



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 12:31 AM GMT

PDB ID : 4LMQ
Title : Development and Preclinical Characterization of a Humanized Antibody Targeting CXCL12
Authors : Zhong, Z.; Wang, J.; Li, B.; Xiang, H.; Ultsch, M.; Coons, M.; Wong, T.; Chiang, N.Y.; Clark, S.; Clark, R.; Quintana, L.; Gribling, P.; Suto, E.; Barck, K.; Corpuz, R.; Yao, J.; Takkar, R.; Lee, W.P.; Damico-Beyer, L.A.; Carano, R.D.; Adams, C.; Kelley, R.F.; Wang, W.; Ferrara, N.
Deposited on : 2013-07-10
Resolution : 2.77 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>

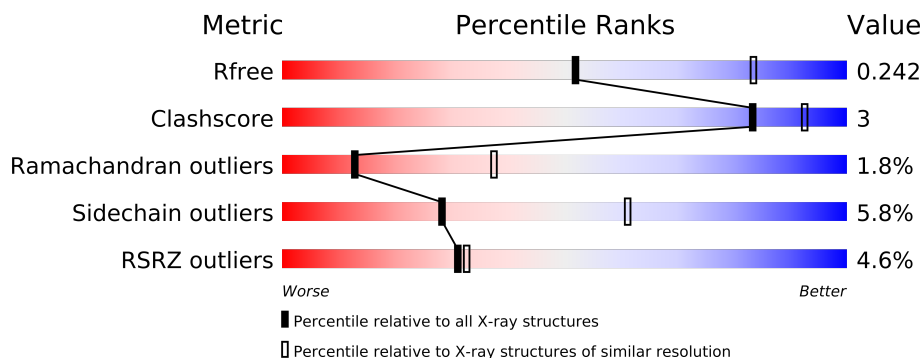
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.77 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	2193 (2.80-2.76)
Clashscore	79885	2751 (2.80-2.76)
Ramachandran outliers	78287	2699 (2.80-2.76)
Sidechain outliers	78261	2701 (2.80-2.76)
RSRZ outliers	66119	2196 (2.80-2.76)

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	D	61	
1	F	61	
2	E	221	
2	H	221	
3	I	214	
3	L	214	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7398 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 Stromal cell-derived factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	55	Total	C	N	O	S	0	0	0
			449	286	85	76	2			
1	F	58	Total	C	N	O	S	0	0	0
			472	300	90	78	4			

- Molecule 2 is a protein called immunoglobulin G1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	195	Total	C	N	O	S	0	0	0
			1474	936	248	285	5			
2	H	220	Total	C	N	O	S	0	0	0
			1636	1031	276	324	5			

- Molecule 3 is a protein called Stromal cell-derived factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	214	Total	C	N	O	S	0	0	0
			1654	1039	274	335	6			
3	L	214	Total	C	N	O	S	0	0	0
			1654	1039	274	335	6			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	8	Total	O	0	0
			8	8		
4	E	10	Total	O	0	0
			10	10		
4	F	7	Total	O	0	0
			7	7		
4	H	11	Total	O	0	0
			11	11		

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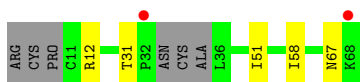
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	11	Total	O	0	0
			11	11		
4	L	12	Total	O	0	0
			12	12		

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.

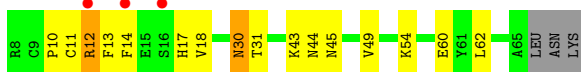
- Molecule 1: Stromal cell-derived factor 1

Chain D: 



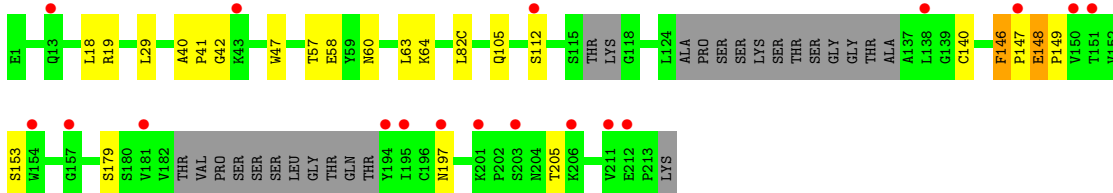
- Molecule 1: Stromal cell-derived factor 1

Chain F: 



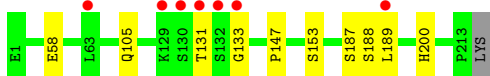
- Molecule 2: immunoglobulin G1 heavy chain

Chain E: 



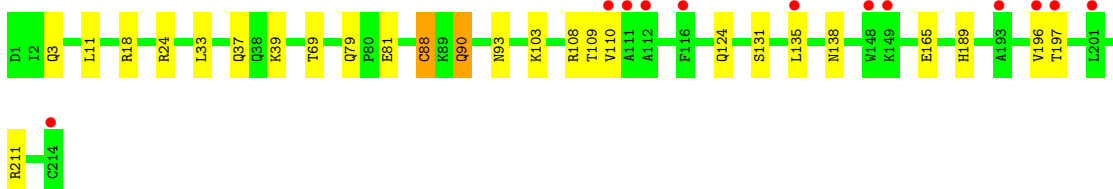
- Molecule 2: immunoglobulin G1 heavy chain

Chain H: 



- Molecule 3: Stromal cell-derived factor 1

Chain I: 



- Molecule 3: Stromal cell-derived factor 1

Chain L: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.95Å 73.10Å 106.63Å 90.00° 90.40° 90.00°	Depositor
Resolution (Å)	55.30 – 2.77 55.30 – 2.77	Depositor EDS
% Data completeness (in resolution range)	94.2 (55.30-2.77) 98.0 (55.30-2.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.253 , 0.301 0.224 , 0.242	Depositor DCC
R_{free} test set	1250 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 14.3	EDS
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 25069 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7398	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	D	0.24	0/455	0.42	0/610
1	F	0.26	0/481	0.51	0/649
2	E	0.24	0/1508	0.46	0/2051
2	H	0.25	0/1675	0.45	0/2284
3	I	0.24	0/1691	0.43	0/2295
3	L	0.24	0/1691	0.43	0/2295
All	All	0.25	0/7501	0.45	0/10184

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
2	E	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	146	PHE	Peptide
2	E	148	GLU	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	D	449	0	0	1	0
1	F	472	0	0	5	0
2	E	1474	0	0	4	0
2	H	1636	0	0	2	0
3	I	1654	0	0	7	0
3	L	1654	0	0	4	0
4	D	8	0	0	1	0
4	E	10	0	0	0	0
4	F	7	0	0	1	0
4	H	11	0	0	0	0
4	I	11	0	0	1	0
4	L	12	0	0	0	0
All	All	7398	0	0	22	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 3.

All (22) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:L:39:LYS:NZ	3:L:81:GLU:O	2.26	0.67
1:F:18:VAL:O	4:F:101:HOH:O	2.16	0.62
3:I:108:ARG:NH2	3:I:109:THR:O	2.35	0.59
1:F:11:CYS:O	1:F:13:PHE:N	2.37	0.58
3:I:103:LYS:NZ	3:I:165:GLU:OE1	2.38	0.56
3:L:90:GLN:OE1	3:L:93:ASN:N	2.39	0.55
2:E:47:TRP:O	2:E:60:ASN:ND2	2.41	0.53
3:I:189:HIS:O	3:I:211:ARG:NE	2.42	0.53
3:I:90:GLN:OE1	3:I:93:ASN:N	2.42	0.52
3:I:39:LYS:NZ	3:I:81:GLU:O	2.46	0.49
1:F:30:ASN:O	1:F:30:ASN:ND2	2.46	0.47
1:D:67:ASN:OD1	4:D:108:HOH:O	2.20	0.47
3:L:108:ARG:NH1	3:L:170:ASP:O	2.48	0.47
2:H:147:PRO:O	2:H:200:HIS:NE2	2.47	0.46
2:E:58:GLU:OE2	1:F:43:LYS:NZ	2.49	0.45
2:E:153:SER:O	2:E:197:ASN:N	2.50	0.45
3:I:124:GLN:OE1	3:I:131:SER:OG	2.37	0.42
1:F:44:ASN:OD1	1:F:45:ASN:N	2.52	0.42
3:L:151:ASP:N	3:L:191:VAL:O	2.53	0.42
2:E:40:ALA:O	2:E:42:GLY:N	2.53	0.41
2:H:187:SER:O	2:H:188:SER:OG	2.39	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:I:37:GLN:NE2	4:I:302:HOH:O	2.54	0.40

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	D	51/61 (84%)	47 (92%)	2 (4%)	2 (4%)	5	14
1	F	56/61 (92%)	51 (91%)	3 (5%)	2 (4%)	5	16
2	E	187/221 (85%)	172 (92%)	9 (5%)	6 (3%)	6	19
2	H	218/221 (99%)	205 (94%)	11 (5%)	2 (1%)	25	61
3	I	212/214 (99%)	198 (93%)	10 (5%)	4 (2%)	12	35
3	L	212/214 (99%)	202 (95%)	9 (4%)	1 (0%)	38	75
All	All	936/992 (94%)	875 (94%)	44 (5%)	17 (2%)	13	37

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	147	PRO
1	F	12	ARG
3	I	196	VAL
3	I	197	THR
1	D	12	ARG
2	E	146	PHE
2	E	149	PRO
3	I	88	CYS
2	E	148	GLU
2	E	41	PRO
3	I	138	ASN
3	L	210	ASN
1	D	31	THR
2	E	112	SER

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Mol	Chain	Res	Type
2	H	189	LEU
1	F	10	PRO
2	H	133	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	D	49/56 (88%)	47 (96%)	2 (4%)	41	77
1	F	52/56 (93%)	43 (83%)	9 (17%)	3	8
2	E	163/184 (89%)	152 (93%)	11 (7%)	23	53
2	H	183/184 (100%)	179 (98%)	4 (2%)	64	92
3	I	190/190 (100%)	179 (94%)	11 (6%)	28	61
3	L	190/190 (100%)	179 (94%)	11 (6%)	28	61
All	All	827/860 (96%)	779 (94%)	48 (6%)	28	61

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	51	ILE
1	D	58	ILE
2	E	18	LEU
2	E	19	ARG
2	E	29	LEU
2	E	57	THR
2	E	63	LEU
2	E	64	LYS
2	E	82(C)	LEU
2	E	105	GLN
2	E	140	CYS
2	E	179	SER
2	E	205	THR
1	F	12	ARG
1	F	14	PHE
1	F	17	HIS

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Mol	Chain	Res	Type
1	F	30	ASN
1	F	31	THR
1	F	49	VAL
1	F	54	LYS
1	F	60	GLU
1	F	62	LEU
2	H	58	GLU
2	H	105	GLN
2	H	131	THR
2	H	153	SER
3	I	3	GLN
3	I	11	LEU
3	I	18	ARG
3	I	24	ARG
3	I	33	LEU
3	I	69	THR
3	I	79	GLN
3	I	88	CYS
3	I	90	GLN
3	I	110	VAL
3	I	135	LEU
3	L	3	GLN
3	L	72	THR
3	L	90	GLN
3	L	100	GLN
3	L	125	LEU
3	L	142	ARG
3	L	169	LYS
3	L	181	LEU
3	L	201	LEU
3	L	211	ARG
3	L	213	GLU

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

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 ⓘ

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 ⓘ

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	D	55/61 (90%)	0.28	2 (3%) 41 43	15, 41, 88, 116	0
1	F	58/61 (95%)	0.28	3 (5%) 26 27	9, 39, 75, 104	0
2	E	195/221 (88%)	0.64	18 (9%) 9 8	10, 60, 109, 132	0
2	H	220/221 (99%)	0.19	7 (3%) 45 48	8, 32, 81, 142	0
3	I	214/214 (100%)	0.39	12 (5%) 24 25	13, 45, 97, 124	0
3	L	214/214 (100%)	0.01	2 (0%) 81 83	7, 30, 67, 113	0
All	All	956/992 (96%)	0.30	44 (4%) 31 33	7, 36, 97, 142	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	132	SER	8.7
3	I	116	PHE	5.8
2	H	130	SER	5.6
3	I	201	LEU	5.3
1	F	16	SER	5.2
2	H	131	THR	4.8
2	E	157	GLY	4.7
2	E	154	TRP	4.5
3	I	197	THR	4.0
2	E	201	LYS	3.6
2	E	197	ASN	3.4
2	H	63	LEU	3.4
2	E	211	VAL	3.2
2	E	147	PRO	3.1
3	L	150	VAL	3.1
3	I	112	ALA	3.0
3	I	214	CYS	3.0
2	E	112	SER	3.0
2	H	129	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
3	I	135	LEU	2.8
2	H	133	GLY	2.7
2	E	151	THR	2.6
2	E	181	VAL	2.6
2	E	138	LEU	2.5
3	I	196	VAL	2.5
3	I	111	ALA	2.4
2	E	43	LYS	2.4
3	I	110	VAL	2.4
2	E	203	SER	2.3
1	D	32	PRO	2.3
1	F	14	PHE	2.3
3	I	193	ALA	2.3
2	E	13	GLN	2.3
2	E	150	VAL	2.2
3	L	210	ASN	2.2
2	E	212	GLU	2.2
2	E	195	ILE	2.2
2	E	194	TYR	2.2
2	E	206	LYS	2.1
2	H	189	LEU	2.1
1	F	12	ARG	2.1
3	I	148	TRP	2.1
3	I	149	LYS	2.1
1	D	68	LYS	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.