



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:14 PM GMT

PDB ID : 4BPX
Title : Crystal structure of human primase in complex with the primase- binding motif of DNA polymerase alpha
Authors : Kilkenny, M.L.; Perera, R.L.; Pellegrini, L.
Deposited on : 2013-05-28
Resolution : 3.40 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

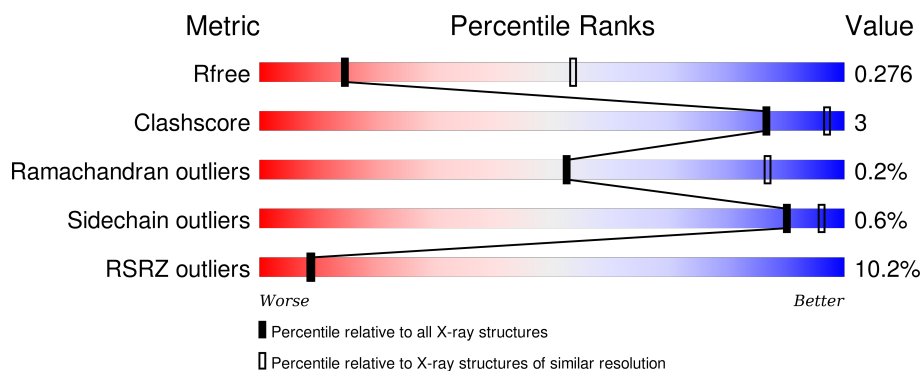
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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. 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	423	
1	C	423	
2	B	269	
2	D	269	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19218 atoms, of which 9629 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 DNA PRIMASE SMALL SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	381	Total	C	H	N	O	S	0	2	0
			6392	2059	3190	558	572	13			
1	C	372	Total	C	H	N	O	S	0	0	0
			6195	2002	3086	537	557	13			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP P49642
A	-1	THR	-	EXPRESSION TAG	UNP P49642
A	0	SER	-	EXPRESSION TAG	UNP P49642
A	72	ALA	LYS	ENGINEERED MUTATION	UNP P49642
A	73	ALA	MET	ENGINEERED MUTATION	UNP P49642
C	-2	GLY	-	EXPRESSION TAG	UNP P49642
C	-1	THR	-	EXPRESSION TAG	UNP P49642
C	0	SER	-	EXPRESSION TAG	UNP P49642
C	72	ALA	LYS	ENGINEERED MUTATION	UNP P49642
C	73	ALA	MET	ENGINEERED MUTATION	UNP P49642

- Molecule 2 is a protein called DNA POLYMERASE ALPHA CATALYTIC SUBUNIT, DNA PRIMASE LARGE SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	181	Total	C	H	N	O	S	0	0	0
			3056	970	1553	258	273	2			
2	D	213	Total	C	H	N	O	S	0	0	0
			3573	1142	1800	300	329	2			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1444	MET	-	EXPRESSION TAG	UNP P09884

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4	THR	-	LINKER	UNP P49643
B	5	GLY	-	LINKER	UNP P49643
B	6	SER	-	LINKER	UNP P49643
B	7	THR	-	LINKER	UNP P49643
B	8	GLY	-	LINKER	UNP P49643
B	9	SER	-	LINKER	UNP P49643
B	10	THR	-	LINKER	UNP P49643
B	11	GLY	-	LINKER	UNP P49643
B	12	SER	-	LINKER	UNP P49643
B	13	THR	-	LINKER	UNP P49643
B	14	GLY	-	LINKER	UNP P49643
B	15	SER	-	LINKER	UNP P49643
B	16	THR	-	LINKER	UNP P49643
B	17	GLY	-	LINKER	UNP P49643
B	18	SER	-	LINKER	UNP P49643
D	1444	MET	-	EXPRESSION TAG	UNP P09884
D	4	THR	-	LINKER	UNP P49643
D	5	GLY	-	LINKER	UNP P49643
D	6	SER	-	LINKER	UNP P49643
D	7	THR	-	LINKER	UNP P49643
D	8	GLY	-	LINKER	UNP P49643
D	9	SER	-	LINKER	UNP P49643
D	10	THR	-	LINKER	UNP P49643
D	11	GLY	-	LINKER	UNP P49643
D	12	SER	-	LINKER	UNP P49643
D	13	THR	-	LINKER	UNP P49643
D	14	GLY	-	LINKER	UNP P49643
D	15	SER	-	LINKER	UNP P49643
D	16	THR	-	LINKER	UNP P49643
D	17	GLY	-	LINKER	UNP P49643
D	18	SER	-	LINKER	UNP P49643

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0
3	C	1	Total Zn 1 1	0	0

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

Chain A:

2% 80% 10% 10%

GLY THR SER MET GLU T3

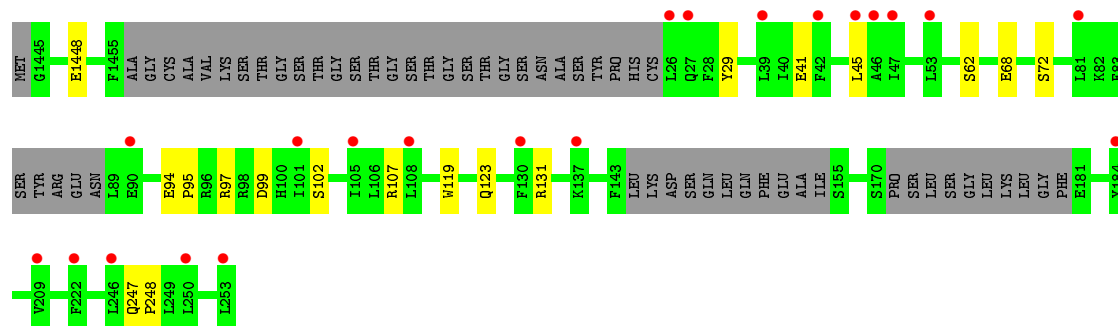
E254 S265 R268 R278 W282 ILE LYS ASN ASP TYR GLY P290 W291 L292 F302 P303 K318 F321 S322 V323 D335 K338 C354 L357 S360 SER THR ASN GLU GLU LYS GLU ASN ALA SER ASP VAL LYS HIS R379 T380 W384

Chain C:

Sequence logo for Chain C. The y-axis represents information content in bits, ranging from 0 to 1.3. The x-axis shows positions 1 to 390. The logo displays the conservation of amino acids at each position, with the most conserved residues (those with the highest information content) shown in larger font and colored blocks. The sequence is: P390, Y391, V392, K393, V394, F395, F398, G408, GLU, LEU, LEU, LYS, LYS, SER, ASP, LEU, GLN, LYS, ASP, PHE, C131, M137, A138, I139, F152, R155, L156, W157, V158, Y159, R163, G164, V165, H166, C167, W168, V169, C170, L228, D232, I233, K237, W240, R252, D253, E254, S285, W269, R278, R282, ILE, LYS, ASN, ASP, LYS, TYR, GLY, P290, W294, Y300, C301, F302, P303, T386, S387, T388, A389.

Chain B:

Residue	Count
Met	1
Gly	1
Tyr	1
Ser	1
Val	1
Asn	1
Leu	1
Ser	1
Lys	1
Phe	1
Ala	1
Gly	1
Cys	1
Ala	1
Val	1
Lys	1
Ser	1
Thr	1
Gly	1
Ser	1
Thr	1
Gly	1
Ser	1
Thr	1
Gly	1
Ser	1
Asn	1
Ala	1
Tyr	1
Pro	1
His	1
Cys	1
Leu	1
Gln	1
Phe	1
Tyr	1
Leu	1
Gln	1
Pro	1
Pro	1
Ser	1
Glu	1
Asn	1
I37	1
L45	1
A46	1
I47	1
D48	1
R49	1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	120.68Å 70.70Å 127.16Å 90.00° 105.83° 90.00°	Depositor
Resolution (Å)	45.33 – 3.40 49.36 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.33-3.40) 99.9 (49.36-3.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 3.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.234 , 0.267 0.239 , 0.276	Depositor DCC
R_{free} test set	1487 reflections (5.45%)	DCC
Wilson B-factor (Å ²)	171.8	Xtriage
Anisotropy	0.334	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 140.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 28768 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19218	wwPDB-VP
Average B, all atoms (Å ²)	218.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0/3297	0.43	0/4449
1	C	0.23	0/3190	0.40	0/4307
2	B	0.23	0/1524	0.41	0/2040
2	D	0.25	0/1803	0.40	0/2420
All	All	0.24	0/9814	0.41	0/13216

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	3202	3190	3167	22	0
1	C	3109	3086	3073	16	0
2	B	1503	1553	1550	5	0
2	D	1773	1800	1794	9	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
All	All	9589	9629	9584	51	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 (51) 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:A:160:SER:O	1:A:318:LYS:NZ	2.19	0.76
2:D:119:TRP:O	2:D:123:GLN:NE2	2.19	0.74
1:A:403:ASP:OD1	1:A:406:ARG:NH2	2.26	0.69
1:C:254:GLU:OE2	1:C:278:ARG:NH2	2.28	0.67
1:C:71:GLN:O	1:C:74:ASN:ND2	2.29	0.66
2:D:29:TYR:O	2:D:107:ARG:NH2	2.28	0.66
1:A:232:ASP:OD1	1:A:265:SER:OG	2.14	0.65
2:B:119:TRP:O	2:B:123:GLN:NE2	2.31	0.64
1:A:92:ASN:OD1	2:D:1448:GLU:N	2.32	0.62
2:B:99:ASP:OD1	2:B:131:ARG:NH2	2.38	0.57
2:D:68:GLU:O	2:D:72:SER:N	2.38	0.56
1:C:111:ASP:OD2	1:C:163:ARG:NH2	2.39	0.56
1:C:104:LYS:NZ	1:C:315:HIS:O	2.36	0.53
1:A:43:ARG:NH1	1:A:81:GLY:O	2.40	0.52
2:B:193:ASP:OD2	2:B:220:ASN:ND2	2.43	0.52
1:A:335:ASP:OD2	1:A:338:LYS:NZ	2.40	0.51
1:C:232:ASP:OD1	1:C:265:SER:OG	2.25	0.51
1:A:237:LYS:HA	1:A:240:TRP:CE2	2.46	0.50
1:C:329:ARG:NH1	1:C:344:PRO:O	2.45	0.50
2:D:99:ASP:OD1	2:D:131:ARG:NH2	2.46	0.49
1:C:121:CYS:SG	1:C:131:CYS:HB3	2.55	0.47
1:A:254:GLU:OE2	1:A:278[A]:ARG:NH2	2.47	0.47
1:C:152:PHE:O	1:C:155:ARG:NH1	2.47	0.47
1:C:128:CYS:SG	1:C:130:LYS:HB2	2.55	0.46
1:A:106:LEU:HB3	1:A:169:VAL:HB	1.96	0.46
1:A:234:LEU:O	1:A:268:ARG:NE	2.49	0.46
2:B:149:LEU:O	2:B:151:PHE:N	2.47	0.46
2:B:125:MET:SD	2:B:223:ARG:NE	2.90	0.46
1:A:135:MET:HE2	1:A:165:VAL:HG23	1.97	0.45
1:A:44:GLU:OE2	1:A:56:ARG:NE	2.44	0.44
1:A:396:GLU:O	1:A:400:GLU:N	2.44	0.44
1:A:302:PHE:CG	1:A:303:PRO:HD2	2.53	0.43
1:C:237:LYS:HA	1:C:240:TRP:CE2	2.52	0.43
2:D:41:GLU:OE2	2:D:97:ARG:NH2	2.47	0.43
2:D:94:GLU:HB2	2:D:95:PRO:HD3	2.01	0.42
1:A:389:ALA:N	1:A:390:PRO:HD2	2.34	0.42
1:A:112:MET:SD	1:A:135:MET:HG2	2.60	0.42
1:A:29:TRP:HB2	1:A:399:LEU:HD21	2.02	0.42
1:A:219:ILE:O	1:A:223:PHE:N	2.51	0.42
1:C:302:PHE:CG	1:C:303:PRO:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:352:PHE:HE1	1:C:387:SER:HG	1.66	0.41
1:C:389:ALA:N	1:C:390:PRO:HD2	2.36	0.41
2:D:45:LEU:HG	2:D:102:SER:HB3	2.01	0.41
2:D:247:GLN:N	2:D:248:PRO:HD2	2.36	0.41
1:C:344:PRO:HA	1:C:347:VAL:HG23	2.02	0.41
1:C:9:LEU:N	1:C:10:PRO:HD2	2.35	0.41
1:A:9:LEU:N	1:A:10:PRO:HD2	2.36	0.40
1:A:121:CYS:SG	1:A:131:CYS:HB3	2.61	0.40
1:A:71:GLN:O	1:A:74:ASN:ND2	2.54	0.40
1:A:23:TYR:CG	1:A:67:GLU:HG2	2.56	0.40
1:C:157:TRP:CD1	1:C:336:LEU:HD21	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	377/423 (89%)	362 (96%)	15 (4%)	0	100	100
1	C	366/423 (86%)	351 (96%)	15 (4%)	0	100	100
2	B	171/269 (64%)	161 (94%)	9 (5%)	1 (1%)	30	72
2	D	203/269 (76%)	192 (95%)	10 (5%)	1 (0%)	34	75
All	All	1117/1384 (81%)	1066 (95%)	49 (4%)	2 (0%)	52	87

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	155	SER
2	D	62	SER

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	356/393 (91%)	354 (99%)	2 (1%)	90	96
1	C	345/393 (88%)	342 (99%)	3 (1%)	84	94
2	B	166/240 (69%)	165 (99%)	1 (1%)	90	96
2	D	196/240 (82%)	196 (100%)	0	100	100
All	All	1063/1266 (84%)	1057 (99%)	6 (1%)	90	96

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	HIS
1	A	240	TRP
2	B	148	GLN
1	C	62	ASN
1	C	240	TRP
1	C	252	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	166	HIS
2	B	220	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	381/423 (90%)	0.25	9 (2%) 62 57	103, 146, 194, 236	0
1	C	372/423 (87%)	0.60	54 (14%) 3 3	148, 228, 287, 302	0
2	B	181/269 (67%)	0.90	33 (18%) 2 2	134, 256, 307, 323	0
2	D	213/269 (79%)	0.38	21 (9%) 9 10	142, 207, 258, 273	0
All	All	1147/1384 (82%)	0.49	117 (10%) 9 9	103, 195, 288, 323	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	110	TYR	14.3
2	B	253	LEU	9.7
1	C	81	GLY	7.8
2	B	52	LEU	7.6
1	C	32	TYR	7.2
1	C	33	GLY	6.1
1	C	166	HIS	6.1
1	C	96	LEU	5.9
2	B	48	ASP	5.6
2	B	135	LEU	5.6
1	C	76	TYR	5.5
2	B	74	LEU	5.5
1	C	29	TRP	5.3
2	D	26	LEU	5.3
2	B	148	GLN	5.2
1	C	321	PHE	5.0
1	C	330	ILE	4.9
2	B	53	LEU	4.9
2	B	252	HIS	4.9
2	B	37	ILE	4.9
2	B	56	VAL	4.8

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Mol	Chain	Res	Type	RSRZ
1	C	156	LEU	4.8
2	D	184	TYR	4.8
1	C	395	PHE	4.7
2	B	237	LEU	4.6
1	C	157	TRP	4.6
1	C	26	TYR	4.6
2	B	109	ALA	4.4
1	C	30	LEU	4.3
2	B	111	CYS	4.3
2	B	132	PHE	4.1
1	C	301	CYS	4.1
1	C	165	VAL	4.1
2	B	151	PHE	4.0
1	C	170	CYS	3.9
2	D	253	LEU	3.9
2	D	108	LEU	3.8
1	C	350	ILE	3.7
1	C	334	ILE	3.5
2	D	42	PHE	3.5
2	B	112	GLN	3.4
1	C	398	PHE	3.4
1	C	354	CYS	3.4
2	B	106	LEU	3.3
1	C	269	TRP	3.2
2	D	105	ILE	3.2
1	C	159	TYR	3.2
1	C	325	PRO	3.1
2	D	53	LEU	3.1
2	B	120	PHE	3.1
2	D	27	GLN	3.1
2	D	47	ILE	3.0
2	D	250	LEU	3.0
2	B	49	ARG	3.0
1	C	109	ASP	3.0
1	C	388	LEU	3.0
1	C	168	TRP	3.0
2	D	45	LEU	3.0
2	B	51	LYS	2.9
1	C	107	VAL	2.9
1	C	58	GLN	2.9
1	C	80	ILE	2.9
2	D	90	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	348	PRO	2.8
1	C	228	LEU	2.7
1	C	27	TYR	2.7
1	C	306	ASP	2.7
1	C	394	VAL	2.7
2	B	45	LEU	2.7
2	D	246	LEU	2.7
1	C	47	PHE	2.7
1	C	35	VAL	2.6
1	C	300	TYR	2.6
2	B	72	SER	2.6
1	A	385	LYS	2.6
2	D	137	LYS	2.6
2	D	209	VAL	2.6
2	B	47	ILE	2.6
1	A	191	LEU	2.5
2	B	134	ILE	2.5
1	C	110	ILE	2.5
1	C	323	VAL	2.5
2	D	101	ILE	2.5
1	A	292	LEU	2.5
1	A	321	PHE	2.5
1	C	137	MET	2.4
1	C	20	LEU	2.4
1	C	340	ASP	2.4
2	B	126	ASP	2.4
1	C	45	PHE	2.4
1	C	139	ILE	2.3
1	A	380	THR	2.3
2	B	76	SER	2.3
1	C	52	ASP	2.3
1	A	388	LEU	2.3
1	C	9	LEU	2.3
1	C	25	GLN	2.3
2	B	180	PHE	2.3
2	D	81	LEU	2.2
1	A	323	VAL	2.2
1	C	294	TRP	2.2
1	C	392	VAL	2.2
2	D	46	ALA	2.2
2	B	138	ASP	2.2
1	C	233	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	336	LEU	2.2
2	D	39	LEU	2.2
2	B	236	SER	2.2
1	C	108	PHE	2.1
1	A	354	CYS	2.1
2	B	150	GLN	2.1
1	A	357	LEU	2.1
2	B	128	LEU	2.1
2	D	130	PHE	2.1
2	D	222	PHE	2.1
1	C	51	ASP	2.0
2	B	75	GLU	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	ZN	A	430	1/1	0.99	0.30	0.69	137,137,137,137	0
3	ZN	C	430	1/1	0.99	0.22	0.47	203,203,203,203	0

6.5 Other polymers [i](#)

There are no such residues in this entry.