Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2023 – 02:46 PM EDT

PDB ID	:	3MZG
Title	:	Crystal structure of a human prolactin receptor antagonist in complex with the extracellular domain of the human prolactin receptor
Authors	:	Kulkarni, M.V.; Tettamanzi, M.C.; Murphy, J.W.; Keeler, C.; Myszka, D.G.; Chayen, N.E.; Lolis, E.J.; Hodsdon, M.E.
Deposited on	:	2010-05-12
Resolution	:	2.10 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

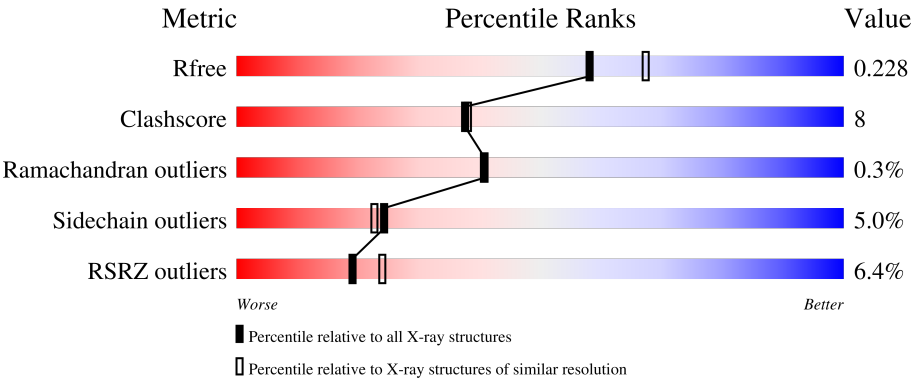
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	186	7% 78% 18%
2	B	210	6% 77% 20%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3505 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 Prolactin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	186	Total	C	N	O	S	0	6	0
			1550	974	271	295	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	MET	-	initiating methionine	UNP P01236
A	129	ARG	GLY	engineered mutation	UNP P01236

- Molecule 2 is a protein called Prolactin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	206	Total	C	N	O	S	0	1	0
			1688	1100	272	305	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P16471

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Na	0	0
			3	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		

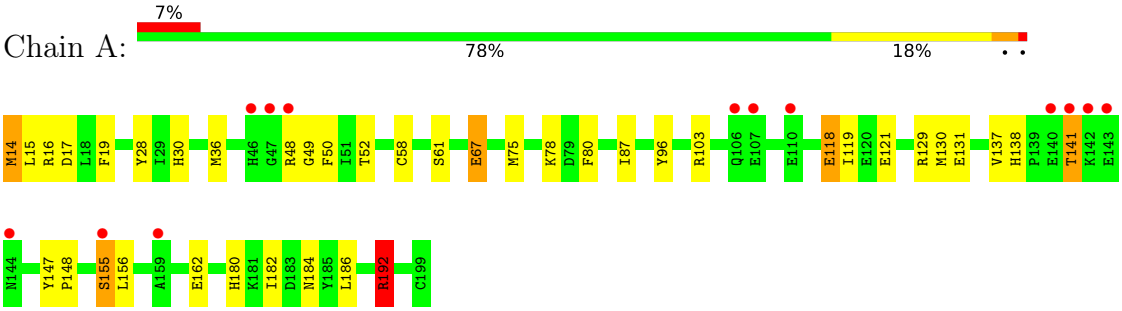
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	109	Total O 109 109	0	0
5	B	154	Total O 154 154	0	0

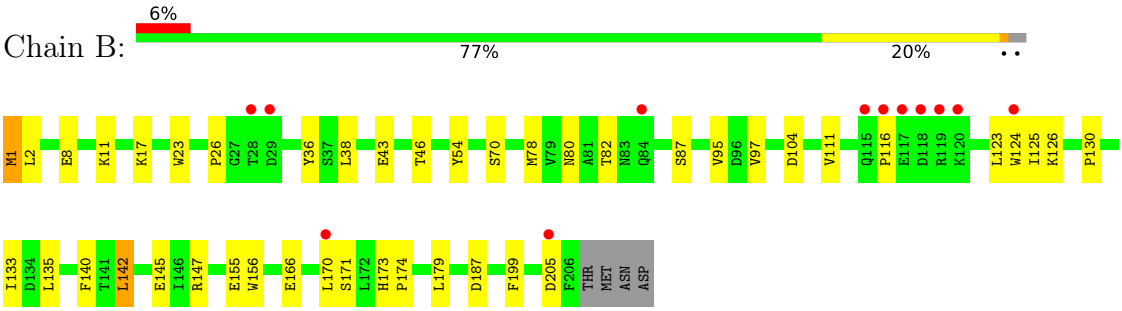
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Prolactin



• Molecule 2: Prolactin receptor



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	123.87Å 123.87Å 72.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.07 – 2.10 31.28 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.0 (32.07-2.10) 99.0 (31.28-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	5.89 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.187 , 0.230 0.186 , 0.228	Depositor DCC
R_{free} test set	1867 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	32.3	Xtriage
Anisotropy	0.713	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.037 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3505	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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, 0.333 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: NA, CL

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	1.13	4/1598 (0.3%)	1.01	5/2155 (0.2%)
2	B	1.21	5/1754 (0.3%)	1.03	3/2395 (0.1%)
All	All	1.18	9/3352 (0.3%)	1.02	8/4550 (0.2%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	121	GLU	CB-CG	8.64	1.68	1.52
1	A	121	GLU	CG-CD	7.12	1.62	1.51
2	B	145	GLU	CB-CG	-6.43	1.40	1.52
1	A	131	GLU	CB-CG	6.18	1.63	1.52
2	B	8	GLU	CG-CD	5.17	1.59	1.51
2	B	17	LYS	CD-CE	-5.15	1.38	1.51
2	B	97	VAL	CB-CG2	5.08	1.63	1.52
1	A	96	TYR	CD2-CE2	5.04	1.47	1.39
2	B	155	GLU	CG-CD	5.04	1.59	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	16	ARG	NE-CZ-NH2	-7.05	116.77	120.30
2	B	95	VAL	CB-CA-C	-6.28	99.46	111.40
1	A	192	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	A	156	LEU	CB-CG-CD1	-6.07	100.68	111.00
2	B	187	ASP	CB-CG-OD1	5.70	123.43	118.30
2	B	142	LEU	CA-CB-CG	5.64	128.27	115.30
1	A	129	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	A	129	ARG	NE-CZ-NH1	5.22	122.91	120.30

There are no chirality outliers.

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	1550	0	1541	25	0
2	B	1688	0	1619	25	0
3	B	3	0	0	0	0
4	B	1	0	0	0	0
5	A	109	0	0	4	1
5	B	154	0	0	4	1
All	All	3505	0	3160	49	1

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 (49) 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:28:TYR:OH	1:A:118[B]:GLU:OE2	2.00	0.80
1:A:155[A]:SER:HB2	5:A:296:HOH:O	1.85	0.74
1:A:118[B]:GLU:OE1	5:A:263:HOH:O	2.06	0.72
1:A:67:GLU:HG2	2:B:70:SER:HB2	1.75	0.68
2:B:111:VAL:CG1	2:B:123:LEU:HD11	2.26	0.65
1:A:48:ARG:HB3	1:A:50:PHE:CE2	2.34	0.62
2:B:126:LYS:NZ	5:B:223:HOH:O	2.32	0.62
1:A:30:HIS:CE1	1:A:180:HIS:HB2	2.36	0.60
2:B:179:LEU:HG	2:B:199:PHE:CE1	2.36	0.60
2:B:124:TRP:CH2	2:B:166:GLU:OE2	2.55	0.59
1:A:48:ARG:HG3	1:A:49:GLY:H	1.67	0.58
1:A:48:ARG:HG3	1:A:49:GLY:N	2.19	0.58
1:A:137:VAL:HG12	1:A:138:HIS:CE1	2.38	0.58
2:B:46:THR:O	5:B:262:HOH:O	2.17	0.58
1:A:155[A]:SER:CB	5:A:296:HOH:O	2.49	0.57
2:B:80:ASN:OD1	2:B:80:ASN:C	2.46	0.54
1:A:48:ARG:CG	1:A:49:GLY:H	2.21	0.53
1:A:14:MET:HG3	1:A:17:ASP:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:LEU:HD11	1:A:137:VAL:HG22	1.91	0.52
2:B:140:PHE:HE1	2:B:142:LEU:HD13	1.76	0.50
1:A:137:VAL:HG12	1:A:138:HIS:ND1	2.28	0.49
2:B:124:TRP:HH2	2:B:166:GLU:OE2	1.94	0.49
2:B:26:PRO:HB3	2:B:36:TYR:OH	2.12	0.49
2:B:133:ILE:HG22	2:B:135:LEU:HG	1.95	0.49
2:B:54:TYR:O	5:B:365:HOH:O	2.20	0.49
1:A:58:CYS:HB3	5:A:215:HOH:O	2.12	0.49
1:A:78:LYS:HD2	1:A:141:THR:HG23	1.95	0.48
2:B:80:ASN:OD1	2:B:80:ASN:O	2.30	0.48
1:A:147:TYR:HB2	1:A:148:PRO:HD2	1.95	0.47
1:A:48:ARG:HB3	1:A:50:PHE:CD2	2.50	0.47
1:A:87:ILE:HG22	1:A:182:ILE:HD11	1.97	0.46
1:A:48:ARG:CG	1:A:49:GLY:N	2.78	0.45
2:B:140:PHE:CE1	2:B:142:LEU:HD13	2.52	0.45
2:B:111:VAL:HG12	2:B:123:LEU:HD11	1.97	0.44
1:A:130:MET:SD	1:A:186:LEU:HD21	2.57	0.44
2:B:147:ARG:HD2	2:B:156:TRP:CD2	2.53	0.44
2:B:125:ILE:O	2:B:166:GLU:HA	2.16	0.44
2:B:78:MET:HE2	5:B:357:HOH:O	2.18	0.43
2:B:82:THR:HG22	2:B:87:SER:CB	2.48	0.43
2:B:11:LYS:HE3	2:B:23:TRP:CZ3	2.53	0.43
2:B:104:ASP:O	2:B:130:PRO:HG3	2.18	0.43
2:B:38:LEU:C	2:B:38:LEU:HD23	2.40	0.42
2:B:82:THR:HG22	2:B:87:SER:HB2	2.02	0.42
2:B:173:HIS:HA	2:B:174:PRO:HD3	1.91	0.42
1:A:15:LEU:HA	1:A:15:LEU:HD23	1.80	0.41
1:A:75:MET:O	1:A:192:ARG:NH2	2.48	0.41
1:A:36:MET:HE1	1:A:119:ILE:HD12	2.04	0.40
1:A:103:ARG:HH11	1:A:103:ARG:HD3	1.71	0.40
2:B:1:MET:O	2:B:1:MET:HG3	2.21	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	Interatomic distance (Å)	Clash overlap (Å)
5:A:277:HOH:O	5:B:226:HOH:O[5_555]	2.11	0.09

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	190/186 (102%)	182 (96%)	8 (4%)	0	100 100
2	B	205/210 (98%)	200 (98%)	4 (2%)	1 (0%)	29 26
All	All	395/396 (100%)	382 (97%)	12 (3%)	1 (0%)	41 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	116	PRO

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	179/173 (104%)	165 (92%)	14 (8%)	12 9
2	B	185/190 (97%)	179 (97%)	6 (3%)	39 41
All	All	364/363 (100%)	344 (94%)	20 (6%)	24 19

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	MET
1	A	19	PHE
1	A	52	THR
1	A	61	SER
1	A	67	GLU

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Mol	Chain	Res	Type
1	A	80	PHE
1	A	118[A]	GLU
1	A	118[B]	GLU
1	A	141	THR
1	A	155[A]	SER
1	A	155[B]	SER
1	A	162	GLU
1	A	184	ASN
1	A	192	ARG
2	B	1	MET
2	B	2	LEU
2	B	43	GLU
2	B	170	LEU
2	B	171	SER
2	B	205	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
2	B	115	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 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

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, 95^{th} 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	186/186 (100%)	0.25	13 (6%)	16	20	23, 39, 74, 89	1 (0%)
2	B	206/210 (98%)	-0.12	12 (5%)	23	28	22, 36, 64, 84	0
All	All	392/396 (98%)	0.06	25 (6%)	19	24	22, 37, 73, 89	1 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	118	ASP	5.4
2	B	116	PRO	5.4
1	A	48	ARG	5.0
1	A	142	LYS	5.0
1	A	144	ASN	5.0
1	A	47	GLY	3.7
2	B	205	ASP	3.7
1	A	46	HIS	3.6
1	A	159	ALA	3.5
1	A	141	THR	3.4
1	A	107	GLU	3.0
2	B	119	ARG	3.0
2	B	120	LYS	2.9
1	A	143	GLU	2.9
1	A	140	GLU	2.8
2	B	28	THR	2.7
1	A	106	GLN	2.5
2	B	124	TRP	2.4
2	B	170	LEU	2.4
2	B	115	GLN	2.3
1	A	155[A]	SER	2.2
2	B	29	ASP	2.2
1	A	110	GLU	2.1
2	B	117	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	84	GLN	2.0

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 monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
3	NA	B	211	1/1	0.98	0.08	35,35,35,35	0
3	NA	B	213	1/1	0.98	0.05	38,38,38,38	0
3	NA	B	214	1/1	0.99	0.14	22,22,22,22	0
4	CL	B	212	1/1	0.99	0.06	33,33,33,33	0

6.5 Other polymers (i)

There are no such residues in this entry.