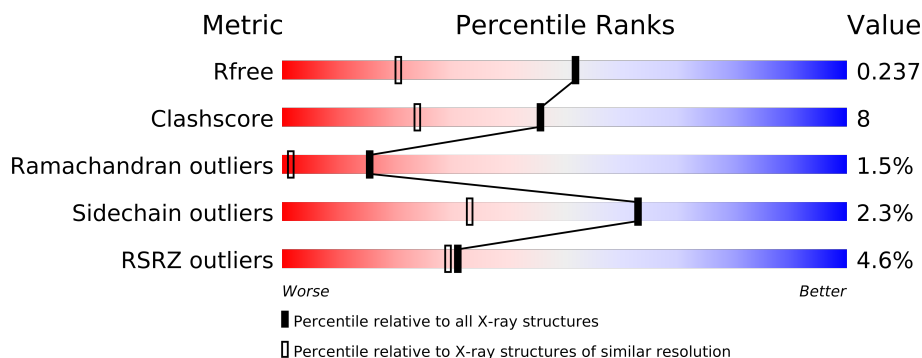
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.65 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	1404 (1.68-1.64)
Clashscore	79885	1001 (1.66-1.66)
Ramachandran outliers	78287	1581 (1.68-1.64)
Sidechain outliers	78261	1580 (1.68-1.64)
RSRZ outliers	66119	1404 (1.68-1.64)

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	352	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2905 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.

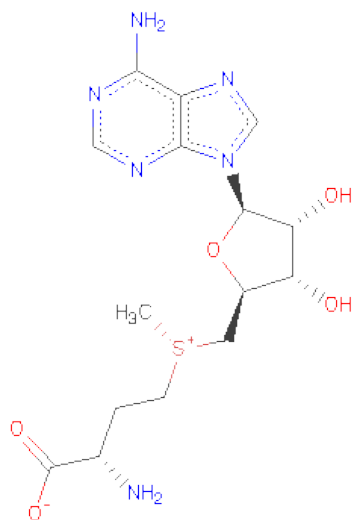
- Molecule 1 is a protein called ISOFLAVONE-O-METHYLTRANSFERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	Se	0	0	0
			2735	1757	448	513	8	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	Modified Residue	UNP O24529
A	31	MSE	MET	Modified Residue	UNP O24529
A	39	MSE	MET	Modified Residue	UNP O24529
A	75	MSE	MET	Modified Residue	UNP O24529
A	114	MSE	MET	Modified Residue	UNP O24529
A	168	MSE	MET	Modified Residue	UNP O24529
A	240	MSE	MET	Modified Residue	UNP O24529
A	289	MSE	MET	Modified Residue	UNP O24529
A	307	MSE	MET	Modified Residue	UNP O24529
A	311	MSE	MET	Modified Residue	UNP O24529

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C₁₅H₂₂N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	27	15	6	5	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	143	Total	O	0	0
			143	143		

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- Molecule 1: ISOFLAVONE-O-METHYLTRANSFERASE

The chart displays the performance of various models across 28 different tasks. The tasks are listed on the y-axis, and the performance score is on the x-axis. Each bar is color-coded: green for scores between 0.5 and 1.0, yellow for scores between 0.0 and 0.5, and grey for scores between -0.5 and 0.0. Red dots indicate the best performance for each task. The tasks are: MSE, ALA, SER, SER, ILE, ASN, GLY, R8, K9, P10, S11, E12, I13, F14, K15, F27, M39, P42, M43, M66, I60, L61, R73, I87, T88, K89, E90, R105, G106, S107, V118, W133, L141, L174, R180, E225, N226, L227, S228, G229, S230, N231, N232, L232.

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.81Å 50.24Å 63.74Å 90.00° 106.76° 90.00°	Depositor
Resolution (Å)	39.28 – 1.65 39.28 – 1.52	Depositor EDS
% Data completeness (in resolution range)	97.6 (39.28-1.65) 95.5 (39.28-1.52)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 1.52Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.218 , 0.235 0.236 , 0.237	Depositor DCC
R_{free} test set	2622 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	25.0	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 28.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 65134 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2905	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.37% 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: SAM

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	0.80	0/2780	0.86	3/3743 (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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	ARG	NE-CZ-NH1	7.70	124.15	120.30
1	A	107	SER	N-CA-C	-6.14	94.43	111.00
1	A	73	ARG	NE-CZ-NH2	-5.40	117.60	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	254	TYR	Sidechain

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	2735	0	2765	39	0
2	A	27	0	20	7	0
3	A	143	0	0	0	1
All	All	2905	0	2785	46	1

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 8.

All (46) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:1699:SAM:C3'	2:A:1699:SAM:C5'	2.30	1.10
2:A:1699:SAM:C5'	2:A:1699:SAM:O4'	2.02	1.05
2:A:1699:SAM:SD	2:A:1699:SAM:C4'	2.48	1.00
2:A:1699:SAM:H5'2	2:A:1699:SAM:C4'	1.48	0.98
2:A:1699:SAM:H5'1	2:A:1699:SAM:C4'	1.48	0.96
1:A:262:LYS:HE2	1:A:266:ARG:NH2	1.84	0.91
1:A:43:ASN:HD21	1:A:105:ARG:H	1.17	0.90
2:A:1699:SAM:C5'	2:A:1699:SAM:C4'	0.88	0.88
1:A:10:PRO:HG2	1:A:12:GLU:HG2	1.54	0.87
1:A:133:TRP:HE1	1:A:315:ASN:HD21	1.23	0.82
1:A:9:LYS:HB3	1:A:10:PRO:HD2	1.65	0.78
1:A:289:MSE:HE1	1:A:307:MSE:HG3	1.67	0.75
1:A:105:ARG:HG3	1:A:105:ARG:HH11	1.55	0.71
1:A:12:GLU:O	1:A:15:LYS:HG3	1.93	0.69
1:A:10:PRO:HD2	1:A:12:GLU:OE1	1.94	0.68
1:A:43:ASN:HD21	1:A:105:ARG:N	1.93	0.66
1:A:230:SER:O	1:A:231:ASN:O	2.19	0.60
1:A:9:LYS:CB	1:A:10:PRO:HD2	2.36	0.53
1:A:56:ASN:O	1:A:60:ILE:HG13	2.09	0.53
1:A:347:LEU:C	1:A:347:LEU:HD13	2.29	0.53
1:A:39:MSE:HE3	1:A:61:LEU:HD22	1.91	0.52
1:A:262:LYS:HE2	1:A:266:ARG:HH21	1.70	0.51
1:A:105:ARG:CG	1:A:105:ARG:HH11	2.24	0.51
1:A:347:LEU:HD13	1:A:348:ILE:N	2.26	0.50
1:A:277:ASN:O	1:A:278:ASP:HB3	2.10	0.50
1:A:10:PRO:CG	1:A:12:GLU:HG2	2.36	0.49
1:A:133:TRP:HE1	1:A:315:ASN:ND2	2.00	0.48
1:A:10:PRO:C	1:A:12:GLU:H	2.16	0.48
1:A:225:GLU:O	1:A:226:ASN:HB2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:15:LYS:C	1:A:15:LYS:HD2	2.35	0.47
1:A:280:LYS:O	1:A:281:ARG:HD2	2.16	0.45
1:A:272:LYS:NZ	1:A:332:GLY:HA3	2.30	0.45
1:A:105:ARG:NH1	1:A:105:ARG:HG3	2.29	0.45
1:A:338:ILE:HG12	1:A:348:ILE:HG12	1.99	0.45
1:A:9:LYS:HB3	1:A:10:PRO:CD	2.42	0.44
1:A:10:PRO:O	1:A:12:GLU:N	2.48	0.44
1:A:233:LEU:HD23	1:A:233:LEU:C	2.37	0.44
1:A:9:LYS:HB3	1:A:12:GLU:OE1	2.19	0.43
1:A:9:LYS:CB	1:A:10:PRO:CD	2.96	0.42
1:A:230:SER:O	1:A:231:ASN:C	2.57	0.42
1:A:272:LYS:HZ3	1:A:332:GLY:HA3	1.85	0.42
2:A:1699:SAM:HE2	2:A:1699:SAM:HB1	1.95	0.42
1:A:347:LEU:C	1:A:347:LEU:CD1	2.88	0.42
1:A:193:VAL:CG1	1:A:250:VAL:HG22	2.49	0.41
1:A:141:LEU:HB3	1:A:313:CYS:HA	2.02	0.40
1:A:8:ARG:HA	1:A:8:ARG:HD2	1.55	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	Distance(Å)	Clash(Å)
3:A:1794:HOH:O	3:A:1794:HOH:O[2_556]	1.79	0.41

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	343/352 (97%)	333 (97%)	5 (2%)	5 (2%)	15 1

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	ASN
1	A	11	SER

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Mol	Chain	Res	Type
1	A	232	ASN
1	A	9	LYS
1	A	10	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	307/302 (102%)	300 (98%)	7 (2%)	63	33

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LYS
1	A	42	PRO
1	A	174	LEU
1	A	180	ARG
1	A	257	HIS
1	A	277	ASN
1	A	294	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	43	ASN
1	A	47	ASN
1	A	70	ASN
1	A	161	ASN
1	A	222	GLN
1	A	246	ASN
1	A	277	ASN
1	A	298	ASN
1	A	315	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 ⓘ

1 ligand 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	$\# Z > 2$
2	SAM	A	1699	-	26,29,29	4.83	10 (38%)	38,42,42	4.76	13 (34%)

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
2	SAM	A	1699	-	1/1/7/7	0/13/33/33	0/1/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1699	SAM	C5'-C4'	-22.55	0.88	1.53
2	A	1699	SAM	O4'-C1'	4.56	1.48	1.41
2	A	1699	SAM	CG-CB	-3.47	1.47	1.52
2	A	1699	SAM	C8-N7	-3.35	1.28	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1699	SAM	C5'-SD	3.00	1.90	1.81
2	A	1699	SAM	O3'-C3'	2.86	1.49	1.43
2	A	1699	SAM	C1'-N9	-2.71	1.40	1.48
2	A	1699	SAM	C2-N3	2.30	1.36	1.32
2	A	1699	SAM	O4'-C4'	2.24	1.50	1.45
2	A	1699	SAM	CG-SD	2.15	1.85	1.80

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1699	SAM	O4'-C1'-N9	18.94	126.05	108.44
2	A	1699	SAM	CG-CB-CA	13.12	131.54	112.22
2	A	1699	SAM	C5'-C4'-C3'	10.10	140.03	116.32
2	A	1699	SAM	N3-C2-N1	-7.78	122.20	128.71
2	A	1699	SAM	C3'-C2'-C1'	4.95	108.66	100.91
2	A	1699	SAM	C8-N9-C1'	-4.79	116.94	126.38
2	A	1699	SAM	C1'-N9-C4	4.38	134.20	126.64
2	A	1699	SAM	C2'-C1'-N9	4.24	124.16	113.27
2	A	1699	SAM	C4-C5-N7	3.75	112.73	109.52
2	A	1699	SAM	C2-N1-C6	3.42	124.94	118.77
2	A	1699	SAM	C5-C4-N9	-3.26	102.46	107.16
2	A	1699	SAM	N6-C6-N1	2.93	125.11	119.36
2	A	1699	SAM	C8-N9-C4	2.52	108.83	106.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1699	SAM	C4'

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	345/352 (98%)	0.30	16 (4%) 31 29	18, 25, 41, 50	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	PRO	5.4
1	A	90	GLU	4.4
1	A	11	SER	4.2
1	A	88	THR	3.8
1	A	89	LYS	3.4
1	A	8	ARG	3.2
1	A	106	GLY	3.0
1	A	87	ILE	2.9
1	A	27	PHE	2.6
1	A	226	ASN	2.5
1	A	307	MSE	2.5
1	A	230	SER	2.3
1	A	278	ASP	2.2
1	A	228	SER	2.1
1	A	118	VAL	2.1
1	A	14	PHE	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, 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
2	SAM	A	1699	27/27	0.11	1.66	19,21,28,31	0

6.5 Other polymers

There are no such residues in this entry.