



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 01:05 am GMT

PDB ID : 3E35  
Title : Actinobacteria-specific protein of unknown function, SCO1997  
Authors : Gao, B.; Gupta, R.S.; Sugiman-Marangos, S.; Junop, M.S.  
Deposited on : 2008-08-06  
Resolution : 2.20 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.

---

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

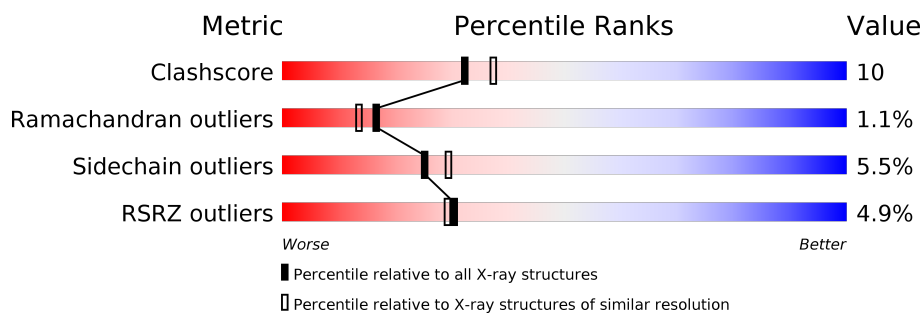
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	325	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2318 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 Uncharacterized protein SCO1997.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	Se	0	0	0
			2086	1319	363	401	3			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	313	LYS	-	EXPRESSION TAG	UNP Q9S2K6
A	314	LEU	-	EXPRESSION TAG	UNP Q9S2K6
A	315	ALA	-	EXPRESSION TAG	UNP Q9S2K6
A	316	ALA	-	EXPRESSION TAG	UNP Q9S2K6
A	317	ALA	-	EXPRESSION TAG	UNP Q9S2K6
A	318	LEU	-	EXPRESSION TAG	UNP Q9S2K6
A	319	GLU	-	EXPRESSION TAG	UNP Q9S2K6
A	320	HIS	-	EXPRESSION TAG	UNP Q9S2K6
A	321	HIS	-	EXPRESSION TAG	UNP Q9S2K6
A	322	HIS	-	EXPRESSION TAG	UNP Q9S2K6
A	323	HIS	-	EXPRESSION TAG	UNP Q9S2K6
A	324	HIS	-	EXPRESSION TAG	UNP Q9S2K6
A	325	HIS	-	EXPRESSION TAG	UNP Q9S2K6

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

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

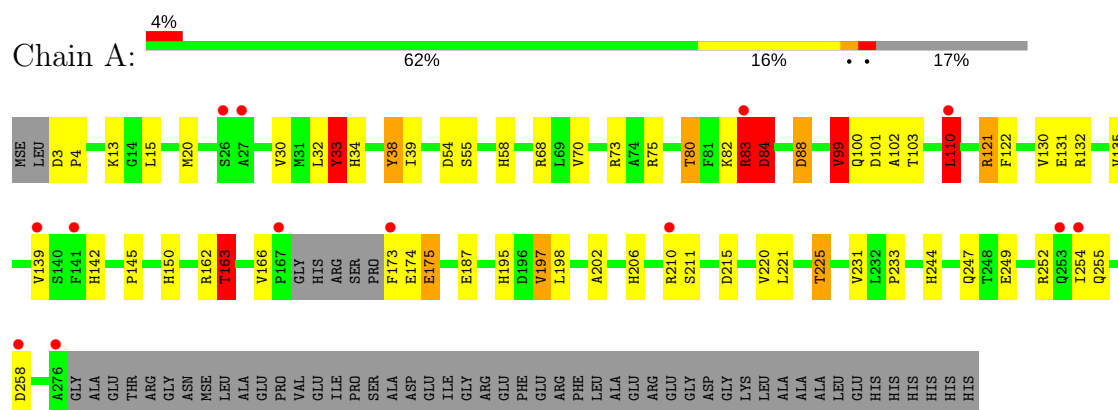
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	230	Total	O	0	0
			230	230		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Uncharacterized protein SCO1997



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.08Å 135.08Å 135.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.35 – 2.20 30.21 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.8 (95.35-2.20) 96.6 (30.21-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.11 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.175 , 0.234 0.177 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	36.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 62.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.025 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	1.42	18/2133 (0.8%)	1.36	16/2910 (0.5%)

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	3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	33	TYR	CE1-CZ	-9.70	1.25	1.38
1	A	73	ARG	CD-NE	-9.01	1.31	1.46
1	A	38	TYR	CD2-CE2	7.58	1.50	1.39
1	A	187	GLU	CB-CG	-6.65	1.39	1.52
1	A	33	TYR	CE2-CZ	-6.53	1.30	1.38
1	A	38	TYR	CB-CG	6.25	1.61	1.51
1	A	33	TYR	CD1-CE1	-6.24	1.29	1.39
1	A	33	TYR	CD2-CE2	-6.19	1.30	1.39
1	A	122	PHE	CD2-CE2	6.16	1.51	1.39
1	A	122	PHE	CE2-CZ	5.77	1.48	1.37
1	A	163	THR	CB-CG2	-5.54	1.34	1.52
1	A	75	ARG	C-O	-5.47	1.12	1.23
1	A	33	TYR	CB-CG	-5.33	1.43	1.51
1	A	249	GLU	CG-CD	5.28	1.59	1.51
1	A	73	ARG	CG-CD	5.19	1.65	1.51
1	A	131	GLU	CG-CD	5.12	1.59	1.51
1	A	33	TYR	CG-CD1	-5.08	1.32	1.39
1	A	102	ALA	CA-CB	5.05	1.63	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	ARG	NE-CZ-NH2	-27.40	106.60	120.30
1	A	73	ARG	NE-CZ-NH1	15.01	127.80	120.30
1	A	110	LEU	CB-CG-CD2	8.83	126.02	111.00
1	A	132	ARG	NE-CZ-NH1	8.09	124.35	120.30
1	A	162	ARG	NE-CZ-NH2	-7.95	116.32	120.30
1	A	13	LYS	CD-CE-NZ	-7.72	93.95	111.70
1	A	121	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	A	88	ASP	CB-CG-OD1	6.88	124.50	118.30
1	A	211	SER	CB-CA-C	-6.37	98.01	110.10
1	A	55	SER	CB-CA-C	-5.90	98.89	110.10
1	A	187	GLU	CG-CD-OE2	-5.61	107.08	118.30
1	A	99	VAL	CA-CB-CG2	5.48	119.12	110.90
1	A	215	ASP	CB-CG-OD1	-5.36	113.47	118.30
1	A	197	VAL	CB-CA-C	5.29	121.45	111.40
1	A	73	ARG	NH1-CZ-NH2	5.28	125.20	119.40
1	A	70	VAL	CG1-CB-CG2	-5.25	102.49	110.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	197	VAL	Peptide
1	A	210	ARG	Peptide
1	A	83	ARG	Peptide

## 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	2086	0	2014	41	0
2	A	2	0	0	0	0
3	A	230	0	0	15	0
All	All	2318	0	2014	41	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (41) 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:68:ARG:NH1	1:A:121:ARG:HH22	1.71	0.86
1:A:80:THR:HG22	3:A:350:HOH:O	1.79	0.82
1:A:3:ASP:HB3	1:A:4:PRO:HD3	1.65	0.78
1:A:3:ASP:N	3:A:522:HOH:O	2.17	0.77
1:A:83:ARG:HB2	1:A:84:ASP:OD1	1.92	0.69
1:A:173:PHE:CD2	1:A:174:GLU:HB2	2.28	0.69
1:A:20:MSE:HE1	3:A:411:HOH:O	1.92	0.69
1:A:68:ARG:HH12	1:A:121:ARG:HH22	1.42	0.68
1:A:195:HIS:HE1	3:A:428:HOH:O	1.75	0.68
1:A:33:TYR:CD1	1:A:33:TYR:N	2.63	0.65
1:A:68:ARG:NH1	1:A:121:ARG:NH2	2.45	0.64
1:A:101:ASP:OD1	1:A:103:THR:HB	1.97	0.63
1:A:83:ARG:CB	1:A:84:ASP:OD1	2.48	0.61
1:A:58:HIS:HB3	1:A:99:VAL:HB	1.84	0.59
1:A:80:THR:HG23	1:A:88:ASP:HB3	1.86	0.58
1:A:139:VAL:HA	1:A:198:LEU:O	2.09	0.53
1:A:39:ILE:HD13	3:A:495:HOH:O	2.09	0.52
1:A:33:TYR:HD1	1:A:33:TYR:N	2.05	0.52
1:A:163:THR:HB	3:A:402:HOH:O	2.10	0.51
1:A:221:LEU:O	1:A:225:THR:HB	2.11	0.50
1:A:254:ILE:HG13	1:A:255:GLN:N	2.26	0.50
1:A:3:ASP:HB3	1:A:4:PRO:CD	2.40	0.50
1:A:142:HIS:HE1	3:A:465:HOH:O	1.94	0.49
1:A:150:HIS:HD2	1:A:247:GLN:HE22	1.59	0.49
1:A:82:LYS:O	1:A:83:ARG:HB2	2.12	0.49
1:A:54:ASP:OD1	3:A:537:HOH:O	2.20	0.48
1:A:244:HIS:HB3	3:A:441:HOH:O	2.14	0.46
1:A:80:THR:CG2	3:A:350:HOH:O	2.49	0.46
1:A:33:TYR:HB3	1:A:110:LEU:HB3	1.98	0.45
1:A:38:TYR:CG	1:A:39:ILE:N	2.85	0.45
1:A:225:THR:HG22	3:A:400:HOH:O	2.18	0.43
1:A:33:TYR:CB	1:A:110:LEU:HB3	2.48	0.43
1:A:34:HIS:HD2	3:A:532:HOH:O	2.02	0.43
1:A:145:PRO:HB2	1:A:206:HIS:ND1	2.34	0.42
1:A:142:HIS:CE1	3:A:465:HOH:O	2.71	0.42
1:A:130:VAL:HG13	1:A:135:VAL:HB	2.01	0.42
1:A:231:VAL:HG23	1:A:233:PRO:HD3	2.01	0.42
1:A:100:GLN:NE2	3:A:473:HOH:O	2.50	0.42
1:A:202:ALA:HB2	1:A:220:VAL:HG23	2.02	0.42
1:A:175:GLU:HG3	1:A:175:GLU:O	2.21	0.41

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:ARG:HG3	3:A:380:HOH:O	2.20	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	265/325 (82%)	255 (96%)	7 (3%)	3 (1%)	17 13

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	ASP
1	A	258	ASP
1	A	83	ARG

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	217/255 (85%)	205 (94%)	12 (6%)	25 29

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	30	VAL
1	A	32	LEU
1	A	33	TYR
1	A	80	THR
1	A	84	ASP
1	A	99	VAL
1	A	110	LEU
1	A	163	THR
1	A	166	VAL
1	A	175	GLU
1	A	225	THR

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	34	HIS
1	A	100	GLN
1	A	142	HIS
1	A	159	HIS
1	A	195	HIS
1	A	244	HIS
1	A	247	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	266/325 (81%)	-0.05	13 (4%) 30 29	26, 33, 42, 55	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	173	PHE	3.8
1	A	276	ALA	3.8
1	A	83	ARG	3.0
1	A	110	LEU	2.9
1	A	167	PRO	2.6
1	A	258	ASP	2.6
1	A	141	PHE	2.6
1	A	253	GLN	2.6
1	A	139	VAL	2.4
1	A	27	ALA	2.4
1	A	210	ARG	2.3
1	A	254	ILE	2.2
1	A	26	SER	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(Å <sup>2</sup> )	Q<0.9
2	MG	A	327	1/1	0.99	0.05	-	38,38,38,38	1
2	MG	A	326	1/1	0.98	0.03	-	37,37,37,37	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.