



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:11 pm BST

PDB ID : 3EW3
Title : the 1:2 complex between a Nterminal elongated prolactin and the extra cellular domain of the rat prolactin receptor
Authors : Broutin, I.; Jomain, J.B.; England, P.; Goffin, V.
Deposited on : 2008-10-14
Resolution : 3.80 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

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	2.11
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)	:	2.11

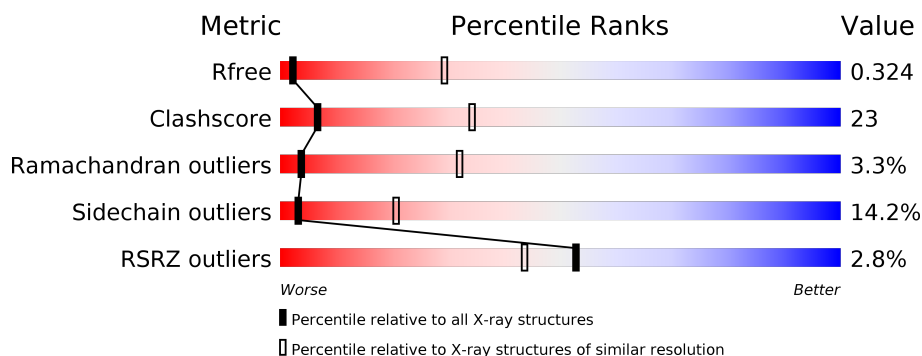
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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))
R_{free}	130704	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RSRZ outliers	127900	1121 (4.00-3.60)

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 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 $\leq 5\%$. 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	203	<div> <div></div> <div>43%</div> <div>39%</div> <div>8%</div> <div>9%</div> </div>
2	B	221	<div> <div>3%</div> <div>42%</div> <div>44%</div> <div>6%</div> <div>8%</div> </div>
2	C	221	<div> <div>4%</div> <div>40%</div> <div>33%</div> <div>8%</div> <div>18%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4694 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	185	Total	C	N	O	S	0	0	0
			1513	954	267	283	9			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	INITIATING METHIONINE	UNP P01236
A	-2	ALA	-	SEE REMARK 999	UNP P01236
A	-1	GLN	-	SEE REMARK 999	UNP P01236
A	0	HIS	-	SEE REMARK 999	UNP P01236
A	1	PRO	-	SEE REMARK 999	UNP P01236
A	2	PRO	-	SEE REMARK 999	UNP P01236
A	3	TYR	-	SEE REMARK 999	UNP P01236
A	4	CYS	-	SEE REMARK 999	UNP P01236
A	5	ARG	-	SEE REMARK 999	UNP P01236
A	6	ASN	-	SEE REMARK 999	UNP P01236
A	7	GLN	-	SEE REMARK 999	UNP P01236
A	8	PRO	-	SEE REMARK 999	UNP P01236
A	9	GLY	-	SEE REMARK 999	UNP P01236
A	10	LYS	-	SEE REMARK 999	UNP P01236
A	11	CYS	-	SEE REMARK 999	UNP P01236
A	12	GLN	-	SEE REMARK 999	UNP P01236
A	13	ILE	-	SEE REMARK 999	UNP P01236
A	14	PRO	-	SEE REMARK 999	UNP P01236

- Molecule 2 is a protein called Prolactin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	203	Total	C	N	O	S	0	0	0
			1676	1078	268	321	9			
2	C	181	Total	C	N	O	S	0	0	0
			1505	971	240	287	7			

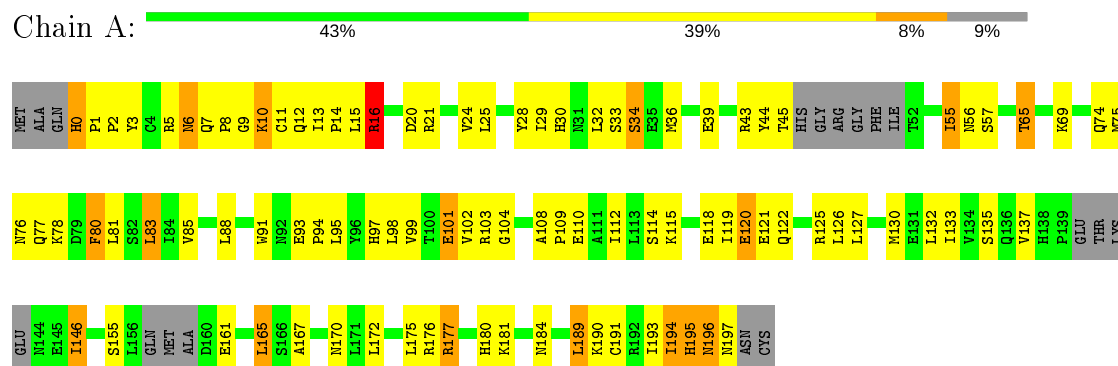
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	INITIATING METHIONINE	UNP P05710
B	211	ARG	-	EXPRESSION TAG	UNP P05710
B	212	SER	-	EXPRESSION TAG	UNP P05710
B	213	ARG	-	EXPRESSION TAG	UNP P05710
B	214	SER	-	EXPRESSION TAG	UNP P05710
B	215	HIS	-	EXPRESSION TAG	UNP P05710
B	216	HIS	-	EXPRESSION TAG	UNP P05710
B	217	HIS	-	EXPRESSION TAG	UNP P05710
B	218	HIS	-	EXPRESSION TAG	UNP P05710
B	219	HIS	-	EXPRESSION TAG	UNP P05710
B	220	HIS	-	EXPRESSION TAG	UNP P05710
C	0	MET	-	INITIATING METHIONINE	UNP P05710
C	211	ARG	-	EXPRESSION TAG	UNP P05710
C	212	SER	-	EXPRESSION TAG	UNP P05710
C	213	ARG	-	EXPRESSION TAG	UNP P05710
C	214	SER	-	EXPRESSION TAG	UNP P05710
C	215	HIS	-	EXPRESSION TAG	UNP P05710
C	216	HIS	-	EXPRESSION TAG	UNP P05710
C	217	HIS	-	EXPRESSION TAG	UNP P05710
C	218	HIS	-	EXPRESSION TAG	UNP P05710
C	219	HIS	-	EXPRESSION TAG	UNP P05710
C	220	HIS	-	EXPRESSION TAG	UNP P05710

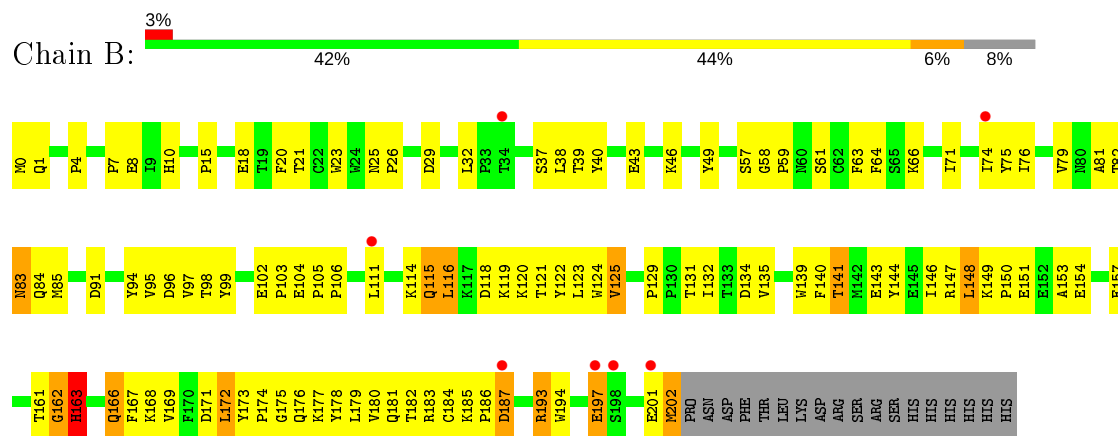
3 Residue-property plots

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.

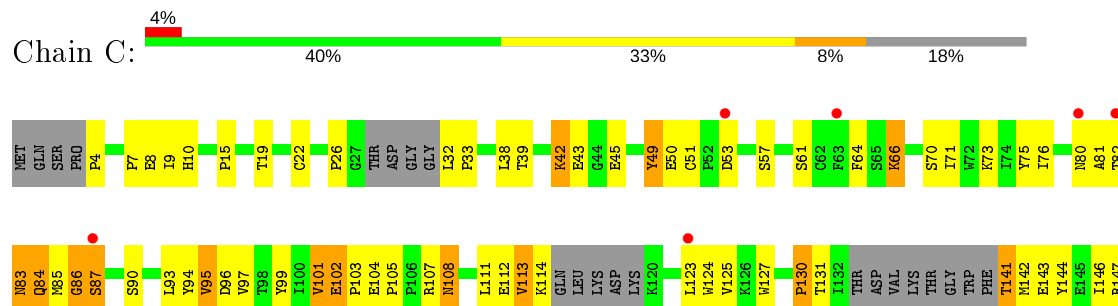
• Molecule 1: Prolactin

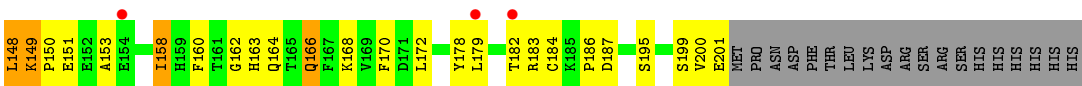


• Molecule 2: Prolactin receptor



• Molecule 2: Prolactin receptor





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.12Å 92.12Å 215.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.80 84.73 – 3.70	Depositor EDS
% Data completeness (in resolution range)	98.7 (15.00-3.80) 98.8 (84.73-3.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.64 (at 3.67Å)	Xtriage
Refinement program	CNS, PHENIX ?	Depositor
R, R_{free}	0.252 , 0.324 0.261 , 0.324	Depositor DCC
R_{free} test set	547 reflections (5.25%)	wwPDB-VP
Wilson B-factor (Å ²)	88.1	Xtriage
Anisotropy	0.597	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 77.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	4694	wwPDB-VP
Average B, all atoms (Å ²)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.45	0/1544	0.65	0/2086
2	B	0.46	0/1734	0.63	0/2363
2	C	0.42	0/1556	0.57	0/2118
All	All	0.44	0/4834	0.62	0/6567

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	1513	0	1495	77	1
2	B	1676	0	1595	79	1
2	C	1505	0	1424	72	0
All	All	4694	0	4514	216	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 23.

All (216) 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)
2:C:146:ILE:HG22	2:C:182:THR:HG22	1.44	1.00

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:75:TYR:HB2	2:C:95:VAL:HG23	1.52	0.91
1:A:15:LEU:HD11	1:A:133:ILE:HD11	1.53	0.91
1:A:36:MET:HG3	1:A:115:LYS:HB2	1.54	0.89
2:B:7:PRO:HG3	2:B:81:ALA:HB2	1.59	0.82
1:A:5:ARG:HG3	1:A:6:ASN:H	1.44	0.82
1:A:13:ILE:H	1:A:13:ILE:HD12	1.45	0.81
2:C:32:LEU:HD23	2:C:33:PRO:HD2	1.62	0.80
2:B:32:LEU:HD13	2:B:83:ASN:OD1	1.82	0.79
2:C:66:LYS:H	2:C:66:LYS:HD3	1.49	0.78
2:C:149:LYS:HD2	2:C:151:GLU:H	1.50	0.77
2:B:175:GLY:HA2	2:B:202:MET:O	1.84	0.76
1:A:2:PRO:HG3	2:C:99:TYR:CD2	2.19	0.76
2:B:183:ARG:HD3	2:B:194:TRP:CZ2	2.23	0.74
2:B:146:ILE:HG22	2:B:182:THR:HG22	1.68	0.74
2:B:1:GLN:O	2:B:85:MET:CE	2.37	0.72
2:C:42:LYS:HE3	2:C:49:TYR:OH	1.90	0.72
2:B:111:LEU:HD22	2:B:180:VAL:HG11	1.72	0.71
1:A:5:ARG:HG3	1:A:6:ASN:N	2.06	0.70
2:B:183:ARG:HD3	2:B:194:TRP:CH2	2.28	0.69
2:B:1:GLN:O	2:B:85:MET:HE3	1.92	0.69
2:B:141:THR:O	2:B:187:ASP:N	2.26	0.68
2:C:160:PHE:CE1	2:C:162:GLY:HA2	2.30	0.67
2:B:149:LYS:HD2	2:B:153:ALA:HB3	1.77	0.66
2:B:106:PRO:HD3	2:B:184:CYS:SG	2.36	0.66
2:B:76:ILE:HG23	2:B:94:TYR:CE2	2.32	0.65
2:B:150:PRO:HD3	2:B:178:TYR:CE1	2.32	0.65
1:A:99:VAL:O	1:A:103:ARG:HB2	1.97	0.64
2:C:200:VAL:HG22	2:C:201:GLU:H	1.60	0.64
2:B:176:GLN:HB3	2:B:178:TYR:CE2	2.33	0.64
1:A:80:PHE:HB3	1:A:189:LEU:HD21	1.79	0.63
1:A:78:LYS:NZ	1:A:137:VAL:HG12	2.14	0.63
2:C:149:LYS:HD3	2:C:153:ALA:O	1.99	0.63
1:A:32:LEU:HD22	1:A:119:ILE:HG12	1.81	0.62
2:B:181:GLN:HG3	2:B:197:GLU:HB3	1.81	0.62
2:B:141:THR:HG23	2:B:187:ASP:HB2	1.82	0.62
2:B:129:PRO:HG3	2:B:144:TYR:OH	2.00	0.61
2:C:147:ARG:HB3	2:C:158:ILE:HG23	1.82	0.61
1:A:15:LEU:HD11	1:A:133:ILE:CD1	2.27	0.61
1:A:33:SER:HB2	1:A:175:LEU:CD2	2.30	0.61
1:A:33:SER:HB2	1:A:175:LEU:HD23	1.82	0.60
1:A:196:ASN:ND2	1:A:196:ASN:N	2.48	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ASN:ND2	1:A:196:ASN:H	1.99	0.60
2:C:7:PRO:HB2	2:C:90:SER:HB3	1.83	0.60
1:A:161:GLU:O	1:A:165:LEU:HB2	2.02	0.60
1:A:76:ASN:HD21	1:A:78:LYS:HB2	1.66	0.60
2:C:76:ILE:HG12	2:C:94:TYR:CE2	2.37	0.59
2:B:151:GLU:OE1	2:B:177:LYS:HD3	2.01	0.59
1:A:3:TYR:CD2	1:A:14:PRO:HD3	2.37	0.59
2:C:166:GLN:C	2:C:166:GLN:HE21	2.04	0.59
2:B:176:GLN:HB3	2:B:178:TYR:HE2	1.67	0.59
1:A:69:LYS:HD2	2:B:139:TRP:CD1	2.37	0.59
1:A:15:LEU:O	1:A:16:ARG:C	2.41	0.59
1:A:30:HIS:O	1:A:34:SER:HB2	2.03	0.59
2:C:82:THR:HG23	2:C:87:SER:HB3	1.84	0.59
1:A:2:PRO:HG3	2:C:99:TYR:CE2	2.38	0.58
2:B:1:GLN:O	2:B:85:MET:HE2	2.03	0.58
2:C:149:LYS:HD2	2:C:151:GLU:N	2.17	0.58
2:B:75:TYR:HB2	2:B:95:VAL:O	2.03	0.58
1:A:65:THR:HG21	1:A:181:LYS:HD3	1.85	0.58
1:A:3:TYR:CE2	1:A:14:PRO:HD3	2.38	0.58
2:B:125:VAL:HG23	2:B:167:PHE:O	2.03	0.58
1:A:195:HIS:H	1:A:195:HIS:CD2	2.22	0.58
2:B:8:GLU:HB2	2:B:25:ASN:HB2	1.86	0.57
2:C:15:PRO:HA	2:C:102:GLU:O	2.04	0.57
2:B:147:ARG:HA	2:B:157:GLU:O	2.04	0.56
1:A:177:ARG:HB3	1:A:177:ARG:HH11	1.70	0.56
2:C:4:PRO:N	2:C:86:GLY:HA2	2.20	0.56
1:A:25:LEU:HD13	1:A:126:LEU:HB2	1.88	0.56
2:B:146:ILE:HG22	2:B:182:THR:CG2	2.36	0.56
1:A:21:ARG:NH1	2:C:71:ILE:O	2.38	0.56
2:B:32:LEU:HD22	2:B:84:GLN:HB3	1.88	0.56
2:C:70:SER:HB3	2:C:73:LYS:HE2	1.87	0.56
1:A:32:LEU:HD22	1:A:119:ILE:CG1	2.36	0.56
1:A:97:HIS:O	1:A:101:GLU:HB2	2.07	0.55
2:B:124:TRP:CD1	2:B:168:LYS:HG2	2.41	0.55
2:C:7:PRO:O	2:C:90:SER:HB2	2.06	0.54
1:A:32:LEU:HD23	1:A:32:LEU:O	2.07	0.54
2:B:143:GLU:HA	2:B:163:HIS:H	1.71	0.54
1:A:81:LEU:O	1:A:85:VAL:HG23	2.08	0.54
2:B:114:LYS:HB2	2:B:122:TYR:CZ	2.42	0.54
2:C:170:PHE:O	2:C:172:LEU:HD12	2.08	0.54
1:A:127:LEU:HD23	1:A:127:LEU:O	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:GLY:O	1:A:10:LYS:HB2	2.08	0.53
2:C:108:ASN:O	2:C:127:TRP:HA	2.07	0.53
1:A:127:LEU:O	1:A:130:MET:HB2	2.08	0.53
2:B:37:SER:O	2:B:79:VAL:HG23	2.09	0.53
2:B:131:THR:HG23	2:B:132:ILE:HD13	1.90	0.53
1:A:95:LEU:HB3	1:A:120:GLU:HG2	1.90	0.53
2:C:75:TYR:HB2	2:C:95:VAL:CG2	2.33	0.53
2:C:45:GLU:HG2	2:C:45:GLU:O	2.09	0.52
1:A:32:LEU:HB3	1:A:119:ILE:HD11	1.91	0.52
2:B:124:TRP:HE1	2:B:166:GLN:HE21	1.57	0.52
2:B:38:LEU:HD23	2:B:39:THR:N	2.25	0.52
2:B:21:THR:OG1	2:B:63:PHE:HD1	1.93	0.52
2:C:101:VAL:HB	2:C:186:PRO:HG3	1.90	0.52
2:B:167:PHE:HE1	2:C:163:HIS:HB2	1.75	0.52
2:C:114:LYS:HG3	2:C:114:LYS:O	2.09	0.51
2:C:9:ILE:HG21	2:C:93:LEU:HD22	1.91	0.51
2:B:105:PRO:HD3	2:B:193:ARG:CD	2.40	0.51
2:C:178:TYR:HB2	2:C:200:VAL:HG12	1.92	0.51
2:C:19:THR:HB	2:C:64:PHE:O	2.11	0.51
1:A:44:TYR:HB3	1:A:165:LEU:HD21	1.93	0.51
2:B:115:GLN:OE1	2:B:121:THR:HG22	2.11	0.51
1:A:5:ARG:O	1:A:7:GLN:N	2.44	0.51
2:B:111:LEU:HD11	2:B:123:LEU:HG	1.92	0.51
2:C:141:THR:HG22	2:C:142:MET:H	1.76	0.51
1:A:69:LYS:HB2	2:B:139:TRP:CE2	2.46	0.51
1:A:30:HIS:NE2	1:A:180:HIS:HB2	2.26	0.51
1:A:195:HIS:CD2	1:A:195:HIS:N	2.78	0.50
2:C:124:TRP:HZ3	2:C:168:LYS:HD2	1.77	0.50
2:C:103:PRO:HG2	2:C:186:PRO:HD3	1.92	0.50
2:B:18:GLU:OE1	2:B:66:LYS:HE2	2.11	0.50
2:B:135:VAL:HG12	2:B:140:PHE:O	2.11	0.49
2:B:175:GLY:H	2:B:202:MET:HG3	1.77	0.49
2:C:143:GLU:HA	2:C:162:GLY:O	2.12	0.49
1:A:88:LEU:CD1	1:A:130:MET:HG3	2.43	0.49
2:B:105:PRO:HD3	2:B:193:ARG:HD2	1.95	0.49
1:A:190:LYS:O	1:A:194:ILE:HB	2.12	0.49
2:C:149:LYS:HD2	2:C:151:GLU:HA	1.95	0.49
2:C:148:LEU:HA	2:C:179:LEU:O	2.12	0.48
1:A:55:ILE:HD11	1:A:57:SER:O	2.13	0.48
2:C:33:PRO:O	2:C:83:ASN:HB3	2.13	0.48
2:B:124:TRP:HD1	2:B:168:LYS:HG2	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:178:TYR:O	2:C:199:SER:HA	2.14	0.48
2:C:124:TRP:CE3	2:C:168:LYS:HG3	2.48	0.48
2:C:200:VAL:HG22	2:C:201:GLU:N	2.28	0.48
2:C:105:PRO:HB3	2:C:195:SER:HA	1.96	0.48
1:A:93:GLU:N	1:A:94:PRO:HD2	2.29	0.47
2:B:179:LEU:HD22	2:B:197:GLU:OE1	2.15	0.47
2:C:113:VAL:HG12	2:C:114:LYS:H	1.79	0.47
2:B:102:GLU:HA	2:B:103:PRO:HD3	1.66	0.47
2:B:111:LEU:HD11	2:B:123:LEU:CG	2.44	0.47
2:C:38:LEU:HD23	2:C:39:THR:N	2.29	0.47
2:C:4:PRO:CA	2:C:86:GLY:HA2	2.44	0.47
2:B:76:ILE:HG12	2:B:94:TYR:CE2	2.50	0.47
2:C:57:SER:HB2	2:C:61:SER:OG	2.13	0.47
2:B:161:THR:O	2:B:162:GLY:C	2.52	0.47
1:A:28:TYR:O	1:A:32:LEU:HB2	2.14	0.47
2:B:176:GLN:HE21	2:B:177:LYS:H	1.63	0.47
2:B:23:TRP:CD1	2:B:61:SER:HB3	2.50	0.47
2:B:74:ILE:HG22	2:B:74:ILE:O	2.14	0.47
2:B:105:PRO:HD3	2:B:193:ARG:NE	2.30	0.47
2:C:150:PRO:O	2:C:151:GLU:HB3	2.14	0.47
2:B:171:ASP:C	2:B:172:LEU:HG	2.35	0.46
2:B:58:GLY:HA3	2:B:59:PRO:HD3	1.75	0.46
2:C:124:TRP:HE3	2:C:168:LYS:HG3	1.81	0.46
1:A:98:LEU:O	1:A:102:VAL:HG23	2.16	0.46
1:A:56:ASN:HD22	2:B:43:GLU:HG3	1.80	0.46
2:C:39:THR:HG22	2:C:50:GLU:HA	1.98	0.46
1:A:76:ASN:ND2	1:A:78:LYS:HB2	2.30	0.46
1:A:36:MET:HG3	1:A:115:LYS:CB	2.37	0.46
2:B:181:GLN:CG	2:B:197:GLU:HB3	2.44	0.46
2:C:84:GLN:O	2:C:85:MET:HG2	2.15	0.46
2:C:166:GLN:O	2:C:166:GLN:NE2	2.39	0.45
2:C:144:TYR:CE1	2:C:184:CYS:HB3	2.51	0.45
2:C:130:PRO:HB2	2:C:131:THR:H	1.67	0.45
2:C:144:TYR:HA	2:C:183:ARG:O	2.17	0.45
1:A:65:THR:HG21	1:A:181:LYS:NZ	2.32	0.45
2:B:111:LEU:HD11	2:B:123:LEU:HD21	1.98	0.45
2:C:143:GLU:O	2:C:184:CYS:HA	2.17	0.45
1:A:21:ARG:NH2	2:C:96:ASP:OD2	2.48	0.44
1:A:189:LEU:O	1:A:193:ILE:HG13	2.17	0.44
1:A:20:ASP:O	1:A:24:VAL:HG23	2.18	0.44
1:A:75:MET:HB3	1:A:80:PHE:CE1	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:MET:O	1:A:133:ILE:HG22	2.18	0.44
1:A:146:ILE:HG13	1:A:146:ILE:H	1.57	0.44
2:B:167:PHE:CE1	2:C:163:HIS:HB2	2.53	0.44
2:B:186:PRO:O	2:B:187:ASP:C	2.56	0.44
2:B:38:LEU:HD23	2:B:38:LEU:C	2.38	0.44
2:C:160:PHE:CE1	2:C:162:GLY:CA	3.00	0.44
1:A:108:ALA:HA	1:A:109:PRO:HD3	1.86	0.44
2:C:111:LEU:HB3	2:C:123:LEU:HD11	2.00	0.44
1:A:7:GLN:HA	1:A:8:PRO:HD2	1.79	0.44
2:B:20:PHE:CE2	2:B:64:PHE:CD1	3.06	0.44
2:B:4:PRO:HD3	2:B:83:ASN:ND2	2.33	0.44
2:C:81:ALA:O	2:C:87:SER:HA	2.17	0.44
1:A:130:MET:HA	1:A:133:ILE:HG22	1.99	0.43
1:A:15:LEU:CD1	1:A:133:ILE:CD1	2.95	0.43
1:A:91:TRP:O	1:A:94:PRO:HG2	2.18	0.43
1:A:55:ILE:HD13	1:A:170:ASN:CG	2.39	0.43
2:B:96:ASP:OD2	2:B:96:ASP:O	2.35	0.43
2:B:143:GLU:OE1	2:B:185:LYS:HE3	2.18	0.43
2:C:149:LYS:HD2	2:C:151:GLU:CA	2.49	0.42
2:B:111:LEU:HD11	2:B:123:LEU:CD2	2.49	0.42
1:A:15:LEU:CD1	1:A:133:ILE:HD11	2.38	0.42
1:A:83:LEU:HA	1:A:83:LEU:HD22	1.77	0.42
2:C:42:LYS:HD3	2:C:73:LYS:NZ	2.34	0.42
1:A:0:HIS:HD2	1:A:1:PRO:HD2	1.84	0.42
2:C:112:GLU:HB3	2:C:124:TRP:HB3	2.00	0.42
1:A:36:MET:CG	1:A:115:LYS:HB2	2.38	0.42
2:C:111:LEU:N	2:C:111:LEU:HD12	2.35	0.42
2:B:173:TYR:HB2	2:C:170:PHE:CZ	2.54	0.42
2:B:116:LEU:HB3	2:B:120:LYS:HZ3	1.83	0.42
2:B:116:LEU:HB3	2:B:120:LYS:NZ	2.35	0.42
1:A:109:PRO:O	1:A:110:GLU:C	2.58	0.41
1:A:43:ARG:C	1:A:44:TYR:CD1	2.93	0.41
2:B:25:ASN:HA	2:B:26:PRO:HD2	1.92	0.41
1:A:122:GLN:NE2	1:A:125:ARG:HH21	2.19	0.41
1:A:25:LEU:O	1:A:29:ILE:HG13	2.21	0.41
2:C:112:GLU:O	2:C:113:VAL:O	2.38	0.41
1:A:118:GLU:O	1:A:122:GLN:HG2	2.20	0.41
2:C:104:GLU:O	2:C:105:PRO:C	2.59	0.41
2:C:4:PRO:N	2:C:86:GLY:CA	2.83	0.41
1:A:69:LYS:HE2	2:B:134:ASP:OD2	2.20	0.41
2:C:22:CYS:O	2:C:61:SER:HA	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:THR:HG21	2:B:57:SER:OG	2.22	0.40
1:A:155:SER:HB2	1:A:167:ALA:HB1	2.02	0.40
2:B:174:PRO:HB3	2:B:202:MET:HE1	2.03	0.40
1:A:30:HIS:CD2	1:A:180:HIS:HB2	2.56	0.40
2:B:148:LEU:HA	2:B:179:LEU:O	2.22	0.40
2:B:40:TYR:CE2	2:B:49:TYR:HB2	2.56	0.40
2:C:150:PRO:HG3	2:C:178:TYR:CE1	2.57	0.40
1:A:0:HIS:HA	1:A:1:PRO:HD3	1.89	0.40
2:B:125:VAL:O	2:B:166:GLN:HA	2.22	0.40
2:B:169:VAL:HA	2:C:164:GLN:OE1	2.22	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)
1:A:74:GLN:OE1	2:B:0:MET:O[3_554]	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	177/203 (87%)	148 (84%)	22 (12%)	7 (4%)	3	28
2	B	201/221 (91%)	178 (89%)	18 (9%)	5 (2%)	5	36
2	C	173/221 (78%)	148 (86%)	19 (11%)	6 (4%)	3	31
All	All	551/645 (85%)	474 (86%)	59 (11%)	18 (3%)	4	32

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	163	HIS
2	C	113	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	16	ARG
2	B	187	ASP
2	C	26	PRO
2	C	130	PRO
1	A	6	ASN
1	A	12	GLN
2	B	118	ASP
2	C	10	HIS
2	B	119	LYS
1	A	10	LYS
1	A	11	CYS
2	B	162	GLY
2	C	108	ASN
2	C	86	GLY
1	A	194	ILE
1	A	104	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	A	173/187 (92%)	145 (84%)	28 (16%)	2	15
2	B	190/208 (91%)	165 (87%)	25 (13%)	4	22
2	C	171/208 (82%)	148 (86%)	23 (14%)	4	22
All	All	534/603 (89%)	458 (86%)	76 (14%)	3	21

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	16	ARG
1	A	34	SER
1	A	39	GLU
1	A	45	THR
1	A	55	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	65	THR
1	A	77	GLN
1	A	80	PHE
1	A	83	LEU
1	A	101	GLU
1	A	112	ILE
1	A	114	SER
1	A	120	GLU
1	A	121	GLU
1	A	132	LEU
1	A	135	SER
1	A	146	ILE
1	A	165	LEU
1	A	172	LEU
1	A	176	ARG
1	A	177	ARG
1	A	184	ASN
1	A	189	LEU
1	A	191	CYS
1	A	195	HIS
1	A	196	ASN
1	A	197	ASN
2	B	10	HIS
2	B	15	PRO
2	B	29	ASP
2	B	46	LYS
2	B	71	ILE
2	B	82	THR
2	B	83	ASN
2	B	91	ASP
2	B	97	VAL
2	B	98	THR
2	B	99	TYR
2	B	104	GLU
2	B	115	GLN
2	B	116	LEU
2	B	125	VAL
2	B	141	THR
2	B	148	LEU
2	B	154	GLU
2	B	163	HIS
2	B	166	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	172	LEU
2	B	193	ARG
2	B	197	GLU
2	B	201	GLU
2	B	202	MET
2	C	8	GLU
2	C	42	LYS
2	C	43	GLU
2	C	49	TYR
2	C	51	CYS
2	C	53	ASP
2	C	66	LYS
2	C	80	ASN
2	C	83	ASN
2	C	84	GLN
2	C	87	SER
2	C	95	VAL
2	C	97	VAL
2	C	101	VAL
2	C	102	GLU
2	C	107	ARG
2	C	125	VAL
2	C	141	THR
2	C	148	LEU
2	C	149	LYS
2	C	158	ILE
2	C	166	GLN
2	C	187	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	7	GLN
1	A	31	ASN
1	A	56	ASN
1	A	184	ASN
1	A	196	ASN
1	A	197	ASN
2	B	1	GLN
2	B	84	GLN
2	B	159	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	166	GLN
2	B	176	GLN
2	B	188	HIS
2	C	176	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](#)

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 ⓘ

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	A	185/203 (91%)	0.30	0 100 100	70, 94, 162, 178	0
2	B	203/221 (91%)	0.61	7 (3%) 45 37	77, 95, 145, 167	0
2	C	181/221 (81%)	0.69	9 (4%) 28 25	90, 122, 154, 168	0
All	All	569/645 (88%)	0.54	16 (2%) 53 43	70, 103, 154, 178	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	201	GLU	4.4
2	C	80	ASN	4.2
2	C	82	THR	3.7
2	C	123	LEU	3.6
2	C	154	GLU	3.4
2	B	187	ASP	2.8
2	B	198	SER	2.7
2	C	87	SER	2.6
2	C	179	LEU	2.5
2	B	197	GLU	2.5
2	C	53	ASP	2.5
2	B	111	LEU	2.4
2	C	63	PHE	2.3
2	C	182	THR	2.3
2	B	74	ILE	2.1
2	B	34	THR	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 [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.