Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	1G2Z
Title	:	DIMERIZATION DOMAIN OF HNF-1ALPHA WITH A LEU 13 SELENOMETHIONINE SUBSTITUTION
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Deposited on	:	2000-10-23
Resolution	:	1.15 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

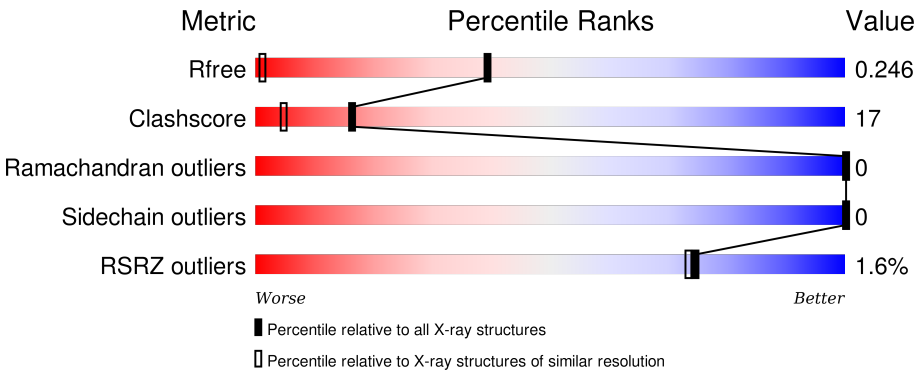
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.15 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	1495 (1.20-1.08)
Clashscore	102246	1593 (1.20-1.08)
Ramachandran outliers	100387	1521 (1.20-1.08)
Sidechain outliers	100360	1518 (1.20-1.08)
RSRZ outliers	91569	1498 (1.20-1.08)

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. 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 <=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	32	78% 22%
1	B	32	3% 56% 34% 6% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 561 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 HEPATOCYTE NUCLEAR FACTOR 1-ALPHA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	32	235	148	37	48	1	1	0	0	0
			Total	C	N	O	Se				
1	B	31	227	143	36	47	1		0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	MSE	LEU	Engineered	UNP P22361
B	13	MSE	LEU	Engineered	UNP P22361

- Molecule 2 is water.

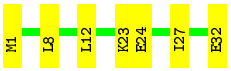
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	55	55	55	0	0
			Total	O		
2	B	44	44	44	0	0

3 Residue-property plots (i)

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: HEPATOCYTE NUCLEAR FACTOR 1-ALPHA

Chain A:



- Molecule 1: HEPATOCYTE NUCLEAR FACTOR 1-ALPHA

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	37.10Å 41.20Å 42.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.50 – 1.15 18.75 – 1.03	Depositor EDS
% Data completeness (in resolution range)	96.0 (29.50-1.15) 91.3 (18.75-1.03)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 1.03Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.243 0.215 , 0.246	Depositor DCC
R_{free} test set	1124 reflections (4.97%)	DCC
Wilson B-factor (Å^2)	11.4	Xtriage
Anisotropy	0.324	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 96.6	EDS
Estimated twinning fraction	0.014 for -h,l,k	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 29550 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	561	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	1.19	2/233 (0.9%)	1.11	1/309 (0.3%)
1	B	1.15	2/225 (0.9%)	1.25	2/299 (0.7%)
All	All	1.17	4/458 (0.9%)	1.18	3/608 (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	B	2	0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	24	GLU	CD-OE2	6.65	1.32	1.25
1	A	32	GLU	CD-OE2	6.03	1.32	1.25
1	B	32	GLU	CD-OE2	5.89	1.32	1.25
1	B	18	GLU	CD-OE2	5.32	1.31	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	3	SER	N-CA-CB	11.08	127.12	110.50
1	A	1	MET	CA-CB-CG	-7.06	101.30	113.30
1	B	2	VAL	CB-CA-C	5.15	121.19	111.40

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	2	VAL	CA
1	B	3	SER	CA

There are no planarity outliers.

5.2 Too-close contacts (i)

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	235	0	255	5	5
1	B	227	0	243	12	5
2	A	55	0	0	0	0
2	B	44	0	0	2	0
All	All	561	0	498	16	5

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 (16) 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:B:2:VAL:HG12	1:B:6:SER:HB2	1.60	0.84
1:A:8:LEU:O	1:A:12:LEU:HG	1.80	0.82
1:B:2:VAL:HG22	1:B:5:LEU:HD23	1.67	0.76
1:A:23:LYS:NZ	1:A:27:ILE:HD11	2.00	0.75
1:B:22:SER:HB2	1:B:24:GLU:OE1	1.94	0.66
1:B:2:VAL:O	1:B:6:SER:N	2.18	0.62
1:A:23:LYS:HZ3	1:A:27:ILE:HD11	1.65	0.59
1:A:23:LYS:HZ2	1:A:27:ILE:HD11	1.66	0.58
1:B:2:VAL:HA	1:B:5:LEU:HB3	1.86	0.58
1:A:12:LEU:HD22	1:B:12:LEU:HD22	1.87	0.57
1:B:24:GLU:CD	1:B:24:GLU:H	2.05	0.55
1:B:24:GLU:OE1	1:B:24:GLU:N	2.25	0.53
1:B:8:LEU:O	1:B:12:LEU:HG	2.10	0.51
1:B:2:VAL:O	1:B:3:SER:C	2.49	0.50
1:B:13:MSE:HG3	2:B:43:HOH:O	2.12	0.49
1:B:23:LYS:HG2	2:B:51:HOH:O	2.20	0.41

All (5) 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:23:LYS:CE	1:B:27:ILE:CD1[2_756]	0.74	1.46
1:A:23:LYS:NZ	1:B:27:ILE:CD1[2_756]	1.51	0.69
1:A:23:LYS:CE	1:B:27:ILE:CG1[2_756]	1.88	0.32
1:A:23:LYS:NZ	1:B:27:ILE:CG1[2_756]	2.01	0.19
1:A:23:LYS:CD	1:B:27:ILE:CD1[2_756]	2.10	0.10

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	30/32 (94%)	30 (100%)	0	0	100	100
1	B	29/32 (91%)	28 (97%)	1 (3%)	0	100	100
All	All	59/64 (92%)	58 (98%)	1 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	26/25 (104%)	26 (100%)	0	100	100
1	B	25/25 (100%)	25 (100%)	0	100	100
All	All	51/50 (102%)	51 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no

such sidechains identified.

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)

There are no ligands in this entry.

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, 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	31/32 (96%)	-0.06	0 100 100	9, 14, 46, 63	0
1	B	30/32 (93%)	-0.00	1 (3%) 50 48	8, 13, 44, 59	0
All	All	61/64 (95%)	-0.03	1 (1%) 74 73	8, 13, 46, 63	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	VAL	5.9

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.