



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 06:28 pm BST

PDB ID : 4KWV  
Title : Crystal Structure of human apo-QPRT  
Authors : Malik, S.S.; Patterson, D.N.; Ncube, Z.; Toth, E.A.  
Deposited on : 2013-05-24  
Resolution : 2.80 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](mailto: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.

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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

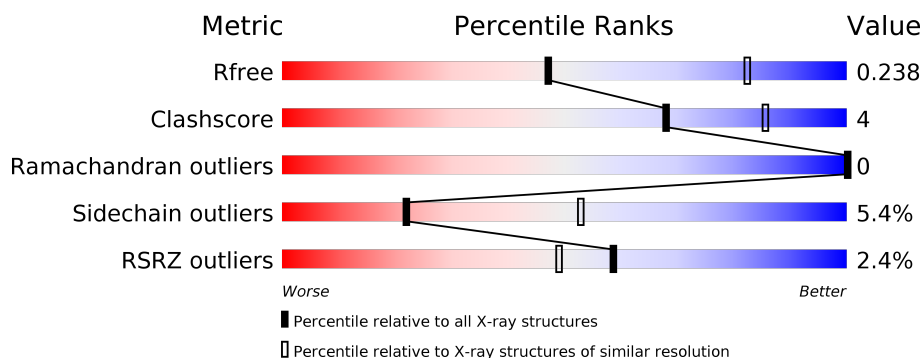
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	301	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>5%</div> </div> </div>
1	B	301	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>5%</div> </div> </div>
1	C	301	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>5%</div> </div> </div>
1	D	301	<div> <div></div> <div> <div></div> <div>85%</div> <div>9%</div> <div>5%</div> </div> </div>
1	E	301	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>5%</div> </div> </div>
1	F	301	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>5%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12001 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 Nicotinate-nucleotide pyrophosphorylase [carboxylating].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			1995	1281	337	368	9			
1	B	286	Total	C	N	O	S	0	0	0
			1976	1268	330	369	9			
1	C	285	Total	C	N	O	S	0	0	0
			1951	1243	331	368	9			
1	D	285	Total	C	N	O	S	0	0	0
			2005	1285	341	370	9			
1	E	288	Total	C	N	O	S	0	0	0
			2023	1295	345	374	9			
1	F	291	Total	C	N	O	S	0	0	0
			2036	1301	345	381	9			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP Q15274
A	-2	PRO	-	EXPRESSION TAG	UNP Q15274
A	-1	GLY	-	EXPRESSION TAG	UNP Q15274
A	0	SER	-	EXPRESSION TAG	UNP Q15274
B	-3	GLY	-	EXPRESSION TAG	UNP Q15274
B	-2	PRO	-	EXPRESSION TAG	UNP Q15274
B	-1	GLY	-	EXPRESSION TAG	UNP Q15274
B	0	SER	-	EXPRESSION TAG	UNP Q15274
C	-3	GLY	-	EXPRESSION TAG	UNP Q15274
C	-2	PRO	-	EXPRESSION TAG	UNP Q15274
C	-1	GLY	-	EXPRESSION TAG	UNP Q15274
C	0	SER	-	EXPRESSION TAG	UNP Q15274
D	-3	GLY	-	EXPRESSION TAG	UNP Q15274
D	-2	PRO	-	EXPRESSION TAG	UNP Q15274
D	-1	GLY	-	EXPRESSION TAG	UNP Q15274
D	0	SER	-	EXPRESSION TAG	UNP Q15274
E	-3	GLY	-	EXPRESSION TAG	UNP Q15274

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	PRO	-	EXPRESSION TAG	UNP Q15274
E	-1	GLY	-	EXPRESSION TAG	UNP Q15274
E	0	SER	-	EXPRESSION TAG	UNP Q15274
F	-3	GLY	-	EXPRESSION TAG	UNP Q15274
F	-2	PRO	-	EXPRESSION TAG	UNP Q15274
F	-1	GLY	-	EXPRESSION TAG	UNP Q15274
F	0	SER	-	EXPRESSION TAG	UNP Q15274

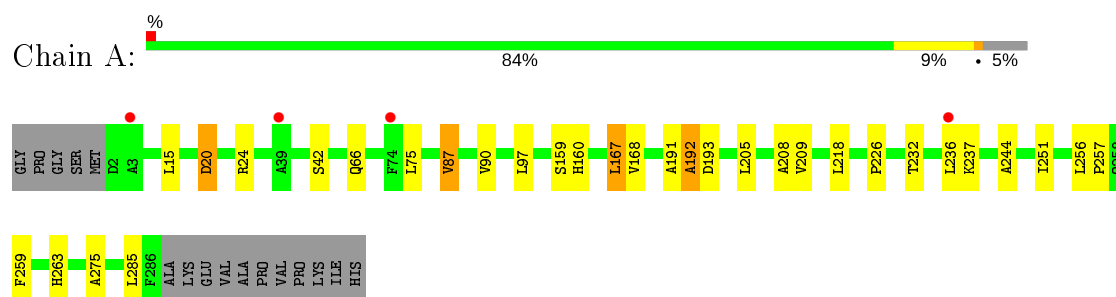
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total O 4 4	0	0
2	B	1	Total O 1 1	0	0
2	C	1	Total O 1 1	0	0
2	D	3	Total O 3 3	0	0
2	E	1	Total O 1 1	0	0
2	F	5	Total O 5 5	0	0

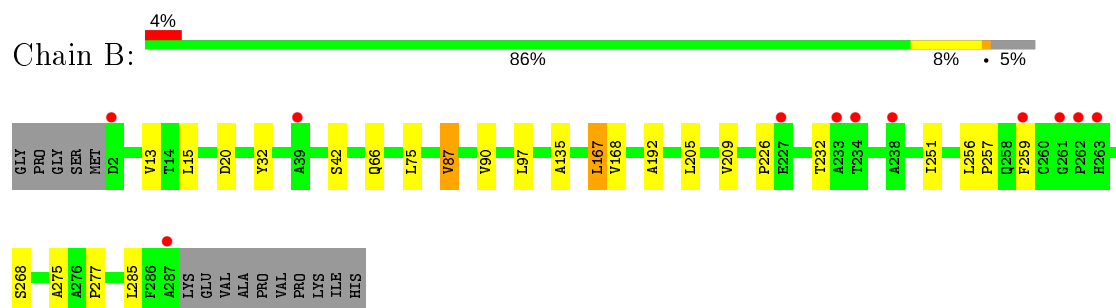
### 3 Residue-property plots [i](#)

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.

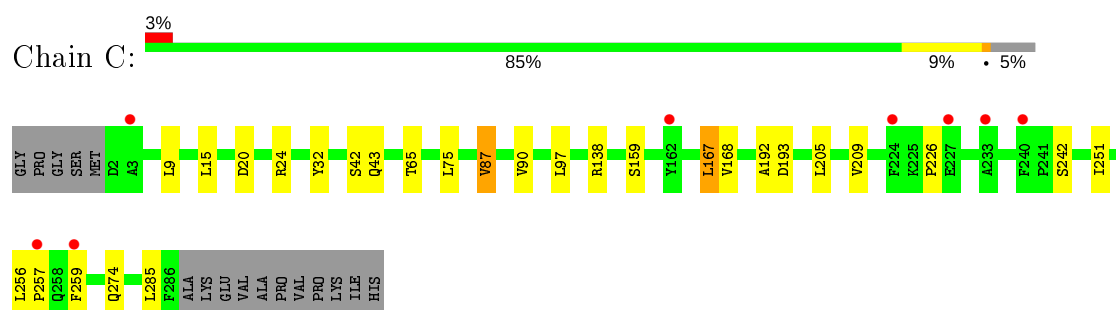
- Molecule 1: Nicotinate-nucleotide pyrophosphorylase [carboxylating]



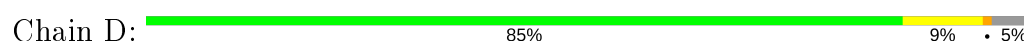
- Molecule 1: Nicotinate-nucleotide pyrophosphorylase [carboxylating]

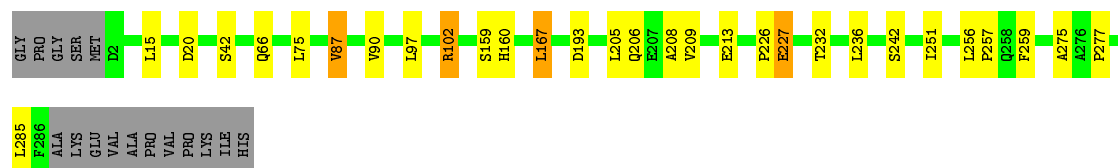


- Molecule 1: Nicotinate-nucleotide pyrophosphorylase [carboxylating]

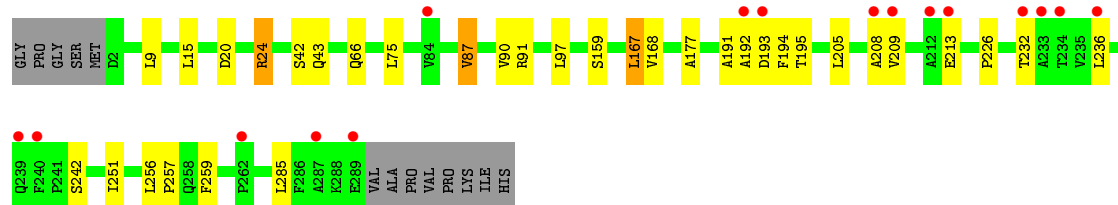
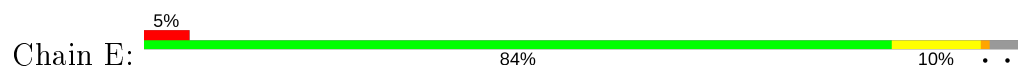


- Molecule 1: Nicotinate-nucleotide pyrophosphorylase [carboxylating]

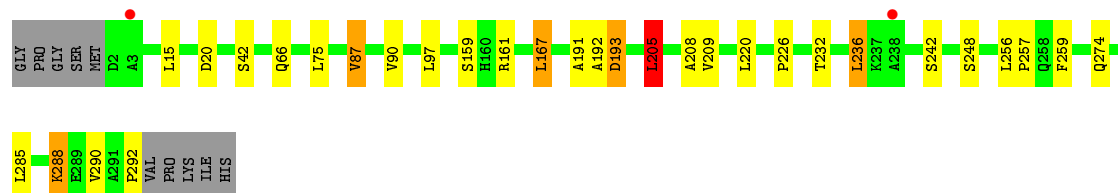
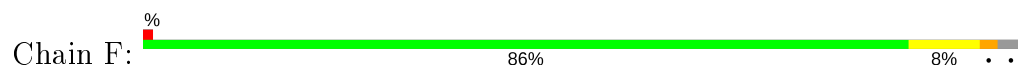




- Molecule 1: Nicotinate-nucleotide pyrophosphorylase [carboxylating]



- Molecule 1: Nicotinate-nucleotide pyrophosphorylase [carboxylating]



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	178.56Å 178.56Å 121.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.93 – 2.80 42.89 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.93-2.80) 99.9 (42.89-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.212 , 0.237 0.212 , 0.238	Depositor DCC
$R_{free}$ test set	2812 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.4	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12001	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [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	0.34	0/2038	0.54	2/2796 (0.1%)
1	B	0.38	0/2018	0.53	0/2773
1	C	0.37	0/1990	0.54	1/2731 (0.0%)
1	D	0.38	0/2048	0.54	0/2806
1	E	0.34	0/2065	0.55	0/2829
1	F	0.51	0/2078	0.60	4/2849 (0.1%)
All	All	0.39	0/12237	0.55	7/16784 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	192	ALA	CB-CA-C	5.88	118.91	110.10
1	F	193	ASP	CB-CA-C	-5.28	99.85	110.40
1	F	292	PRO	N-CA-CB	5.20	109.54	103.30
1	A	275	ALA	CB-CA-C	5.17	117.86	110.10
1	F	205	LEU	CB-CG-CD2	-5.15	102.24	111.00
1	F	274	GLN	CB-CA-C	5.04	120.49	110.40
1	C	274	GLN	CB-CA-C	5.03	120.46	110.40

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	1995	0	1941	15	0
1	B	1976	0	1899	15	0
1	C	1951	0	1861	12	0
1	D	2005	0	1962	16	0
1	E	2023	0	1982	25	0
1	F	2036	0	1986	12	0
2	A	4	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	3	0	0	0	0
2	E	1	0	0	0	0
2	F	5	0	0	0	0
All	All	12001	0	11631	89	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 4.

All (89) 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:E:168:VAL:HG21	1:E:192:ALA:HB2	1.31	1.13
1:D:275:ALA:O	1:D:277:PRO:HD3	1.78	0.83
1:B:275:ALA:O	1:B:277:PRO:HD3	1.79	0.82
1:E:168:VAL:CG2	1:E:192:ALA:HB2	2.11	0.80
1:E:168:VAL:HG21	1:E:192:ALA:CB	2.10	0.79
1:F:20:ASP:OD1	1:F:66:GLN:NE2	2.21	0.73
1:D:20:ASP:OD1	1:D:66:GLN:NE2	2.22	0.72
1:A:208:ALA:HB1	1:A:236:LEU:HD11	1.71	0.72
1:E:20:ASP:OD1	1:E:66:GLN:NE2	2.22	0.71
1:E:43:GLN:HG2	1:E:91:ARG:HG2	1.72	0.71
1:B:20:ASP:OD1	1:B:66:GLN:NE2	2.24	0.70
1:E:208:ALA:HB1	1:E:236:LEU:HD11	1.75	0.66
1:A:20:ASP:OD1	1:A:66:GLN:NE2	2.29	0.65
1:B:168:VAL:HG21	1:B:192:ALA:HB2	1.79	0.64
1:E:193:ASP:OD1	1:E:195:THR:HG23	1.96	0.64
1:D:167:LEU:HD23	1:E:195:THR:HB	1.83	0.61
1:D:208:ALA:HB1	1:D:236:LEU:HD11	1.86	0.57
1:C:168:VAL:HG21	1:C:192:ALA:HB2	1.88	0.56
1:A:168:VAL:HG21	1:A:192:ALA:HB2	1.88	0.55
1:E:177:ALA:HA	1:F:288:LYS:HG3	1.90	0.53
1:C:205:LEU:O	1:C:209:VAL:HG23	2.09	0.53
1:E:194:PHE:CE2	1:E:195:THR:HG22	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:90:VAL:HG12	1:C:97:LEU:HD21	1.93	0.51
1:E:167:LEU:HD12	1:E:167:LEU:C	2.31	0.51
1:A:167:LEU:HD12	1:A:167:LEU:C	2.32	0.51
1:A:205:LEU:O	1:A:209:VAL:HG23	2.10	0.51
1:F:90:VAL:HG12	1:F:97:LEU:HD21	1.93	0.50
1:A:191:ALA:O	1:A:192:ALA:C	2.49	0.50
1:E:191:ALA:O	1:E:192:ALA:C	2.50	0.50
1:E:90:VAL:HG12	1:E:97:LEU:HD21	1.93	0.50
1:B:90:VAL:HG12	1:B:97:LEU:HD21	1.93	0.50
1:D:90:VAL:HG12	1:D:97:LEU:HD21	1.94	0.50
1:B:32:TYR:HA	1:C:9:LEU:CD2	2.42	0.50
1:E:205:LEU:O	1:E:209:VAL:HG23	2.12	0.49
1:B:75:LEU:HD12	1:B:87:VAL:HG13	1.94	0.49
1:F:205:LEU:HB2	1:F:232:THR:HG23	1.93	0.49
1:A:90:VAL:HG12	1:A:97:LEU:HD21	1.94	0.49
1:D:167:LEU:HD12	1:D:167:LEU:C	2.33	0.49
1:A:218:LEU:HG	1:A:244:ALA:HB3	1.95	0.48
1:B:167:LEU:HD12	1:B:167:LEU:C	2.34	0.48
1:C:167:LEU:HD12	1:C:167:LEU:C	2.34	0.48
1:F:167:LEU:C	1:F:167:LEU:HD12	2.33	0.48
1:F:75:LEU:HD12	1:F:87:VAL:HG13	1.95	0.48
1:D:205:LEU:O	1:D:209:VAL:HG23	2.13	0.48
1:D:75:LEU:HD12	1:D:87:VAL:HG13	1.96	0.48
1:A:20:ASP:OD2	1:A:24:ARG:NH2	2.48	0.47
1:B:205:LEU:O	1:B:209:VAL:HG23	2.13	0.47
1:F:226:PRO:HG3	1:F:259:PHE:CE1	2.50	0.47
1:F:208:ALA:HB1	1:F:236:LEU:HD21	1.96	0.47
1:A:75:LEU:HD12	1:A:87:VAL:HG13	1.96	0.47
1:D:226:PRO:HG3	1:D:259:PHE:CE1	2.51	0.46
1:C:75:LEU:HD12	1:C:87:VAL:HG13	1.97	0.46
1:C:226:PRO:HG3	1:C:259:PHE:CE1	2.51	0.46
1:B:226:PRO:HG3	1:B:259:PHE:CE1	2.50	0.46
1:E:226:PRO:HG3	1:E:259:PHE:CE1	2.51	0.46
1:E:75:LEU:HD12	1:E:87:VAL:HG13	1.98	0.46
1:C:138:ARG:CB	1:D:102:ARG:HD3	2.45	0.45
1:E:168:VAL:CG2	1:E:192:ALA:CB	2.85	0.45
1:A:226:PRO:HG3	1:A:259:PHE:CE1	2.52	0.45
1:D:205:LEU:HB2	1:D:232:THR:HG23	1.98	0.45
1:B:13:VAL:HG12	1:E:24:ARG:HD2	1.97	0.45
1:C:32:TYR:HA	1:E:9:LEU:CD2	2.47	0.45
1:B:205:LEU:HB2	1:B:232:THR:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:193:ASP:OD1	1:E:194:PHE:CD1	2.70	0.44
1:D:227:GLU:H	1:D:227:GLU:CD	2.21	0.43
1:F:191:ALA:O	1:F:192:ALA:C	2.55	0.43
1:F:220:LEU:HD11	1:F:248:SER:HB3	2.00	0.43
1:A:205:LEU:HB2	1:A:232:THR:HG23	1.99	0.42
1:F:205:LEU:O	1:F:209:VAL:HG23	2.19	0.42
1:B:251:ILE:HG12	1:B:259:PHE:CE2	2.54	0.42
1:E:193:ASP:OD1	1:E:194:PHE:CE1	2.72	0.42
1:C:251:ILE:HG12	1:C:259:PHE:CE2	2.55	0.42
1:B:135:ALA:O	1:B:268:SER:HA	2.20	0.42
1:F:256:LEU:N	1:F:257:PRO:CD	2.82	0.42
1:B:256:LEU:N	1:B:257:PRO:CD	2.83	0.41
1:A:237:LYS:HG3	1:A:263:HIS:HB3	2.02	0.41
1:D:251:ILE:HG12	1:D:259:PHE:CE2	2.55	0.41
1:E:256:LEU:N	1:E:257:PRO:CD	2.83	0.41
1:C:256:LEU:N	1:C:257:PRO:CD	2.84	0.41
1:E:205:LEU:HB2	1:E:232:THR:HG23	2.01	0.41
1:E:251:ILE:HG12	1:E:259:PHE:CE2	2.54	0.41
1:A:256:LEU:N	1:A:257:PRO:CD	2.84	0.41
1:A:251:ILE:HG12	1:A:259:PHE:CE2	2.55	0.41
1:B:251:ILE:HG12	1:B:259:PHE:CD2	2.56	0.40
1:D:205:LEU:HD13	1:D:232:THR:HG23	2.03	0.40
1:C:251:ILE:HG12	1:C:259:PHE:CD2	2.56	0.40
1:D:256:LEU:N	1:D:257:PRO:CD	2.84	0.40
1:E:251:ILE:HG12	1:E:259:PHE:CD2	2.56	0.40
1:D:251:ILE:HG12	1:D:259:PHE:CD2	2.56	0.40

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	283/301 (94%)	282 (100%)	1 (0%)	0	100	100
1	B	284/301 (94%)	282 (99%)	2 (1%)	0	100	100
1	C	283/301 (94%)	281 (99%)	2 (1%)	0	100	100
1	D	283/301 (94%)	282 (100%)	1 (0%)	0	100	100
1	E	286/301 (95%)	284 (99%)	2 (1%)	0	100	100
1	F	289/301 (96%)	286 (99%)	3 (1%)	0	100	100
All	All	1708/1806 (95%)	1697 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	188/222 (85%)	179 (95%)	9 (5%)	25	58
1	B	183/222 (82%)	178 (97%)	5 (3%)	44	78
1	C	179/222 (81%)	167 (93%)	12 (7%)	16	43
1	D	191/222 (86%)	178 (93%)	13 (7%)	16	42
1	E	192/222 (86%)	183 (95%)	9 (5%)	26	59
1	F	195/222 (88%)	182 (93%)	13 (7%)	16	43
All	All	1128/1332 (85%)	1067 (95%)	61 (5%)	22	53

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	20	ASP
1	A	42	SER
1	A	87	VAL
1	A	159	SER
1	A	160	HIS
1	A	167	LEU

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Mol	Chain	Res	Type
1	A	193	ASP
1	A	285	LEU
1	B	15	LEU
1	B	42	SER
1	B	87	VAL
1	B	167	LEU
1	B	285	LEU
1	C	15	LEU
1	C	20	ASP
1	C	24	ARG
1	C	42	SER
1	C	43	GLN
1	C	65	THR
1	C	87	VAL
1	C	159	SER
1	C	167	LEU
1	C	193	ASP
1	C	242	SER
1	C	285	LEU
1	D	15	LEU
1	D	42	SER
1	D	87	VAL
1	D	102	ARG
1	D	159	SER
1	D	160	HIS
1	D	167	LEU
1	D	193	ASP
1	D	206	GLN
1	D	213	GLU
1	D	227	GLU
1	D	242	SER
1	D	285	LEU
1	E	15	LEU
1	E	24	ARG
1	E	42	SER
1	E	87	VAL
1	E	159	SER
1	E	167	LEU
1	E	213	GLU
1	E	242	SER
1	E	285	LEU
1	F	15	LEU

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Mol	Chain	Res	Type
1	F	42	SER
1	F	87	VAL
1	F	159	SER
1	F	161	ARG
1	F	167	LEU
1	F	193	ASP
1	F	205	LEU
1	F	236	LEU
1	F	242	SER
1	F	285	LEU
1	F	288	LYS
1	F	290	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	43	GLN
1	B	66	GLN
1	B	263	HIS
1	C	43	GLN
1	C	66	GLN
1	D	66	GLN
1	D	206	GLN
1	E	66	GLN
1	F	66	GLN
1	F	160	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	285/301 (94%)	0.04	4 (1%) 75 70	39, 63, 83, 116	0
1	B	286/301 (95%)	0.13	11 (3%) 40 30	40, 63, 89, 107	0
1	C	285/301 (94%)	0.19	8 (2%) 53 43	33, 63, 104, 120	0
1	D	285/301 (94%)	0.03	0 100 100	36, 52, 76, 100	0
1	E	288/301 (95%)	0.17	16 (5%) 24 16	30, 51, 83, 106	0
1	F	291/301 (96%)	-0.11	2 (0%) 87 84	27, 44, 70, 90	0
All	All	1720/1806 (95%)	0.07	41 (2%) 59 49	27, 56, 90, 120	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	39	ALA	4.6
1	C	3	ALA	3.9
1	B	287	ALA	3.3
1	C	233	ALA	3.2
1	C	227	GLU	3.0
1	E	234	THR	3.0
1	E	232	THR	2.9
1	B	227	GLU	2.8
1	E	236	LEU	2.8
1	B	2	ASP	2.8
1	B	238	ALA	2.7
1	C	257	PRO	2.7
1	B	262	PRO	2.7
1	B	233	ALA	2.7
1	A	74	PHE	2.6
1	E	262	PRO	2.6
1	C	259	PHE	2.6
1	B	263	HIS	2.5
1	C	162	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	209	VAL	2.5
1	B	259	PHE	2.5
1	F	238	ALA	2.5
1	E	193	ASP	2.5
1	B	261	GLY	2.4
1	E	233	ALA	2.3
1	A	3	ALA	2.3
1	C	240	PHE	2.3
1	F	3	ALA	2.3
1	E	212	ALA	2.3
1	A	236	LEU	2.2
1	E	287	ALA	2.2
1	E	192	ALA	2.2
1	E	213	GLU	2.2
1	E	289	GLU	2.1
1	C	224	PHE	2.1
1	B	39	ALA	2.1
1	E	239	GLN	2.1
1	E	240	PHE	2.0
1	E	208	ALA	2.0
1	B	234	THR	2.0
1	E	84	VAL	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 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.