



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:39 AM GMT

PDB ID : 2DSQ
Title : Structural Basis for the Inhibition of Insulin-like Growth Factors by IGF Binding Proteins
Authors : Sitar, T.; Popowicz, G.M.; Siwanowicz, I.; Huber, R.; Holak, T.A.
Deposited on : 2006-07-05
Resolution : 2.80 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

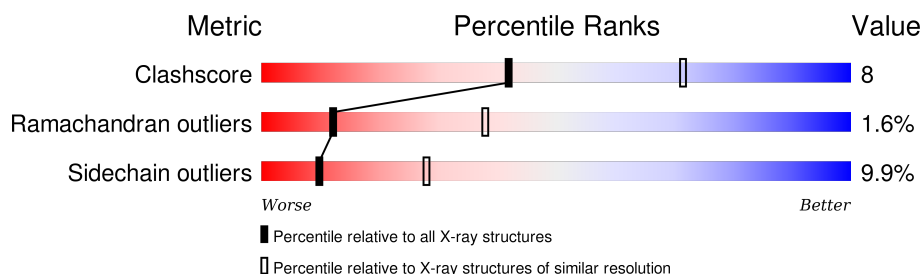
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	92	
1	B	92	
2	C	70	
2	I	70	
3	G	94	
3	H	94	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3072 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 Insulin-like growth factor-binding protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	87	Total	C	N	O	S	0	0	0
			627	386	112	114	15			
1	A	91	Total	C	N	O	S	0	0	0
			651	401	116	119	15			

- Molecule 2 is a protein called Insulin-like growth factor IB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	49	Total	C	N	O	S	0	0	0
			385	243	64	71	7			
2	C	51	Total	C	N	O	S	0	0	0
			392	247	63	75	7			

- Molecule 3 is a protein called Insulin-like growth factor-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	73	Total	C	N	O	S	0	0	0
			567	356	99	105	7			
3	H	58	Total	C	N	O	S	0	0	0
			450	289	75	80	6			

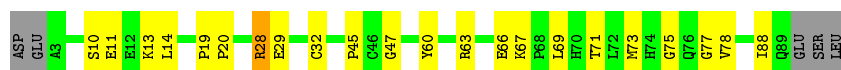
3 Residue-property plots [i](#)

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.


Note EDS was not executed.

- Molecule 1: Insulin-like growth factor-binding protein 4

Chain B: 



- Molecule 1: Insulin-like growth factor-binding protein 4

Chain A: 



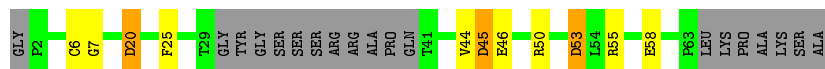
- Molecule 2: Insulin-like growth factor IB

Chain I: 



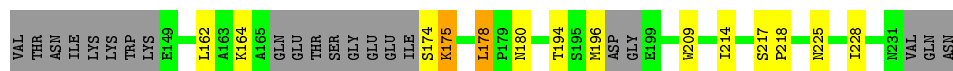
- Molecule 2: Insulin-like growth factor IB

Chain C: 



- Molecule 3: Insulin-like growth factor-binding protein 1

Chain G: 



- Molecule 3: Insulin-like growth factor-binding protein 1

Chain H: 

VAL	THR	ASN	ILE	LYS	TRP	K148	E149	I153	R157	L162	ALA	LYS	ALA	GLN	GLU	THR	SER	GLY	GLU	GLU	ILE	SER	LYS	F176	M180	C183	N182	G185	H188	S189	R190	Q191	C192	GLU	THR	SER	MET	ASP	GLY	GLU	ALA	G201	L202	C205	P224	M225	C226	GLN	ILE	TYR
-----	-----	-----	-----	-----	-----	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	-----	-----	-----

PHE	ASN	VAL	GLN	ASN
-----	-----	-----	-----	-----

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.28 Å 43.66 Å 81.15 Å 90.00° 91.67° 90.00°	Depositor
Resolution (Å)	10.00 – 2.80	Depositor
% Data completeness (in resolution range)	99.8 (10.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.288 , 0.357	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3072	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.39	0/665	0.60	0/902
1	B	0.39	0/641	0.60	0/869
2	C	0.40	0/399	0.54	0/537
2	I	0.42	0/391	0.56	0/523
3	G	0.36	0/581	0.54	0/787
3	H	0.41	0/464	0.55	0/631
All	All	0.40	0/3141	0.57	0/4249

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	651	0	626	8	0
1	B	627	0	606	12	0
2	C	392	0	361	6	0
2	I	385	0	362	7	0
3	G	567	0	512	10	0
3	H	450	0	400	16	0
All	All	3072	0	2867	50	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 8.

All (50) 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)
3:H:191:GLN:HA	3:H:192:CYS:HB2	1.29	1.07
2:I:6:CYS:HA	2:I:10:LEU:HB2	1.48	0.93
3:H:148:LYS:HG3	3:H:149:GLU:H	1.34	0.92
3:H:191:GLN:CA	3:H:192:CYS:HB2	2.06	0.85
1:B:63:ARG:HE	1:B:88:ILE:HG23	1.53	0.74
3:H:182:ASN:HB3	3:H:188:HIS:CE1	2.28	0.68
3:G:214:ILE:HD11	3:G:228:ILE:HD11	1.76	0.66
1:A:45:PRO:HA	1:A:77:GLY:O	1.96	0.65
1:B:47:GLY:HA3	1:B:75:GLY:HA2	1.80	0.64
3:G:174:SER:HA	3:G:175:LYS:C	2.17	0.64
3:H:191:GLN:HA	3:H:192:CYS:CB	2.13	0.63
2:C:25:PHE:HZ	3:H:176:PHE:HZ	1.46	0.63
1:B:63:ARG:NE	1:B:88:ILE:HG23	2.15	0.62
3:G:174:SER:HA	3:G:175:LYS:O	2.00	0.62
1:A:28:ARG:HE	3:G:228:ILE:HG23	1.65	0.61
3:H:149:GLU:CG	3:H:185:GLY:HA3	2.31	0.60
1:A:65:VAL:HG21	1:A:71:THR:HG21	1.84	0.60
2:C:7:GLY:HA3	3:H:180:ASN:HB3	1.85	0.59
1:A:63:ARG:CZ	1:A:88:ILE:HG12	2.32	0.59
2:C:25:PHE:HZ	3:H:176:PHE:CZ	2.21	0.56
3:H:153:ILE:O	3:H:157:ARG:HG2	2.04	0.56
1:A:34:CYS:O	3:G:209:TRP:HZ3	1.88	0.56
3:H:148:LYS:HG3	3:H:149:GLU:N	2.15	0.54
1:A:63:ARG:NE	1:A:88:ILE:HG12	2.24	0.53
3:H:149:GLU:HG3	3:H:185:GLY:HA3	1.89	0.53
2:C:20:ASP:N	2:C:20:ASP:OD2	2.40	0.50
2:C:44:VAL:O	2:C:46:GLU:N	2.42	0.49
1:B:69:LEU:HD13	2:I:5:LEU:HD12	1.94	0.49
2:C:53:ASP:OD1	2:C:55:ARG:HG3	2.14	0.48
3:H:189:SER:O	3:H:205:CYS:HA	2.13	0.48
1:B:88:ILE:HG22	1:B:88:ILE:O	2.14	0.47
1:A:28:ARG:HH21	1:A:28:ARG:CG	2.27	0.47
2:I:6:CYS:HA	2:I:10:LEU:CB	2.33	0.46
1:B:32:CYS:SG	3:G:196:MET:HB2	2.56	0.46
2:I:7:GLY:HA2	3:G:178:LEU:HB3	1.97	0.45
3:H:149:GLU:HG2	3:H:185:GLY:HA3	1.99	0.45
1:B:69:LEU:O	1:B:73:MET:HG2	2.17	0.45
1:A:25:GLU:HG2	1:A:39:ALA:HB2	1.99	0.45
3:H:224:PRO:HB2	3:H:225:ASN:HA	1.98	0.45
1:B:28:ARG:HG3	1:B:29:GLU:O	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:ARG:NH2	1:B:88:ILE:HA	2.32	0.44
2:I:64:LEU:H	2:I:64:LEU:HD12	1.82	0.44
1:B:67:LYS:O	1:B:71:THR:HG23	2.18	0.43
3:G:175:LYS:HA	3:G:194:THR:O	2.18	0.43
1:B:19:PRO:HA	1:B:20:PRO:HD3	1.88	0.43
2:I:7:GLY:HA3	3:G:180:ASN:ND2	2.34	0.42
3:H:148:LYS:CG	3:H:149:GLU:H	2.15	0.42
2:I:6:CYS:HB2	2:I:7:GLY:H	1.55	0.42
3:G:217:SER:HA	3:G:218:PRO:HD3	1.93	0.42
1:B:45:PRO:HA	1:B:77:GLY:O	2.20	0.41

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	89/92 (97%)	79 (89%)	8 (9%)	2 (2%)	8	28
1	B	85/92 (92%)	83 (98%)	2 (2%)	0	100	100
2	C	47/70 (67%)	44 (94%)	2 (4%)	1 (2%)	9	29
2	I	45/70 (64%)	43 (96%)	2 (4%)	0	100	100
3	G	67/94 (71%)	57 (85%)	7 (10%)	3 (4%)	3	10
3	H	52/94 (55%)	49 (94%)	3 (6%)	0	100	100
All	All	385/512 (75%)	355 (92%)	24 (6%)	6 (2%)	12	38

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	ARG
1	A	22	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	G	164	LYS
2	C	45	ASP
3	G	225	ASN
3	G	175	LYS

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	71/75 (95%)	63 (89%)	8 (11%)	7	22
1	B	69/75 (92%)	61 (88%)	8 (12%)	7	20
2	C	43/57 (75%)	37 (86%)	6 (14%)	4	13
2	I	42/57 (74%)	39 (93%)	3 (7%)	18	46
3	G	60/84 (71%)	58 (97%)	2 (3%)	45	79
3	H	48/84 (57%)	42 (88%)	6 (12%)	6	17
All	All	333/432 (77%)	300 (90%)	33 (10%)	10	28

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	10	SER
1	B	11	GLU
1	B	13	LYS
1	B	14	LEU
1	B	28	ARG
1	B	60	TYR
1	B	66	GLU
1	B	78	VAL
2	I	27	LYS
2	I	55	ARG
2	I	58	GLU
1	A	14	LEU
1	A	28	ARG
1	A	58	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	66	GLU
1	A	71	THR
1	A	73	MET
1	A	78	VAL
1	A	89	GLN
2	C	6	CYS
2	C	20	ASP
2	C	45	ASP
2	C	50	ARG
2	C	53	ASP
2	C	58	GLU
3	G	162	LEU
3	G	178	LEU
3	H	149	GLU
3	H	176	PHE
3	H	180	ASN
3	H	189	SER
3	H	202	LEU
3	H	225	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	70	HIS
3	G	180	ASN
3	H	184	ASN
3	H	188	HIS

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

There are no ligands in this entry.

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.