



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 04:59 am BST

PDB ID : 1H6E
Title : MU2 ADAPTIN SUBUNIT (AP50) OF AP2 ADAPTOR (SECOND DOMAIN), COMPLEXED WITH CTLA-4 INTERNALIZATION PEPTIDE TTGVYVKMPPT
Authors : Rowsell, S.; Paupit, R.A.
Deposited on : 2001-06-12
Resolution : 3.60 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	:	2.11
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

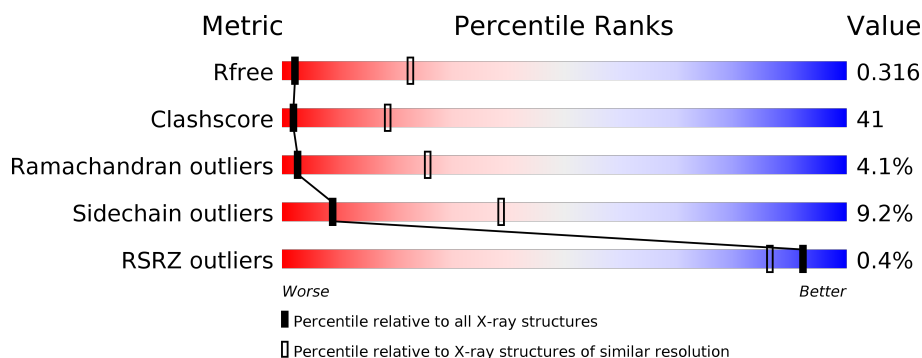
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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 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	288	
2	P	11	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1816 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 CLATHRIN COAT ASSEMBLY PROTEIN AP50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1741	1126	295	308	12			

- Molecule 2 is a protein called CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	10	Total	C	N	O	S	0	0	0
			75	50	11	13	1			

- Molecule 1: CLATHRIN COAT ASSEMBLY PROTEIN AP50

• Molecule 2: CYTOTOXIC T-LYMPHOCYTE PROTEIN 4

T197	T198	G199	V200	Y201	V202	K203	M204	P205	P206	THR
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4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	126.78 Å 126.78 Å 74.16 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	7.99 – 3.60 48.19 – 3.60	Depositor EDS
% Data completeness (in resolution range)	74.4 (7.99-3.60) 74.5 (48.19-3.60)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.50 (at 3.57 Å)	Xtriage
Refinement program	CNX 2000	Depositor
R, R_{free}	0.278 , 0.317 0.279 , 0.316	Depositor DCC
R_{free} test set	726 reflections (10.87%)	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.149 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.74	EDS
Total number of atoms	1816	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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	0.40	0/1775	0.67	0/2388
2	P	0.49	0/77	0.67	0/105
All	All	0.40	0/1852	0.67	0/2493

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

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	1741	0	1824	143	0
2	P	75	0	79	13	0
All	All	1816	0	1903	152	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 41.

All (152) 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:P:203:LYS:HD2	2:P:203:LYS:H	1.17	1.04
1:A:210:PRO:HG3	1:A:408:GLU:HB2	1.41	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:SER:HB3	1:A:192:LEU:HD11	1.41	0.98
1:A:184:LEU:HD12	1:A:192:LEU:HB2	1.46	0.98
1:A:217:ASN:HD21	1:A:400:LYS:HB2	1.31	0.93
1:A:173:LEU:HD11	1:A:420:LYS:HG3	1.51	0.91
1:A:192:LEU:H	1:A:192:LEU:HD12	1.35	0.90
1:A:195:HIS:HA	1:A:283:ILE:CD1	2.09	0.83
1:A:202:MET:CE	1:A:404:LEU:HD11	2.09	0.83
1:A:307:ILE:HD11	1:A:358:MET:HE1	1.60	0.81
2:P:197:THR:HB	2:P:200:VAL:HG11	1.61	0.81
2:P:203:LYS:CD	2:P:203:LYS:H	1.93	0.80
2:P:197:THR:HB	2:P:200:VAL:CG1	2.12	0.79
1:A:217:ASN:ND2	1:A:400:LYS:HB2	1.99	0.77
1:A:179:GLU:OE1	1:A:395:ALA:HB1	1.86	0.75
1:A:202:MET:HE2	1:A:404:LEU:HD11	1.67	0.75
1:A:196:VAL:HG22	1:A:279:THR:HG22	1.70	0.74
1:A:294:ARG:HB3	1:A:302:GLU:HB2	1.69	0.73
1:A:284:ILE:O	1:A:286:PRO:HD3	1.89	0.73
2:P:203:LYS:N	2:P:203:LYS:HD2	2.00	0.72
1:A:415:ASP:C	1:A:417:ASP:H	1.91	0.72
1:A:399:LEU:O	1:A:400:LYS:HG3	1.91	0.71
1:A:185:MET:HB3	1:A:433:THR:HG23	1.71	0.71
2:P:204:MET:C	2:P:206:PRO:HD3	2.11	0.71
1:A:186:SER:CB	1:A:192:LEU:HD11	2.19	0.70
1:A:177:VAL:HB	1:A:424:TYR:HD2	1.55	0.70
1:A:192:LEU:CD1	1:A:192:LEU:H	2.05	0.70
1:A:390:PHE:CE1	1:A:428:SER:HB3	2.27	0.69
1:A:335:VAL:HG12	1:A:368:ALA:CB	2.24	0.67
1:A:166:ILE:HG22	1:A:208:GLY:H	1.59	0.67
1:A:312:LYS:HE2	1:A:314:SER:HB2	1.77	0.67
1:A:179:GLU:OE2	1:A:396:PRO:HD2	1.94	0.67
1:A:199:ARG:HB3	1:A:276:ARG:HD3	1.77	0.66
1:A:328:LEU:N	1:A:328:LEU:HD12	2.11	0.66
1:A:175:LEU:HD12	1:A:401:VAL:HG11	1.78	0.66
1:A:199:ARG:HA	1:A:276:ARG:HA	1.79	0.65
1:A:328:LEU:HD12	1:A:328:LEU:H	1.62	0.65
1:A:183:LEU:HD12	1:A:184:LEU:H	1.63	0.64
1:A:329:ASN:HD22	1:A:372:LEU:HD22	1.63	0.63
1:A:320:ILE:HB	1:A:355:ILE:HB	1.80	0.63
1:A:411:LEU:HD12	1:A:411:LEU:N	2.14	0.62
1:A:187:PRO:HD3	1:A:434:ARG:HB2	1.80	0.62
1:A:366:ILE:O	1:A:366:ILE:HG23	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:GLN:OE1	1:A:188:GLN:N	2.34	0.61
1:A:331:SER:OG	1:A:373:LEU:HD23	2.01	0.61
1:A:192:LEU:N	1:A:192:LEU:HD12	2.11	0.61
1:A:177:VAL:HG21	1:A:424:TYR:HE2	1.66	0.60
1:A:373:LEU:HD13	1:A:374:PRO:N	2.15	0.60
1:A:177:VAL:HB	1:A:424:TYR:CD2	2.37	0.60
1:A:202:MET:HE3	1:A:404:LEU:HD11	1.81	0.59
1:A:175:LEU:HB2	1:A:422:VAL:HG23	1.84	0.59
1:A:214:PHE:O	1:A:262:SER:HA	2.03	0.58
1:A:414:SER:HB3	1:A:417:ASP:HB2	1.86	0.57
1:A:326:THR:HB	1:A:327:PRO:HD2	1.87	0.56
1:A:265:PHE:HE2	1:A:272:PHE:HZ	1.53	0.56
1:A:423:ARG:HG2	2:P:201:TYR:CE1	2.40	0.56
1:A:412:ASN:N	1:A:412:ASN:HD22	2.04	0.56
1:A:294:ARG:HH21	1:A:296:VAL:HG22	1.71	0.56
1:A:185:MET:HG3	1:A:186:SER:N	2.22	0.55
1:A:215:GLY:O	1:A:216:MET:HB3	2.07	0.55
1:A:296:VAL:HG12	1:A:297:GLY:N	2.21	0.55
1:A:305:VAL:HG21	1:A:386:ILE:HD13	1.88	0.55
2:P:197:THR:HB	2:P:200:VAL:HG12	1.89	0.55
1:A:318:GLN:O	1:A:319:LYS:HB2	2.08	0.54
1:A:390:PHE:N	1:A:428:SER:OG	2.40	0.54
1:A:415:ASP:C	1:A:417:ASP:N	2.60	0.54
1:A:175:LEU:CB	1:A:422:VAL:HG23	2.37	0.54
1:A:277:TYR:HD1	1:A:277:TYR:H	1.56	0.54
1:A:399:LEU:HD12	1:A:400:LYS:H	1.73	0.53
1:A:335:VAL:HG12	1:A:368:ALA:HB2	1.90	0.53
1:A:373:LEU:HD13	1:A:374:PRO:HD2	1.91	0.52
1:A:185:MET:HB3	1:A:433:THR:CG2	2.38	0.52
1:A:373:LEU:HD13	1:A:374:PRO:CD	2.39	0.52
1:A:196:VAL:HG21	1:A:397:SER:HB3	1.91	0.52
1:A:185:MET:O	1:A:434:ARG:HG2	2.10	0.51
2:P:204:MET:O	2:P:206:PRO:HD3	2.10	0.51
1:A:307:ILE:CD1	1:A:358:MET:HE1	2.38	0.51
1:A:418:VAL:HG12	1:A:419:ILE:N	2.26	0.51
1:A:315:LEU:HB3	1:A:393:PRO:HG3	1.91	0.51
1:A:411:LEU:CD1	1:A:411:LEU:N	2.74	0.51
1:A:296:VAL:HG12	1:A:297:GLY:H	1.74	0.51
1:A:265:PHE:CE2	1:A:272:PHE:HZ	2.28	0.51
1:A:183:LEU:CD1	1:A:184:LEU:H	2.24	0.50
1:A:198:GLY:O	1:A:276:ARG:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:TRP:CG	1:A:366:ILE:HD12	2.47	0.50
1:A:179:GLU:OE2	1:A:396:PRO:CD	2.59	0.49
1:A:268:PRO:O	1:A:269:ASP:C	2.51	0.49
1:A:216:MET:HB2	1:A:399:LEU:HD11	1.94	0.49
1:A:390:PHE:HZ	1:A:431:TYR:CE2	2.30	0.49
1:A:184:LEU:HD13	1:A:184:LEU:C	2.33	0.49
1:A:185:MET:HG3	1:A:186:SER:H	1.75	0.49
1:A:392:VAL:HG22	1:A:426:GLY:O	2.11	0.49
1:A:177:VAL:HG21	1:A:424:TYR:CE2	2.47	0.49
1:A:216:MET:HA	1:A:400:LYS:O	2.13	0.49
1:A:203:LYS:HG2	1:A:271:GLU:HG3	1.95	0.49
1:A:195:HIS:HA	1:A:283:ILE:HD11	1.91	0.48
1:A:305:VAL:HG12	1:A:306:VAL:N	2.27	0.48
1:A:301:LEU:HD13	1:A:370:ILE:HD12	1.96	0.48
1:A:173:LEU:HD23	1:A:206:LEU:HD11	1.95	0.48
1:A:180:SER:HA	1:A:427:ARG:O	2.13	0.48
1:A:175:LEU:CD1	1:A:401:VAL:HG11	2.44	0.48
1:A:183:LEU:HG	1:A:184:LEU:N	2.29	0.48
1:A:195:HIS:HA	1:A:283:ILE:HD13	1.92	0.48
1:A:318:GLN:NE2	2:P:198:THR:HB	2.29	0.48
1:A:176:ASP:OD2	1:A:203:LYS:NZ	2.47	0.48
1:A:302:GLU:OE1	1:A:369:GLU:HG3	2.14	0.47
1:A:421:TRP:CZ3	2:P:203:LYS:HG3	2.49	0.47
1:A:181:VAL:O	1:A:181:VAL:HG13	2.15	0.47
1:A:287:PHE:HA	1:A:308:LYS:O	2.14	0.47
1:A:389:ASN:O	1:A:390:PHE:HB3	2.14	0.47
1:A:172:GLU:HG2	1:A:419:ILE:HB	1.96	0.47
1:A:291:PRO:HB3	1:A:305:VAL:HG22	1.97	0.47
1:A:342:ALA:HB2	1:A:353:TRP:HA	1.97	0.46
1:A:415:ASP:O	1:A:417:ASP:N	2.47	0.46
1:A:173:LEU:O	1:A:173:LEU:HD12	2.16	0.46
1:A:190:GLN:O	1:A:192:LEU:HD12	2.15	0.46
1:A:294:ARG:CZ	1:A:302:GLU:HG3	2.46	0.46
1:A:290:ILE:O	1:A:290:ILE:HG13	2.16	0.46
1:A:394:PHE:C	1:A:394:PHE:CD1	2.90	0.45
1:A:390:PHE:CZ	1:A:428:SER:HB3	2.51	0.45
1:A:345:LYS:HD2	1:A:348:GLU:OE1	2.16	0.45
1:A:209:MET:N	1:A:210:PRO:HD3	2.32	0.45
1:A:301:LEU:HB3	1:A:370:ILE:HB	1.98	0.45
1:A:374:PRO:O	1:A:375:THR:HB	2.16	0.45
1:A:210:PRO:HB3	1:A:407:PHE:C	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:LEU:CG	1:A:184:LEU:N	2.80	0.44
1:A:174:PHE:CD1	1:A:174:PHE:N	2.83	0.44
1:A:288:ARG:HB3	1:A:308:LYS:HB2	1.98	0.44
2:P:200:VAL:HG13	2:P:200:VAL:O	2.17	0.44
1:A:187:PRO:HB2	1:A:188:GLN:OE1	2.18	0.44
1:A:351:ILE:O	1:A:351:ILE:HG22	2.18	0.44
1:A:309:SER:O	1:A:361:MET:HA	2.18	0.44
1:A:343:LYS:N	1:A:343:LYS:HD2	2.33	0.43
1:A:214:PHE:CE1	1:A:401:VAL:HG13	2.54	0.43
1:A:323:ARG:O	1:A:325:PRO:HD3	2.18	0.43
1:A:349:ASN:O	1:A:349:ASN:OD1	2.35	0.43
1:A:266:ILE:HA	1:A:267:PRO:HD2	1.72	0.43
1:A:201:VAL:HA	1:A:273:GLU:HA	1.98	0.43
1:A:412:ASN:N	1:A:412:ASN:ND2	2.63	0.43
1:A:329:ASN:O	1:A:373:LEU:HB2	2.20	0.42
1:A:196:VAL:HG22	1:A:279:THR:CG2	2.45	0.42
1:A:408:GLU:HG3	1:A:408:GLU:O	2.20	0.42
1:A:184:LEU:HD12	1:A:192:LEU:CB	2.34	0.41
1:A:173:LEU:C	1:A:174:PHE:CD1	2.93	0.41
1:A:296:VAL:CG1	1:A:297:GLY:H	2.32	0.41
1:A:265:PHE:CE2	1:A:272:PHE:CZ	3.08	0.41
1:A:393:PRO:O	1:A:424:TYR:HB2	2.20	0.41
1:A:216:MET:HB2	1:A:399:LEU:CD1	2.50	0.41
1:A:175:LEU:HA	1:A:175:LEU:HD23	1.84	0.40
1:A:185:MET:C	1:A:192:LEU:HD13	2.42	0.40
1:A:215:GLY:O	1:A:216:MET:CB	2.70	0.40
1:A:401:VAL:HG12	2:P:204:MET:HE1	2.03	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	213/288 (74%)	156 (73%)	49 (23%)	8 (4%)	3	27
2	P	8/11 (73%)	6 (75%)	1 (12%)	1 (12%)	0	5
All	All	221/299 (74%)	162 (73%)	50 (23%)	9 (4%)	3	26

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	269	ASP
1	A	274	LEU
1	A	296	VAL
1	A	216	MET
1	A	189	GLY
1	A	372	LEU
2	P	205	PRO
1	A	192	LEU
1	A	416	HIS

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	197/261 (76%)	179 (91%)	18 (9%)	9	39
2	P	9/10 (90%)	8 (89%)	1 (11%)	6	31
All	All	206/271 (76%)	187 (91%)	19 (9%)	9	39

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	173	LEU
1	A	174	PHE
1	A	196	VAL
1	A	199	ARG
1	A	202	MET
1	A	280	THR
1	A	291	PRO

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Mol	Chain	Res	Type
1	A	301	LEU
1	A	314	SER
1	A	329	ASN
1	A	343	LYS
1	A	385	PRO
1	A	412	ASN
1	A	417	ASP
1	A	420	LYS
1	A	427	ARG
1	A	433	THR
1	A	435	CYS
2	P	203	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	217	ASN
1	A	318	GLN
1	A	329	ASN
1	A	349	ASN
1	A	412	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](#)

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 [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	219/288 (76%)	0.10	1 (0%) 91 83	1, 37, 83, 111	0
2	P	10/11 (90%)	-0.05	0 100 100	4, 46, 97, 117	0
All	All	229/299 (76%)	0.10	1 (0%) 92 86	1, 37, 84, 117	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	263	ILE	2.5

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.