



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 16, 2021 – 12:08 PM JST

PDB ID : 7E4W
Title : Human Transcriptional Co-activator PC4 (C-terminal Domain) in space group P1211
Authors : Dev, A.; Pandey, B.; Basu, G.
Deposited on : 2021-02-15
Resolution : 2.90 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:

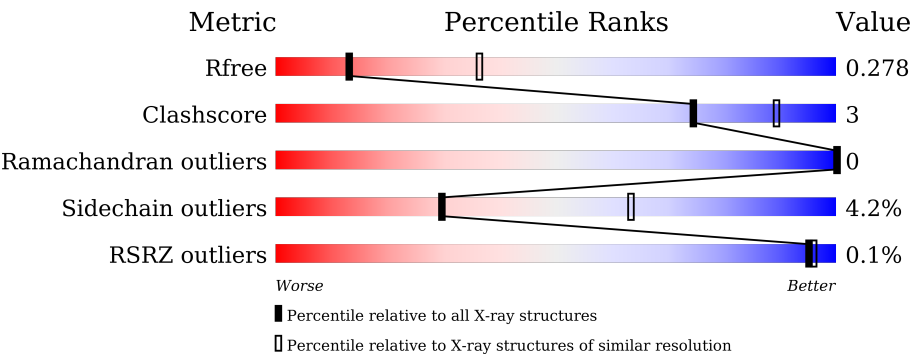
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.1

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 2.90 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.



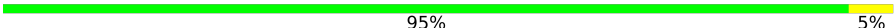









Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	66	<div><div></div><div>86%14%</div></div>
1	B	66	<div><div></div><div>92%8%</div></div>
1	C	66	<div><div></div><div>89%11%</div></div>
1	D	66	<div><div></div><div>91%9%</div></div>
1	E	66	<div><div></div><div>85%14%. </div></div>
1	F	66	<div><div></div><div>85%14%. </div></div>

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Mol	Chain	Length	Quality of chain
1	G	66	 95% 5%
1	H	66	 92% 6% •
1	I	66	 86% 12% •
1	J	66	 82% 17% •
1	K	66	 94% 6%
1	L	66	 89% 9% •
1	M	66	 86% 14%
1	N	66	 86% 12% •
1	O	66	 88% 12%
1	P	66	 95% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8792 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 Activated RNA polymerase II transcriptional coactivator p15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	66	Total	C	N	O	S	0	0	0
			545	346	95	100	4			
1	B	66	Total	C	N	O	S	0	0	0
			539	344	91	100	4			
1	C	66	Total	C	N	O	S	0	0	0
			545	346	95	100	4			
1	D	66	Total	C	N	O	S	0	0	0
			539	342	93	100	4			
1	E	66	Total	C	N	O	S	0	0	0
			545	346	95	100	4			
1	F	66	Total	C	N	O	S	0	0	0
			545	346	95	100	4			
1	G	66	Total	C	N	O	S	0	0	0
			525	334	87	100	4			
1	H	66	Total	C	N	O	S	0	0	0
			540	345	94	97	4			
1	I	66	Total	C	N	O	S	0	0	0
			542	345	95	98	4			
1	J	66	Total	C	N	O	S	0	0	0
			537	342	92	99	4			
1	K	66	Total	C	N	O	S	0	0	0
			541	345	94	98	4			
1	L	66	Total	C	N	O	S	0	0	0
			544	346	94	100	4			
1	M	66	Total	C	N	O	S	0	0	0
			545	346	95	100	4			
1	N	66	Total	C	N	O	S	0	0	0
			543	345	94	100	4			
1	O	66	Total	C	N	O	S	0	0	0
			542	345	93	100	4			
1	P	66	Total	C	N	O	S	0	0	0
			544	346	94	100	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	ALA	-	expression tag	UNP P53999
B	62	ALA	-	expression tag	UNP P53999
C	62	ALA	-	expression tag	UNP P53999
D	62	ALA	-	expression tag	UNP P53999
E	62	ALA	-	expression tag	UNP P53999
F	62	ALA	-	expression tag	UNP P53999
G	62	ALA	-	expression tag	UNP P53999
H	62	ALA	-	expression tag	UNP P53999
I	62	ALA	-	expression tag	UNP P53999
J	62	ALA	-	expression tag	UNP P53999
K	62	ALA	-	expression tag	UNP P53999
L	62	ALA	-	expression tag	UNP P53999
M	62	ALA	-	expression tag	UNP P53999
N	62	ALA	-	expression tag	UNP P53999
O	62	ALA	-	expression tag	UNP P53999
P	62	ALA	-	expression tag	UNP P53999

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	7	Total O 7 7	0	0
2	B	10	Total O 10 10	0	0
2	C	6	Total O 6 6	0	0
2	D	7	Total O 7 7	0	0
2	E	6	Total O 6 6	0	0
2	F	7	Total O 7 7	0	0
2	G	4	Total O 4 4	0	0
2	H	4	Total O 4 4	0	0
2	I	5	Total O 5 5	0	0
2	J	6	Total O 6 6	0	0
2	K	14	Total O 14 14	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	L	9	Total 9	O 9	0	0
2	M	11	Total 11	O 11	0	0
2	N	11	Total 11	O 11	0	0
2	O	10	Total 10	O 10	0	0
2	P	14	Total 14	O 14	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.

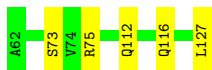
- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain A:  86% 14%




- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain B:  92% 8%



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain C:  89% 11%




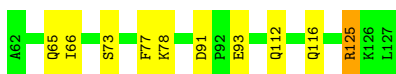
- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain D:  91% 9%




- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain E:  85% 14% .



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain F:  85% 14% .



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain G:  95% 5%




- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain H:  92% 6%




- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain I:  2% 86% 12%



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain J:  82% 17%




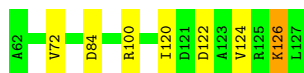
- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain K:  94% 6%



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

Chain L:  89% 9%

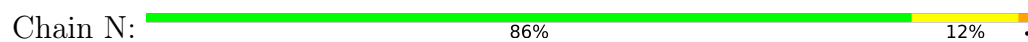


- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15

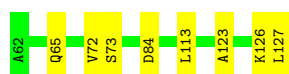
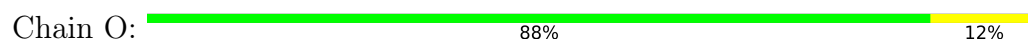
Chain M:  86% 14%



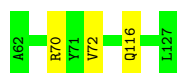
- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15



- Molecule 1: Activated RNA polymerase II transcriptional coactivator p15



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.01Å 166.84Å 108.31Å 90.00° 93.27° 90.00°	Depositor
Resolution (Å)	108.13 – 2.90 43.65 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (108.13-2.90) 99.7 (43.65-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.228 , 0.278 0.231 , 0.278	Depositor DCC
R_{free} test set	1868 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.625	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8792	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.43 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.7077e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [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	0.61	0/555	0.83	0/740
1	B	0.62	0/549	0.86	0/733
1	C	0.60	0/555	0.83	0/740
1	D	0.60	0/549	0.79	0/734
1	E	0.62	0/555	0.84	0/740
1	F	0.60	0/555	0.81	0/740
1	G	0.58	0/535	0.77	0/718
1	H	0.61	0/550	0.80	0/734
1	I	0.53	0/552	0.80	0/737
1	J	0.55	0/547	0.78	0/728
1	K	0.57	0/551	0.82	0/736
1	L	0.57	0/554	0.77	0/738
1	M	0.59	0/555	0.80	0/740
1	N	0.60	0/553	0.87	0/738
1	O	0.60	0/552	0.83	0/736
1	P	0.60	0/554	0.78	0/738
All	All	0.59	0/8821	0.81	0/11770

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	545	0	551	3	0
1	B	539	0	537	1	0
1	C	545	0	551	4	0
1	D	539	0	533	4	0
1	E	545	0	551	7	0
1	F	545	0	551	9	0
1	G	525	0	507	1	0
1	H	540	0	547	2	0
1	I	542	0	547	6	0
1	J	537	0	531	8	0
1	K	541	0	547	2	0
1	L	544	0	549	3	0
1	M	545	0	551	4	0
1	N	543	0	544	4	0
1	O	542	0	546	5	0
1	P	544	0	549	2	0
2	A	7	0	0	0	0
2	B	10	0	0	0	0
2	C	6	0	0	0	0
2	D	7	0	0	0	0
2	E	6	0	0	1	0
2	F	7	0	0	0	0
2	G	4	0	0	0	0
2	H	4	0	0	0	0
2	I	5	0	0	0	0
2	J	6	0	0	0	0
2	K	14	0	0	0	0
2	L	9	0	0	0	0
2	M	11	0	0	0	0
2	N	11	0	0	0	0
2	O	10	0	0	0	0
2	P	14	0	0	0	0
All	All	8792	0	8692	55	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 3.

All (55) 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:125:ARG:HD2	2:E:203:HOH:O	1.92	0.68
1:E:77:PHE:CE1	1:E:78:LYS:HE2	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:123:ALA:O	1:O:127:LEU:HD13	1.95	0.65
1:M:123:ALA:O	1:M:127:LEU:HD13	1.97	0.64
1:F:126:LYS:C	1:F:127:LEU:HD12	2.18	0.64
1:M:126:LYS:C	1:M:127:LEU:HD12	2.18	0.64
1:C:123:ALA:O	1:C:127:LEU:HD13	1.98	0.63
1:A:123:ALA:O	1:A:127:LEU:HD13	1.98	0.63
1:K:123:ALA:O	1:K:127:LEU:HD13	1.99	0.63
1:O:126:LYS:C	1:O:127:LEU:HD12	2.20	0.63
1:O:65:GLN:O	1:P:116:GLN:NE2	2.32	0.62
1:A:126:LYS:C	1:A:127:LEU:HD12	2.21	0.62
1:L:120:ILE:O	1:L:124:VAL:HG23	1.99	0.61
1:C:126:LYS:C	1:C:127:LEU:HD12	2.21	0.61
1:D:126:LYS:C	1:D:127:LEU:HD12	2.19	0.61
1:D:123:ALA:O	1:D:127:LEU:HD13	2.03	0.59
1:K:126:LYS:C	1:K:127:LEU:HD12	2.22	0.58
1:F:77:PHE:O	1:F:78:LYS:HG2	2.05	0.56
1:N:70:ARG:HD3	1:N:87:GLU:HG2	1.88	0.55
1:J:82:LEU:HD22	1:J:104:SER:HB3	1.89	0.54
1:C:116:GLN:NE2	1:D:65:GLN:O	2.40	0.54
1:G:81:VAL:HG21	1:H:127:LEU:HD11	1.90	0.54
1:F:123:ALA:O	1:F:127:LEU:HD13	2.08	0.53
1:H:91:ASP:HB2	1:H:92:PRO:HD2	1.90	0.52
1:J:77:PHE:C	1:J:77:PHE:CD1	2.85	0.50
1:I:116:GLN:NE2	1:J:65:GLN:O	2.45	0.50
1:A:77:PHE:CE1	1:A:78:LYS:HD2	2.47	0.49
1:I:121:ASP:O	1:I:125:ARG:HG2	2.12	0.49
1:M:116:GLN:NE2	1:N:65:GLN:O	2.46	0.49
1:N:112:GLN:O	1:N:116:GLN:HG3	2.12	0.48
1:I:109:GLN:HA	1:J:66:ILE:O	2.14	0.48
1:D:78:LYS:O	1:D:78:LYS:CG	2.60	0.47
1:E:112:GLN:O	1:E:116:GLN:HG3	2.14	0.47
1:I:119:ASP:N	1:I:119:ASP:OD1	2.47	0.47
1:E:93:GLU:N	1:E:93:GLU:OE1	2.49	0.46
1:J:112:GLN:O	1:J:116:GLN:HG3	2.16	0.46
1:L:122:ASP:O	1:L:126:LYS:HG2	2.16	0.45
1:N:127:LEU:N	1:N:127:LEU:CD1	2.80	0.45
1:E:65:GLN:O	1:F:116:GLN:NE2	2.50	0.45
1:F:77:PHE:CE2	1:F:78:LYS:CE	3.00	0.44
1:J:65:GLN:HA	1:J:71:TYR:CD1	2.53	0.44
1:F:112:GLN:O	1:F:116:GLN:HG3	2.17	0.44
1:O:113:LEU:CD1	1:P:72:VAL:HG21	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:127:LEU:HD12	1:F:127:LEU:N	2.33	0.43
1:J:64:PHE:CD1	1:J:64:PHE:N	2.88	0.42
1:E:77:PHE:CZ	1:E:78:LYS:HE2	2.56	0.41
1:I:117:ILE:HD11	1:J:117:ILE:CD1	2.51	0.41
1:E:66:ILE:O	1:F:109:GLN:HA	2.20	0.41
1:O:72:VAL:HA	1:O:84:ASP:O	2.21	0.41
1:B:112:GLN:O	1:B:116:GLN:HG3	2.21	0.41
1:I:112:GLN:O	1:I:116:GLN:HG3	2.21	0.40
1:C:112:GLN:O	1:C:116:GLN:HG3	2.20	0.40
1:M:72:VAL:HA	1:M:84:ASP:O	2.22	0.40
1:F:77:PHE:CE2	1:F:78:LYS:HE3	2.57	0.40
1:L:72:VAL:HA	1:L:84:ASP:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	B	64/66 (97%)	64 (100%)	0	0	100	100
1	C	64/66 (97%)	62 (97%)	2 (3%)	0	100	100
1	D	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	E	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	F	64/66 (97%)	62 (97%)	2 (3%)	0	100	100
1	G	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	H	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	I	64/66 (97%)	62 (97%)	2 (3%)	0	100	100
1	J	64/66 (97%)	62 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	L	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	M	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	N	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
1	O	64/66 (97%)	62 (97%)	2 (3%)	0	100	100
1	P	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
All	All	1024/1056 (97%)	1004 (98%)	20 (2%)	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	59/59 (100%)	55 (93%)	4 (7%)	16	42
1	B	57/59 (97%)	54 (95%)	3 (5%)	22	54
1	C	59/59 (100%)	57 (97%)	2 (3%)	37	71
1	D	57/59 (97%)	56 (98%)	1 (2%)	59	85
1	E	59/59 (100%)	56 (95%)	3 (5%)	24	56
1	F	59/59 (100%)	56 (95%)	3 (5%)	24	56
1	G	55/59 (93%)	53 (96%)	2 (4%)	35	69
1	H	58/59 (98%)	55 (95%)	3 (5%)	23	55
1	I	58/59 (98%)	55 (95%)	3 (5%)	23	55
1	J	56/59 (95%)	53 (95%)	3 (5%)	22	54
1	K	58/59 (98%)	57 (98%)	1 (2%)	60	86
1	L	59/59 (100%)	57 (97%)	2 (3%)	37	71
1	M	59/59 (100%)	56 (95%)	3 (5%)	24	56
1	N	58/59 (98%)	54 (93%)	4 (7%)	15	41
1	O	58/59 (98%)	57 (98%)	1 (2%)	60	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	59/59 (100%)	58 (98%)	1 (2%)	60	86
All	All	928/944 (98%)	889 (96%)	39 (4%)	30	63

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LYS
1	A	73	SER
1	A	93	GLU
1	A	100	ARG
1	B	73	SER
1	B	75	ARG
1	B	127	LEU
1	C	100	ARG
1	C	111	SER
1	D	70	ARG
1	E	73	SER
1	E	91	ASP
1	E	125	ARG
1	F	73	SER
1	F	78	LYS
1	F	100	ARG
1	G	73	SER
1	G	126	LYS
1	H	100	ARG
1	H	126	LYS
1	H	127	LEU
1	I	73	SER
1	I	100	ARG
1	I	119	ASP
1	J	77	PHE
1	J	78	LYS
1	J	93	GLU
1	K	100	ARG
1	L	100	ARG
1	L	126	LYS
1	M	73	SER
1	M	75	ARG
1	M	100	ARG
1	N	73	SER
1	N	78	LYS
1	N	100	ARG

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Mol	Chain	Res	Type
1	N	127	LEU
1	O	73	SER
1	P	70	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	B	116	GLN
1	C	116	GLN
1	E	116	GLN
1	J	65	GLN
1	M	116	GLN
1	N	116	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](#)

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	66/66 (100%)	-0.21	0 100 100	20, 35, 64, 79	0
1	B	66/66 (100%)	-0.26	0 100 100	21, 35, 71, 100	0
1	C	66/66 (100%)	0.01	0 100 100	32, 48, 96, 103	0
1	D	66/66 (100%)	-0.16	0 100 100	33, 45, 74, 93	0
1	E	66/66 (100%)	-0.22	0 100 100	21, 37, 78, 96	0
1	F	66/66 (100%)	-0.20	0 100 100	25, 39, 77, 102	0
1	G	66/66 (100%)	-0.17	0 100 100	31, 46, 72, 98	0
1	H	66/66 (100%)	-0.12	0 100 100	29, 50, 78, 90	0
1	I	66/66 (100%)	0.02	1 (1%) 73 73	29, 56, 94, 111	0
1	J	66/66 (100%)	-0.01	0 100 100	34, 54, 91, 95	0
1	K	66/66 (100%)	-0.07	0 100 100	31, 45, 74, 109	0
1	L	66/66 (100%)	-0.20	0 100 100	31, 47, 75, 96	0
1	M	66/66 (100%)	-0.22	0 100 100	24, 36, 69, 92	0
1	N	66/66 (100%)	-0.23	0 100 100	24, 37, 69, 80	0
1	O	66/66 (100%)	-0.18	0 100 100	24, 38, 59, 80	0
1	P	66/66 (100%)	-0.33	0 100 100	27, 38, 79, 95	0
All	All	1056/1056 (100%)	-0.16	1 (0%) 95 96	20, 44, 83, 111	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	77	PHE	2.7

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 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.