wwPDB X-ray Structure Validation Summary Report (i)

Jun 22, 2024 – 11:27 PM EDT

PDB ID	:	5HLZ
Title	:	Structure of Pro-Activin A Complex at 2.85 A resolution
Authors	:	Wang, X.; Fischer, G.; Hyvonen, M.
Deposited on	:	2016-01-15
Resolution	:	2.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

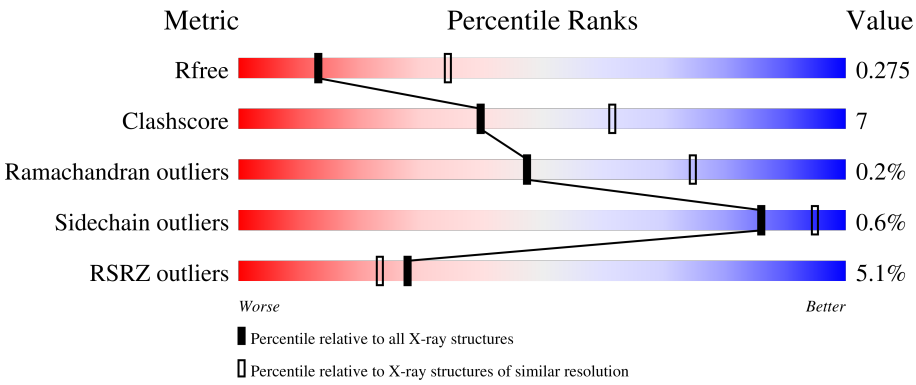
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	270	% 63% 12% 24%
1	C	270	% 61% 14% 24%
1	E	270	2% 63% 13% 24%
1	G	270	2% 62% 13% 24%
2	B	116	8% 53% 21% • 26%

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Mol	Chain	Length	Quality of chain
2	D	116	8% 59% 12% 29%
2	F	116	11% 54% 19% • 26%
2	H	116	9% 53% 17% • 28%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9163 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 Inhibin beta A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	1626	1020	295	304	7	0	0	0
1	C	204	1626	1020	295	304	7	0	0	0
1	E	204	1626	1020	295	304	7	0	0	0
1	G	204	1626	1020	295	304	7	0	0	0

There are 176 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	expression tag	UNP P08476
A	21	SER	-	expression tag	UNP P08476
A	22	HIS	-	expression tag	UNP P08476
A	23	HIS	-	expression tag	UNP P08476
A	24	HIS	-	expression tag	UNP P08476
A	25	HIS	-	expression tag	UNP P08476
A	26	HIS	-	expression tag	UNP P08476
A	27	HIS	-	expression tag	UNP P08476
A	28	SER	-	expression tag	UNP P08476
A	29	MET	-	expression tag	UNP P08476
A	35	SER	CYS	engineered mutation	UNP P08476
A	38	SER	CYS	engineered mutation	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	GLU	deletion	UNP P08476
A	?	-	GLU	deletion	UNP P08476
A	?	-	GLU	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	LYS	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	GLU	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	ALA	deletion	UNP P08476
A	?	-	GLY	deletion	UNP P08476
A	?	-	ALA	deletion	UNP P08476
A	?	-	ASP	deletion	UNP P08476
A	306	LEU	-	cloning artifact	UNP P08476
A	307	GLU	-	cloning artifact	UNP P08476
A	308	VAL	-	cloning artifact	UNP P08476
A	309	LEU	-	cloning artifact	UNP P08476
A	310	PHE	-	cloning artifact	UNP P08476
A	310A	GLN	-	cloning artifact	UNP P08476
A	310B	GLY	-	cloning artifact	UNP P08476
A	310C	PRO	-	cloning artifact	UNP P08476
C	20	MET	-	expression tag	UNP P08476
C	21	SER	-	expression tag	UNP P08476
C	22	HIS	-	expression tag	UNP P08476
C	23	HIS	-	expression tag	UNP P08476
C	24	HIS	-	expression tag	UNP P08476
C	25	HIS	-	expression tag	UNP P08476
C	26	HIS	-	expression tag	UNP P08476
C	27	HIS	-	expression tag	UNP P08476
C	28	SER	-	expression tag	UNP P08476
C	29	MET	-	expression tag	UNP P08476
C	35	SER	CYS	engineered mutation	UNP P08476
C	38	SER	CYS	engineered mutation	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	GLU	deletion	UNP P08476
C	?	-	GLU	deletion	UNP P08476

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	GLU	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	GLU	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	LYS	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	GLU	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	ALA	deletion	UNP P08476
C	?	-	GLY	deletion	UNP P08476
C	?	-	ALA	deletion	UNP P08476
C	?	-	ASP	deletion	UNP P08476
C	306	LEU	-	cloning artifact	UNP P08476
C	307	GLU	-	cloning artifact	UNP P08476
C	308	VAL	-	cloning artifact	UNP P08476
C	309	LEU	-	cloning artifact	UNP P08476
C	310	PHE	-	cloning artifact	UNP P08476
C	310A	GLN	-	cloning artifact	UNP P08476
C	310B	GLY	-	cloning artifact	UNP P08476
C	310C	PRO	-	cloning artifact	UNP P08476
E	20	MET	-	expression tag	UNP P08476
E	21	SER	-	expression tag	UNP P08476
E	22	HIS	-	expression tag	UNP P08476
E	23	HIS	-	expression tag	UNP P08476
E	24	HIS	-	expression tag	UNP P08476
E	25	HIS	-	expression tag	UNP P08476
E	26	HIS	-	expression tag	UNP P08476
E	27	HIS	-	expression tag	UNP P08476
E	28	SER	-	expression tag	UNP P08476
E	29	MET	-	expression tag	UNP P08476
E	35	SER	CYS	engineered mutation	UNP P08476
E	38	SER	CYS	engineered mutation	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	GLU	deletion	UNP P08476
E	?	-	GLU	deletion	UNP P08476
E	?	-	GLU	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	GLU	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	LYS	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	GLU	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	ALA	deletion	UNP P08476
E	?	-	GLY	deletion	UNP P08476
E	?	-	ALA	deletion	UNP P08476
E	?	-	ASP	deletion	UNP P08476
E	306	LEU	-	cloning artifact	UNP P08476
E	307	GLU	-	cloning artifact	UNP P08476
E	308	VAL	-	cloning artifact	UNP P08476
E	309	LEU	-	cloning artifact	UNP P08476
E	310	PHE	-	cloning artifact	UNP P08476
E	310A	GLN	-	cloning artifact	UNP P08476
E	310B	GLY	-	cloning artifact	UNP P08476
E	310C	PRO	-	cloning artifact	UNP P08476
G	20	MET	-	expression tag	UNP P08476
G	21	SER	-	expression tag	UNP P08476
G	22	HIS	-	expression tag	UNP P08476
G	23	HIS	-	expression tag	UNP P08476
G	24	HIS	-	expression tag	UNP P08476
G	25	HIS	-	expression tag	UNP P08476
G	26	HIS	-	expression tag	UNP P08476
G	27	HIS	-	expression tag	UNP P08476
G	28	SER	-	expression tag	UNP P08476
G	29	MET	-	expression tag	UNP P08476
G	35	SER	CYS	engineered mutation	UNP P08476
G	38	SER	CYS	engineered mutation	UNP P08476
G	?	-	LYS	deletion	UNP P08476
G	?	-	LYS	deletion	UNP P08476
G	?	-	LYS	deletion	UNP P08476

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	LYS	deletion	UNP P08476
G	?	-	LYS	deletion	UNP P08476
G	?	-	GLU	deletion	UNP P08476
G	?	-	GLU	deletion	UNP P08476
G	?	-	GLU	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	GLU	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	LYS	deletion	UNP P08476
G	?	-	LYS	deletion	UNP P08476
G	?	-	LYS	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	GLU	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	ALA	deletion	UNP P08476
G	?	-	GLY	deletion	UNP P08476
G	?	-	ALA	deletion	UNP P08476
G	?	-	ASP	deletion	UNP P08476
G	306	LEU	-	cloning artifact	UNP P08476
G	307	GLU	-	cloning artifact	UNP P08476
G	308	VAL	-	cloning artifact	UNP P08476
G	309	LEU	-	cloning artifact	UNP P08476
G	310	PHE	-	cloning artifact	UNP P08476
G	310A	GLN	-	cloning artifact	UNP P08476
G	310B	GLY	-	cloning artifact	UNP P08476
G	310C	PRO	-	cloning artifact	UNP P08476

- Molecule 2 is a protein called Inhibin beta A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	86	674	425	109	128	12	0	0	0
			Total	C	N	O	S			
2	D	82	644	405	104	123	12	0	0	0
			Total	C	N	O	S			
2	F	86	674	425	109	128	12	0	0	0
			Total	C	N	O	S			
2	H	84	657	413	106	126	12	0	0	0

- Molecule 3 is water.

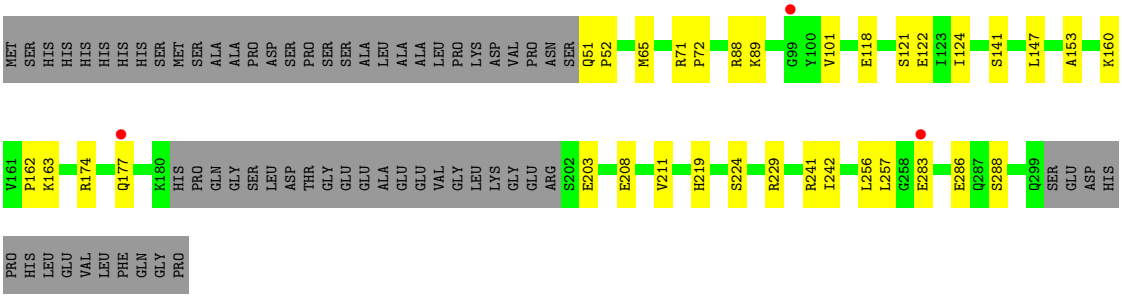
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	2	2	2	0	0
			Total	O		
3	C	2	2	2	0	0
			Total	O		
3	E	2	2	2	0	0
			Total	O		
3	G	4	4	4	0	0

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.

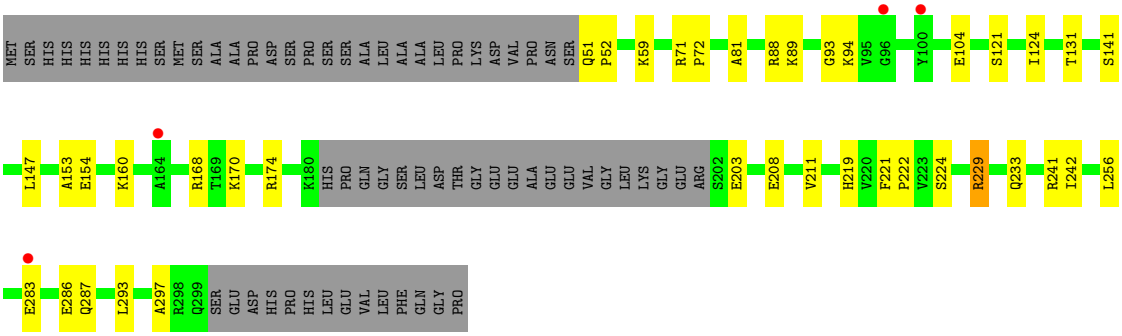
• Molecule 1: Inhibin beta A chain

Chain A:



• Molecule 1: Inhibin beta A chain

Chain C:

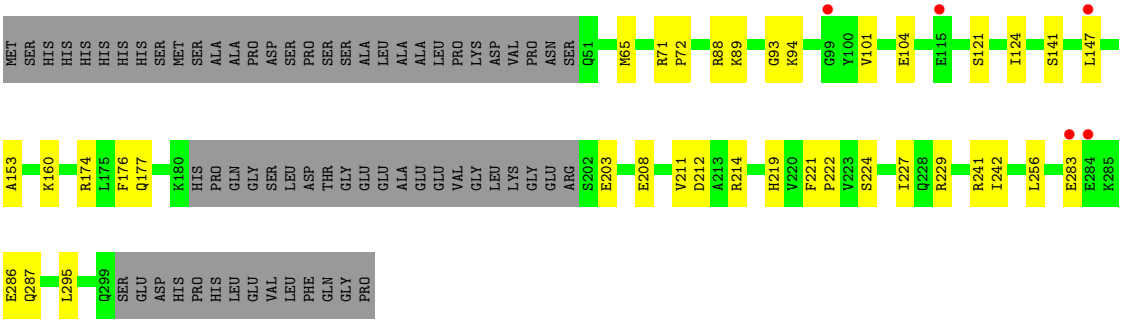


• Molecule 1: Inhibin beta A chain

Chain E:

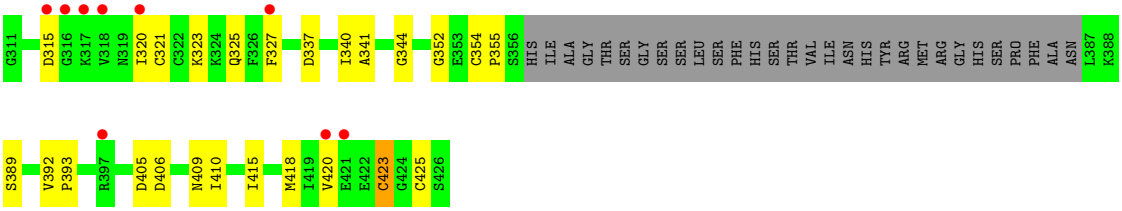
• Molecule 1: Inhibin beta A chain

Chain G:



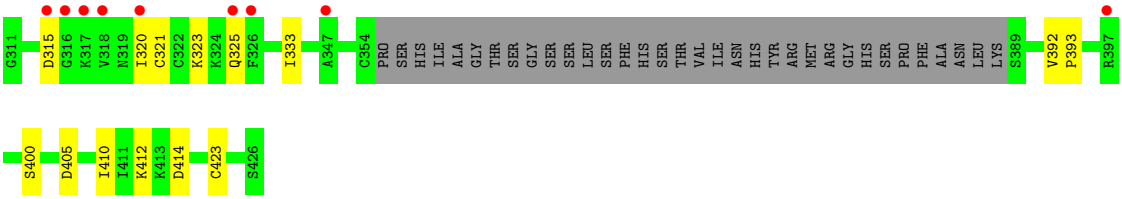
• Molecule 2: Inhibin beta A chain

Chain B:



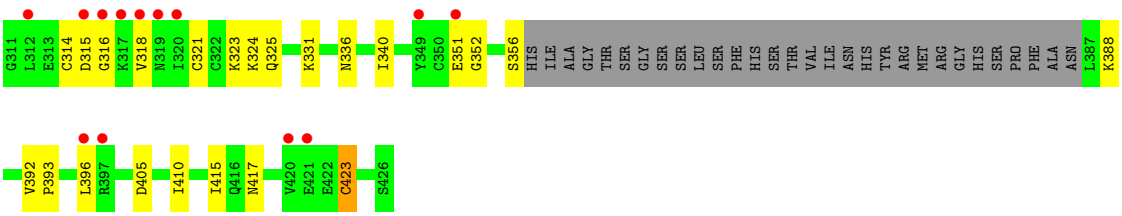
• Molecule 2: Inhibin beta A chain

Chain D:



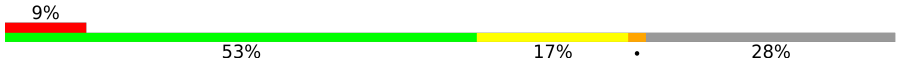
• Molecule 2: Inhibin beta A chain

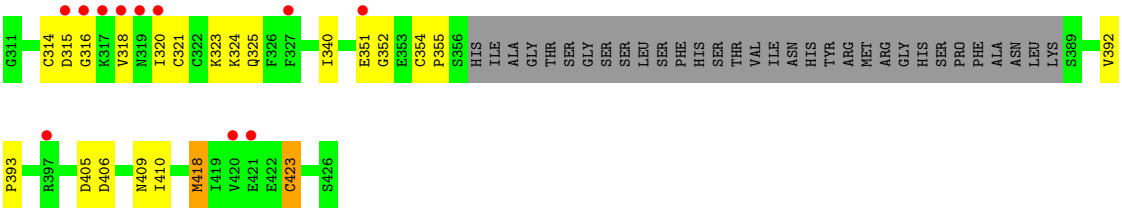
Chain F:



• Molecule 2: Inhibin beta A chain

Chain H:


9%
53%
17%
28%


G311 C314 D315 G316 K317 V318 N319 I320 C321 C322 K323 K324 Q325 F326 F327 I340 E351 G352 E353 C354 P355 S356 HIS ILE ALA GLY THR SER GLY SER SER LEU SER PHE HIS SER THR VAL ILE ASN HIS TYR ARG MET ARG GLY HIS SER PRO PHE ALA ASN LEU LYS S389 V392
P393 R397 D405 D406 N409 I410 M418 I419 V420 E421 E422 C423 S426

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	47.23Å 47.23Å 445.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.90 – 2.85 40.90 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.90-2.85) 92.7 (40.90-2.85)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.14	Depositor
$< I/\sigma(I) >$ [1]	1.23 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.10pre_2084: ???)	Depositor
R, R_{free}	0.220 , 0.274 0.220 , 0.275	Depositor DCC
R_{free} test set	1338 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å^2)	62.1	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 43.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.467 for -h,-k,l 0.469 for h,-h-k,-l 0.469 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	9163	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.78% 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 (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	0.26	0/1648	0.43	0/2214
1	C	0.26	0/1648	0.43	0/2214
1	E	0.27	0/1648	0.43	0/2214
1	G	0.27	0/1648	0.45	0/2214
2	B	0.28	0/688	0.44	0/923
2	D	0.27	0/657	0.47	0/881
2	F	0.26	0/688	0.42	0/923
2	H	0.27	0/671	0.45	0/901
All	All	0.27	0/9296	0.44	0/12484

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 (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	1626	0	1676	23	0
1	C	1626	0	1676	26	0
1	E	1626	0	1676	22	0
1	G	1626	0	1676	23	0
2	B	674	0	640	19	0
2	D	644	0	604	12	0
2	F	674	0	640	16	0
2	H	657	0	616	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	2	0	0	0	0
3	C	2	0	0	1	0
3	E	2	0	0	0	0
3	G	4	0	0	1	0
All	All	9163	0	9204	133	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 7.

The worst 5 of 133 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:H:393:PRO:HA	2:H:423:CYS:HB3	1.57	0.86
2:F:393:PRO:HA	2:F:423:CYS:HB3	1.58	0.83
2:D:393:PRO:HA	2:D:423:CYS:HB3	1.59	0.82
2:F:405:ASP:OD2	1:G:141:SER:OG	2.00	0.80
2:B:392:VAL:HG21	2:D:392:VAL:HG21	1.63	0.79

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	200/270 (74%)	194 (97%)	6 (3%)	0	100	100
1	C	200/270 (74%)	196 (98%)	4 (2%)	0	100	100
1	E	200/270 (74%)	194 (97%)	6 (3%)	0	100	100
1	G	200/270 (74%)	194 (97%)	6 (3%)	0	100	100
2	B	82/116 (71%)	79 (96%)	3 (4%)	0	100	100
2	D	78/116 (67%)	76 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	82/116 (71%)	80 (98%)	1 (1%)	1 (1%)	13	35
2	H	80/116 (69%)	76 (95%)	3 (4%)	1 (1%)	12	33
All	All	1122/1544 (73%)	1089 (97%)	31 (3%)	2 (0%)	47	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	316	GLY
2	H	316	GLY

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	182/237 (77%)	181 (100%)	1 (0%)	88	96
1	C	182/237 (77%)	181 (100%)	1 (0%)	88	96
1	E	182/237 (77%)	182 (100%)	0	100	100
1	G	182/237 (77%)	182 (100%)	0	100	100
2	B	77/102 (76%)	76 (99%)	1 (1%)	69	88
2	D	73/102 (72%)	73 (100%)	0	100	100
2	F	77/102 (76%)	76 (99%)	1 (1%)	69	88
2	H	75/102 (74%)	73 (97%)	2 (3%)	44	74
All	All	1030/1356 (76%)	1024 (99%)	6 (1%)	86	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	418	MET
2	H	423	CYS
1	C	229	ARG
2	B	423	CYS
1	A	257	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	ASN

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)

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	204/270 (75%)	0.04	3 (1%)	73	72	35, 62, 95, 130	0
1	C	204/270 (75%)	0.05	4 (1%)	65	62	37, 62, 94, 126	0
1	E	204/270 (75%)	0.07	5 (2%)	57	54	38, 62, 99, 119	0
1	G	204/270 (75%)	-0.01	5 (2%)	57	54	36, 61, 97, 127	0
2	B	86/116 (74%)	0.45	9 (10%)	6	4	48, 80, 120, 133	0
2	D	82/116 (70%)	0.58	9 (10%)	5	4	47, 78, 120, 132	0
2	F	86/116 (74%)	0.59	13 (15%)	2	1	46, 82, 124, 137	0
2	H	84/116 (72%)	0.54	11 (13%)	3	2	46, 82, 124, 133	0
All	All	1154/1544 (74%)	0.18	59 (5%)	28	23	35, 65, 113, 137	0

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	318	VAL	7.9
1	G	99	GLY	7.1
1	E	99	GLY	6.2
2	B	316	GLY	6.0
2	H	316	GLY	6.0

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.