



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:55 PM UTC

PDB ID : 4NSC / pdb_00004nsc
Title : Crystal Structure of CBARA1 in the Apo-form
Authors : Wang, L.; Yang, X.; Li, S.; Shen, Y.
Deposited on : 2013-11-28
Resolution : 3.20 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 ⓘ 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

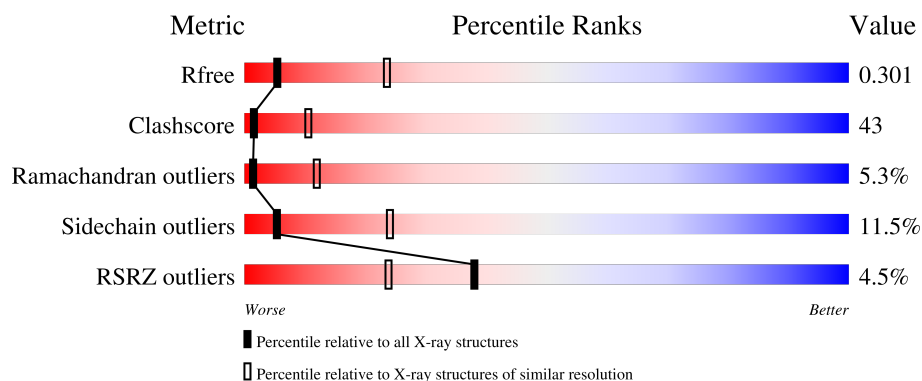
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 $\leq 5\%$. 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	401	5% 26% 38% 12% • 23%
1	B	401	4% 28% 38% 10% • 21%
1	C	401	5% 23% 49% 9% • 18%
1	D	401	4% 31% 38% 11% • 19%
1	E	401	2% 31% 38% 11% • 18%

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Mol	Chain	Length	Quality of chain
1	F	401	2% 30% 36% 10% • 23%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15349 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 Calcium uptake protein 1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2472	1583	419	454	16			
1	B	316	Total	C	N	O	S	0	0	0
			2539	1622	426	473	18			
1	C	330	Total	C	N	O	S	0	0	0
			2619	1673	442	486	18			
1	D	326	Total	C	N	O	S	0	0	0
			2604	1662	438	487	17			
1	E	330	Total	C	N	O	S	0	0	0
			2598	1657	439	487	15			
1	F	310	Total	C	N	O	S	0	0	0
			2504	1601	422	468	13			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	MET	-	expression tag	UNP Q9BPX6
A	77	HIS	-	expression tag	UNP Q9BPX6
A	78	HIS	-	expression tag	UNP Q9BPX6
A	79	HIS	-	expression tag	UNP Q9BPX6
A	80	HIS	-	expression tag	UNP Q9BPX6
A	81	HIS	-	expression tag	UNP Q9BPX6
A	82	HIS	-	expression tag	UNP Q9BPX6
A	83	SER	-	expression tag	UNP Q9BPX6
A	84	SER	-	expression tag	UNP Q9BPX6
A	85	GLY	-	expression tag	UNP Q9BPX6
A	86	LEU	-	expression tag	UNP Q9BPX6
A	87	GLU	-	expression tag	UNP Q9BPX6
A	88	VAL	-	expression tag	UNP Q9BPX6
A	89	LEU	-	expression tag	UNP Q9BPX6
A	90	PHE	-	expression tag	UNP Q9BPX6
A	91	GLN	-	expression tag	UNP Q9BPX6
A	92	GLY	-	expression tag	UNP Q9BPX6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	93	PRO	-	expression tag	UNP Q9BPX6
A	94	GLY	-	expression tag	UNP Q9BPX6
A	95	SER	-	expression tag	UNP Q9BPX6
A	96	MET	-	expression tag	UNP Q9BPX6
B	76	MET	-	expression tag	UNP Q9BPX6
B	77	HIS	-	expression tag	UNP Q9BPX6
B	78	HIS	-	expression tag	UNP Q9BPX6
B	79	HIS	-	expression tag	UNP Q9BPX6
B	80	HIS	-	expression tag	UNP Q9BPX6
B	81	HIS	-	expression tag	UNP Q9BPX6
B	82	HIS	-	expression tag	UNP Q9BPX6
B	83	SER	-	expression tag	UNP Q9BPX6
B	84	SER	-	expression tag	UNP Q9BPX6
B	85	GLY	-	expression tag	UNP Q9BPX6
B	86	LEU	-	expression tag	UNP Q9BPX6
B	87	GLU	-	expression tag	UNP Q9BPX6
B	88	VAL	-	expression tag	UNP Q9BPX6
B	89	LEU	-	expression tag	UNP Q9BPX6
B	90	PHE	-	expression tag	UNP Q9BPX6
B	91	GLN	-	expression tag	UNP Q9BPX6
B	92	GLY	-	expression tag	UNP Q9BPX6
B	93	PRO	-	expression tag	UNP Q9BPX6
B	94	GLY	-	expression tag	UNP Q9BPX6
B	95	SER	-	expression tag	UNP Q9BPX6
B	96	MET	-	expression tag	UNP Q9BPX6
C	76	MET	-	expression tag	UNP Q9BPX6
C	77	HIS	-	expression tag	UNP Q9BPX6
C	78	HIS	-	expression tag	UNP Q9BPX6
C	79	HIS	-	expression tag	UNP Q9BPX6
C	80	HIS	-	expression tag	UNP Q9BPX6
C	81	HIS	-	expression tag	UNP Q9BPX6
C	82	HIS	-	expression tag	UNP Q9BPX6
C	83	SER	-	expression tag	UNP Q9BPX6
C	84	SER	-	expression tag	UNP Q9BPX6
C	85	GLY	-	expression tag	UNP Q9BPX6
C	86	LEU	-	expression tag	UNP Q9BPX6
C	87	GLU	-	expression tag	UNP Q9BPX6
C	88	VAL	-	expression tag	UNP Q9BPX6
C	89	LEU	-	expression tag	UNP Q9BPX6
C	90	PHE	-	expression tag	UNP Q9BPX6
C	91	GLN	-	expression tag	UNP Q9BPX6
C	92	GLY	-	expression tag	UNP Q9BPX6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	93	PRO	-	expression tag	UNP Q9BPX6
C	94	GLY	-	expression tag	UNP Q9BPX6
C	95	SER	-	expression tag	UNP Q9BPX6
C	96	MET	-	expression tag	UNP Q9BPX6
D	76	MET	-	expression tag	UNP Q9BPX6
D	77	HIS	-	expression tag	UNP Q9BPX6
D	78	HIS	-	expression tag	UNP Q9BPX6
D	79	HIS	-	expression tag	UNP Q9BPX6
D	80	HIS	-	expression tag	UNP Q9BPX6
D	81	HIS	-	expression tag	UNP Q9BPX6
D	82	HIS	-	expression tag	UNP Q9BPX6
D	83	SER	-	expression tag	UNP Q9BPX6
D	84	SER	-	expression tag	UNP Q9BPX6
D	85	GLY	-	expression tag	UNP Q9BPX6
D	86	LEU	-	expression tag	UNP Q9BPX6
D	87	GLU	-	expression tag	UNP Q9BPX6
D	88	VAL	-	expression tag	UNP Q9BPX6
D	89	LEU	-	expression tag	UNP Q9BPX6
D	90	PHE	-	expression tag	UNP Q9BPX6
D	91	GLN	-	expression tag	UNP Q9BPX6
D	92	GLY	-	expression tag	UNP Q9BPX6
D	93	PRO	-	expression tag	UNP Q9BPX6
D	94	GLY	-	expression tag	UNP Q9BPX6
D	95	SER	-	expression tag	UNP Q9BPX6
D	96	MET	-	expression tag	UNP Q9BPX6
E	76	MET	-	expression tag	UNP Q9BPX6
E	77	HIS	-	expression tag	UNP Q9BPX6
E	78	HIS	-	expression tag	UNP Q9BPX6
E	79	HIS	-	expression tag	UNP Q9BPX6
E	80	HIS	-	expression tag	UNP Q9BPX6
E	81	HIS	-	expression tag	UNP Q9BPX6
E	82	HIS	-	expression tag	UNP Q9BPX6
E	83	SER	-	expression tag	UNP Q9BPX6
E	84	SER	-	expression tag	UNP Q9BPX6
E	85	GLY	-	expression tag	UNP Q9BPX6
E	86	LEU	-	expression tag	UNP Q9BPX6
E	87	GLU	-	expression tag	UNP Q9BPX6
E	88	VAL	-	expression tag	UNP Q9BPX6
E	89	LEU	-	expression tag	UNP Q9BPX6
E	90	PHE	-	expression tag	UNP Q9BPX6
E	91	GLN	-	expression tag	UNP Q9BPX6
E	92	GLY	-	expression tag	UNP Q9BPX6

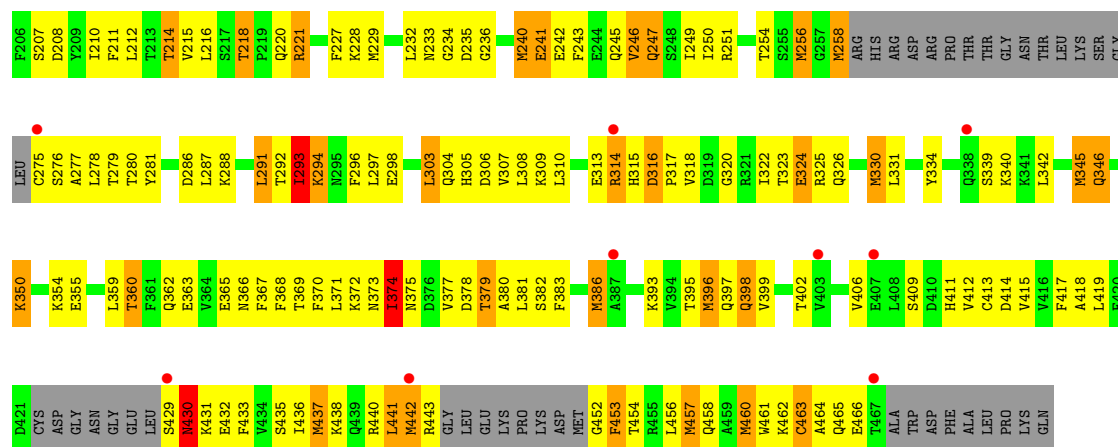
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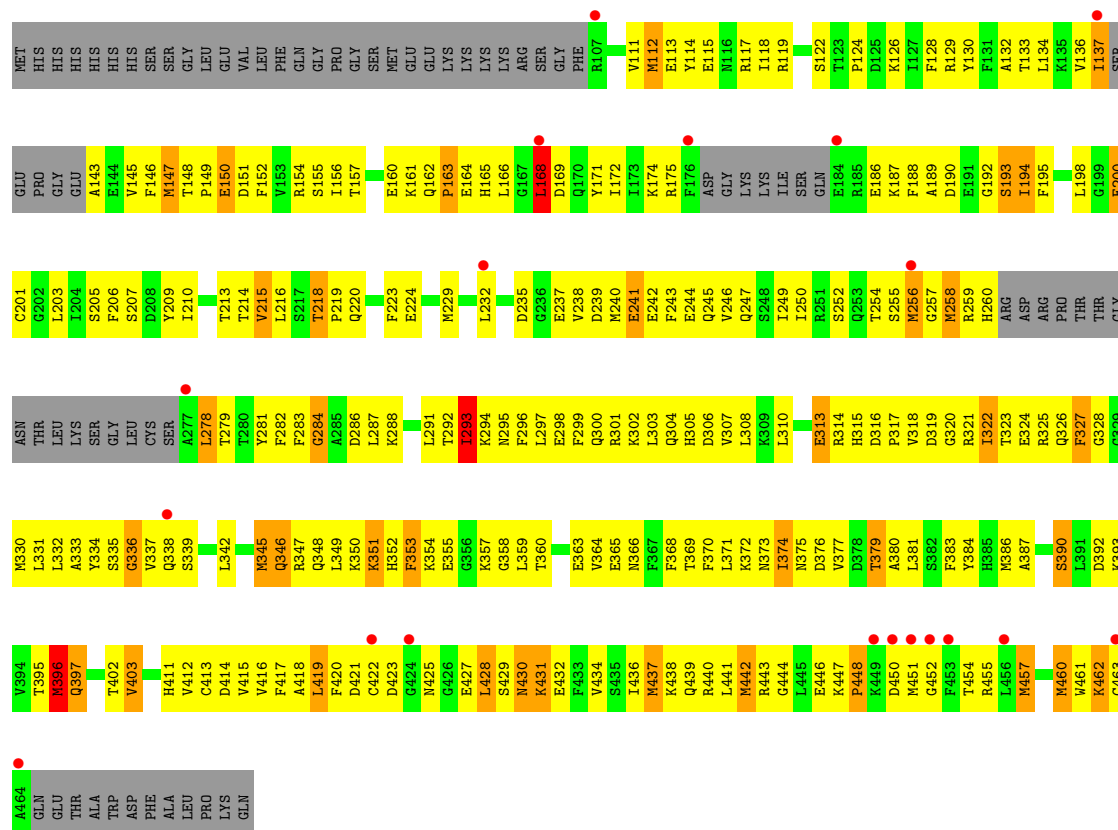
Chain	Residue	Modelled	Actual	Comment	Reference
E	93	PRO	-	expression tag	UNP Q9BPX6
E	94	GLY	-	expression tag	UNP Q9BPX6
E	95	SER	-	expression tag	UNP Q9BPX6
E	96	MET	-	expression tag	UNP Q9BPX6
F	76	MET	-	expression tag	UNP Q9BPX6
F	77	HIS	-	expression tag	UNP Q9BPX6
F	78	HIS	-	expression tag	UNP Q9BPX6
F	79	HIS	-	expression tag	UNP Q9BPX6
F	80	HIS	-	expression tag	UNP Q9BPX6
F	81	HIS	-	expression tag	UNP Q9BPX6
F	82	HIS	-	expression tag	UNP Q9BPX6
F	83	SER	-	expression tag	UNP Q9BPX6
F	84	SER	-	expression tag	UNP Q9BPX6
F	85	GLY	-	expression tag	UNP Q9BPX6
F	86	LEU	-	expression tag	UNP Q9BPX6
F	87	GLU	-	expression tag	UNP Q9BPX6
F	88	VAL	-	expression tag	UNP Q9BPX6
F	89	LEU	-	expression tag	UNP Q9BPX6
F	90	PHE	-	expression tag	UNP Q9BPX6
F	91	GLN	-	expression tag	UNP Q9BPX6
F	92	GLY	-	expression tag	UNP Q9BPX6
F	93	PRO	-	expression tag	UNP Q9BPX6
F	94	GLY	-	expression tag	UNP Q9BPX6
F	95	SER	-	expression tag	UNP Q9BPX6
F	96	MET	-	expression tag	UNP Q9BPX6

- Molecule 2 is water.

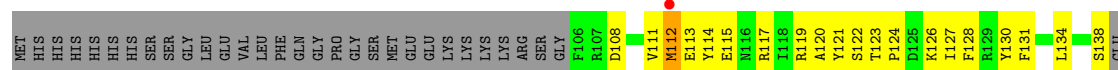
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total O 4 4	0	0
2	B	3	Total O 3 3	0	0
2	C	1	Total O 1 1	0	0
2	D	1	Total O 1 1	0	0
2	F	4	Total O 4 4	0	0



• Molecule 1: Calcium uptake protein 1, mitochondrial



• Molecule 1: Calcium uptake protein 1, mitochondrial







4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.88Å 146.82Å 115.87Å 90.00° 111.08° 90.00°	Depositor
Resolution (Å)	36.72 – 3.20 36.72 – 3.20	Depositor EDS
% Data completeness (in resolution range)	92.3 (36.72-3.20) 92.3 (36.72-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 3.18Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.254 , 0.307 0.254 , 0.301	Depositor DCC
R_{free} test set	2007 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	15349	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 3.12% 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	0.76	21/2517 (0.8%)	1.02	14/3379 (0.4%)
1	B	0.85	24/2581 (0.9%)	1.05	16/3456 (0.5%)
1	C	0.81	23/2665 (0.9%)	1.04	13/3577 (0.4%)
1	D	0.85	19/2649 (0.7%)	1.08	21/3551 (0.6%)
1	E	0.79	14/2644 (0.5%)	1.13	19/3550 (0.5%)
1	F	0.80	11/2549 (0.4%)	1.11	21/3418 (0.6%)
All	All	0.81	112/15605 (0.7%)	1.07	104/20931 (0.5%)

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
1	B	0	1

The worst 5 of 112 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	147	MET	CG-SD	9.55	2.04	1.80
1	D	147	MET	CG-SD	8.58	2.02	1.80
1	D	229	MET	CG-SD	8.15	2.01	1.80
1	F	442	MET	CG-SD	8.13	2.01	1.80
1	D	256	MET	CG-SD	8.09	2.00	1.80

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	454	THR	N-CA-C	-10.69	97.87	112.94
1	E	218	THR	CA-C-N	9.46	129.40	120.03
1	E	218	THR	C-N-CA	9.46	129.40	120.03
1	C	293	ILE	N-CA-C	-9.21	100.96	111.00
1	B	218	THR	CA-C-N	9.06	129.00	119.85

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	196	TYR	Sidechain

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	2472	0	2397	245	0
1	B	2539	0	2496	229	0
1	C	2619	0	2542	262	0
1	D	2604	0	2547	228	0
1	E	2598	0	2494	204	1
1	F	2504	0	2458	204	1
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	F	4	0	0	0	0
All	All	15349	0	14934	1296	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 43.

The worst 5 of 1296 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:D:147:MET:SD	1:D:147:MET:CG	2.02	1.48
1:C:147:MET:CG	1:C:147:MET:SD	2.04	1.44
1:C:323:THR:HB	1:C:326:GLN:HG3	1.23	1.14
1:F:323:THR:HB	1:F:326:GLN:HG3	1.23	1.14
1:E:323:THR:HB	1:E:326:GLN:HG3	1.28	1.14

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:E:171:TYR:O	1:F:357:LYS:NZ[2_756]	2.10	0.10

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	300/401 (75%)	227 (76%)	54 (18%)	19 (6%)	1	8
1	B	304/401 (76%)	235 (77%)	53 (17%)	16 (5%)	1	12
1	C	322/401 (80%)	248 (77%)	56 (17%)	18 (6%)	1	11
1	D	316/401 (79%)	262 (83%)	39 (12%)	15 (5%)	2	14
1	E	322/401 (80%)	261 (81%)	47 (15%)	14 (4%)	2	16
1	F	302/401 (75%)	237 (78%)	49 (16%)	16 (5%)	1	12
All	All	1866/2406 (78%)	1470 (79%)	298 (16%)	98 (5%)	1	12

5 of 98 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	LEU
1	A	172	ILE
1	A	354	LYS
1	A	453	PHE
1	B	374	ILE

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	259/354 (73%)	228 (88%)	31 (12%)	5	23
1	B	273/354 (77%)	242 (89%)	31 (11%)	5	24
1	C	274/354 (77%)	244 (89%)	30 (11%)	6	26
1	D	278/354 (78%)	250 (90%)	28 (10%)	7	30
1	E	269/354 (76%)	233 (87%)	36 (13%)	4	19
1	F	270/354 (76%)	239 (88%)	31 (12%)	5	24
All	All	1623/2124 (76%)	1436 (88%)	187 (12%)	5	24

5 of 187 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	428	LEU
1	E	331	LEU
1	D	445	LEU
1	E	214	THR
1	E	423	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	247	GLN
1	F	326	GLN
1	E	300	GLN
1	E	425	ASN
1	F	411	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides 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	310/401 (77%)	0.79	21 (6%)	23 15	62, 86, 113, 127	0
1	B	316/401 (78%)	0.46	15 (4%)	36 23	41, 73, 104, 122	0
1	C	330/401 (82%)	0.49	19 (5%)	29 18	44, 70, 97, 114	0
1	D	326/401 (81%)	0.33	16 (4%)	35 22	36, 60, 89, 111	0
1	E	330/401 (82%)	0.18	7 (2%)	63 43	32, 59, 107, 122	0
1	F	310/401 (77%)	0.22	9 (2%)	53 35	36, 58, 95, 112	0
All	All	1922/2406 (79%)	0.41	87 (4%)	38 24	32, 69, 104, 127	0

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	277	ALA	4.9
1	C	450	ASP	4.9
1	A	124	PRO	4.5
1	A	339	SER	4.3
1	F	182	SER	3.7

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 oligosaccharides 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.