



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:28 AM GMT

PDB ID : 2AL6  
Title : FERM domain of Focal Adhesion Kinase  
Authors : Ceccarelli, D.F.; Song, H.K.; Poy, F.; Schaller, M.D.; Eck, M.J.  
Deposited on : 2005-08-04  
Resolution : 2.35 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  
<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

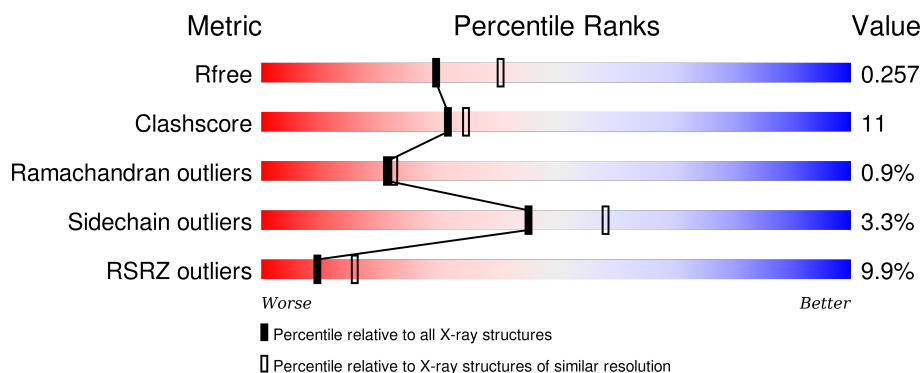
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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. 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	375	
1	B	375	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5718 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 Focal adhesion kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	0	0
			2774	1768	474	520	12			
1	B	351	Total	C	N	O	S	0	0	0
			2840	1811	487	530	12			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	61	Total	O	0	0
			61	61		
2	B	43	Total	O	0	0
			43	43		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.54Å 123.99Å 133.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.35 29.46 – 2.35	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.35) 100.0 (29.46-2.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 2.36Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.215 , 0.252 0.218 , 0.257	Depositor DCC
$R_{free}$ test set	1795 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.3	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 35886 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5718	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.41% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0/2831	0.57	0/3821
1	B	0.39	0/2899	0.56	0/3913
All	All	0.39	0/5730	0.56	0/7734

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	2774	0	2749	50	0
1	B	2840	0	2826	70	0
2	A	61	0	0	2	0
2	B	43	0	0	1	0
All	All	5718	0	5575	120	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 11.

All (120) 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:295:ASP:H	1:A:298:GLN:HE21	1.12	0.96

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ILE:H	1:A:150:GLN:HE22	1.03	0.92
1:B:41:HIS:HD2	1:B:43:PHE:H	1.31	0.78
1:B:317:GLN:HE22	1:B:373:ILE:H	1.32	0.77
1:A:305:SER:HB2	1:A:315:MET:HB2	1.66	0.76
1:B:56:ILE:HD11	1:B:71:ILE:HD11	1.68	0.73
1:A:252:ARG:HH21	1:A:255:LYS:HD3	1.55	0.71
1:A:126:ILE:N	1:A:150:GLN:HE22	1.86	0.69
1:A:134:LEU:O	1:A:138:THR:HG23	1.93	0.67
1:B:177:ARG:NH1	1:B:185:GLY:H	1.93	0.67
1:A:248:SER:HB3	1:A:249:PRO:HD3	1.75	0.67
1:B:185:GLY:HA3	1:B:232:ALA:HB1	1.77	0.66
1:B:231:PHE:HB3	1:B:234:LEU:HD12	1.77	0.66
1:A:169:LEU:HD21	1:A:223:LEU:HB3	1.78	0.66
1:B:308:GLU:CD	1:B:308:GLU:H	1.97	0.65
1:A:212:LEU:HD23	1:A:220:LEU:HD21	1.79	0.65
1:A:41:HIS:HD2	1:A:43:PHE:H	1.44	0.65
1:A:316:LEU:HD11	1:A:341:ALA:HB2	1.79	0.64
1:B:235:ASN:O	1:B:239:SER:HB2	1.98	0.64
1:B:295:ASP:H	1:B:298:GLN:HE21	1.46	0.63
1:A:72:VAL:HG21	1:A:80:VAL:HG13	1.80	0.63
1:B:129:LEU:O	1:B:276:PRO:HB3	1.98	0.62
1:B:218:LYS:HG2	1:B:222:LYS:HE3	1.81	0.61
1:B:108:ARG:O	1:B:112:GLU:HB2	2.02	0.59
1:B:248:SER:HB3	1:B:249:PRO:HD3	1.83	0.59
1:B:215:VAL:HG11	1:B:220:LEU:HD13	1.85	0.58
1:B:87:LEU:HD11	1:B:120:TRP:HB3	1.86	0.58
1:B:183:MET:HG2	1:B:187:ALA:HB3	1.85	0.57
1:A:160:ALA:HB1	1:A:208:PRO:HB3	1.85	0.57
1:A:70:LYS:HE3	1:A:398:ALA:O	2.05	0.57
1:B:191:LYS:HD2	2:B:448:HOH:O	2.05	0.56
1:B:283:LEU:HD21	1:B:290:PRO:HG3	1.87	0.56
1:A:79:ASN:ND2	1:A:136:GLN:HE21	2.03	0.56
1:A:308:GLU:H	1:A:308:GLU:CD	2.09	0.55
1:A:141:LYS:HB3	1:A:142:PRO:HD3	1.89	0.55
1:A:37:LEU:HD13	1:A:108:ARG:HE	1.72	0.55
1:B:362:PRO:HB3	1:B:370:LEU:HD23	1.88	0.55
1:A:281:SER:HB2	1:A:291:THR:O	2.07	0.55
1:B:295:ASP:H	1:B:298:GLN:NE2	2.05	0.55
1:B:221:ARG:O	1:B:225:GLN:HG3	2.08	0.54
1:B:281:SER:HB3	1:B:292:HIS:HA	1.88	0.54
1:B:128:TYR:CE2	1:B:346:GLY:HA3	2.43	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:ASP:HB2	1:B:298:GLN:HE21	1.71	0.53
1:B:281:SER:HB2	1:B:291:THR:O	2.08	0.53
1:A:50:THR:O	1:A:50:THR:HG22	2.10	0.52
1:B:310:LYS:N	1:B:310:LYS:HD2	2.25	0.52
1:A:55:ILE:N	1:A:55:ILE:HD12	2.25	0.52
1:A:295:ASP:H	1:A:298:GLN:NE2	1.94	0.52
1:B:272:LEU:HD12	1:B:340:MET:HE1	1.92	0.51
1:A:128:TYR:CE2	1:A:346:GLY:HA3	2.46	0.51
1:B:63:ASP:OD2	1:B:65:ARG:HB3	2.11	0.50
1:B:202:GLY:O	1:B:205:ARG:HG2	2.12	0.50
1:A:79:ASN:HD21	1:A:136:GLN:HE21	1.59	0.50
1:A:56:ILE:CD1	1:A:400:ILE:HG12	2.42	0.50
1:A:156:MET:HA	1:A:160:ALA:HB2	1.94	0.49
1:B:362:PRO:CG	1:B:367:GLU:HB3	2.43	0.49
1:B:41:HIS:CD2	1:B:43:PHE:HB2	2.48	0.49
1:B:196:VAL:O	1:B:200:ASP:HB3	2.12	0.49
1:B:42:TYR:HB3	1:B:149:GLN:HB2	1.94	0.48
1:A:401:ILE:O	1:A:402:ASP:HB2	2.13	0.48
1:A:99:HIS:HE1	1:A:345:ASP:OD2	1.96	0.48
1:A:257:CYS:HA	1:A:272:LEU:O	2.14	0.48
1:A:216:LYS:HE2	1:A:219:THR:OG1	2.14	0.47
1:A:192:SER:O	1:A:195:GLU:HB3	2.14	0.47
1:B:104:VAL:O	1:B:108:ARG:HG3	2.16	0.46
1:B:211:LEU:O	1:B:215:VAL:HG12	2.15	0.46
1:B:201:VAL:HG12	1:B:205:ARG:HG3	1.97	0.46
1:A:277:GLU:HB2	2:A:443:HOH:O	2.15	0.46
1:B:362:PRO:HG3	1:B:367:GLU:HB3	1.97	0.45
1:A:49:PRO:HA	1:A:52:TRP:CE2	2.52	0.45
1:A:89:HIS:CE1	1:A:91:GLN:HB2	2.51	0.45
1:B:135:ASN:O	1:B:138:THR:HB	2.16	0.45
1:B:242:LYS:O	1:B:246:ILE:HG12	2.17	0.45
1:B:261:ALA:HB1	1:B:267:ILE:HG22	1.98	0.45
1:A:48:GLU:OE2	1:A:50:THR:HB	2.16	0.45
1:B:64:VAL:HB	1:B:100:LEU:HA	1.98	0.45
1:B:48:GLU:HB3	1:B:51:THR:HG23	1.99	0.45
1:B:183:MET:CG	1:B:187:ALA:HB3	2.46	0.44
1:B:175:GLU:HG3	1:B:206:PHE:HD2	1.82	0.44
1:A:271:GLU:HG2	1:A:283:LEU:HD12	1.99	0.44
1:B:274:ILE:HA	1:B:279:GLY:O	2.17	0.44
1:B:257:CYS:HA	1:B:272:LEU:O	2.16	0.44
1:B:136:GLN:HE21	1:B:136:GLN:HB3	1.57	0.44

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:247:LEU:HG	1:B:251:TYR:HB3	1.99	0.44
1:B:129:LEU:HA	1:B:130:PRO:HD3	1.85	0.43
1:B:226:GLN:HE22	1:B:229:ARG:NH1	2.16	0.43
1:A:49:PRO:HA	1:A:52:TRP:CD2	2.53	0.43
1:B:148:TYR:CD1	1:B:240:ILE:HG23	2.53	0.43
1:B:160:ALA:O	1:B:163:VAL:HG12	2.18	0.43
1:B:69:GLN:HG3	1:B:73:ASP:OD2	2.19	0.43
1:B:218:LYS:HG2	1:B:222:LYS:CE	2.46	0.43
1:A:305:SER:HB2	1:A:315:MET:CB	2.45	0.43
1:A:46:SER:O	1:A:47:SER:HB3	2.18	0.43
1:B:65:ARG:HB2	1:B:100:LEU:HB2	2.00	0.43
1:B:250:VAL:HG22	1:B:250:VAL:O	2.19	0.43
1:A:186:ASN:O	1:A:189:GLU:HG2	2.18	0.43
1:B:305:SER:OG	1:B:317:GLN:NE2	2.43	0.42
1:B:163:VAL:HG22	1:B:164:ASP:N	2.35	0.42
1:A:171:LEU:HD22	1:A:243:PHE:CD1	2.54	0.42
1:B:254:ASP:O	1:B:276:PRO:HD2	2.20	0.42
1:A:236:ARG:HG3	2:A:462:HOH:O	2.19	0.42
1:A:306:ASN:ND2	1:A:334:LEU:HD21	2.34	0.42
1:B:49:PRO:HA	1:B:52:TRP:CE2	2.55	0.42
1:A:163:VAL:HG22	1:A:164:ASP:N	2.35	0.42
1:B:116:PRO:HA	1:B:117:PRO:HD3	1.92	0.42
1:A:212:LEU:CD2	1:A:220:LEU:HD21	2.50	0.41
1:A:42:TYR:HB3	1:A:149:GLN:HB2	2.01	0.41
1:B:235:ASN:OD1	1:B:238:GLU:HG2	2.19	0.41
1:B:68:ILE:O	1:B:72:VAL:HG22	2.20	0.41
1:A:63:ASP:OD1	1:A:65:ARG:HB3	2.20	0.41
1:B:154:ASP:HB3	1:B:251:TYR:OH	2.20	0.41
1:B:204:ARG:HE	1:B:209:LYS:HE2	1.85	0.41
1:A:278:GLU:CD	1:A:278:GLU:H	2.24	0.41
1:B:261:ALA:HB1	1:B:267:ILE:CG2	2.50	0.41
1:A:48:GLU:HA	1:A:49:PRO:HD3	1.94	0.41
1:A:250:VAL:HG22	1:A:250:VAL:O	2.21	0.41
1:B:317:GLN:C	1:B:318:LEU:HD12	2.41	0.41
1:B:177:ARG:HH12	1:B:185:GLY:H	1.67	0.40
1:B:305:SER:HA	1:B:370:LEU:O	2.21	0.40
1:B:94:GLU:OE2	1:B:96:HIS:HE1	2.04	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	339/375 (90%)	322 (95%)	16 (5%)	1 (0%)	46	55
1	B	347/375 (92%)	319 (92%)	23 (7%)	5 (1%)	14	12
All	All	686/750 (92%)	641 (93%)	39 (6%)	6 (1%)	21	22

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	185	GLY
1	A	47	SER
1	B	186	ASN
1	B	47	SER
1	B	46	SER
1	B	187	ALA

### 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	302/332 (91%)	294 (97%)	8 (3%)	54	68
1	B	310/332 (93%)	298 (96%)	12 (4%)	39	51
All	All	612/664 (92%)	592 (97%)	20 (3%)	45	58

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	109	GLU
1	A	128	TYR
1	A	188	LEU
1	A	278	GLU
1	A	306	ASN
1	A	308	GLU
1	A	361	ARG
1	B	70	LYS
1	B	100	LEU
1	B	112	GLU
1	B	136	GLN
1	B	188	LEU
1	B	212	LEU
1	B	278	GLU
1	B	306	ASN
1	B	308	GLU
1	B	356	GLN
1	B	367	GLU
1	B	400	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	58	HIS
1	A	75	HIS
1	A	79	ASN
1	A	91	GLN
1	A	96	HIS
1	A	99	HIS
1	A	150	GLN
1	A	225	GLN
1	A	292	HIS
1	A	298	GLN
1	A	300	GLN
1	A	306	ASN
1	A	356	GLN
1	B	41	HIS
1	B	45	ASN
1	B	58	HIS
1	B	75	HIS
1	B	96	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	106	ASN
1	B	136	GLN
1	B	165	GLN
1	B	226	GLN
1	B	230	GLN
1	B	289	ASN
1	B	292	HIS
1	B	298	GLN
1	B	306	ASN
1	B	317	GLN
1	B	352	ASN
1	B	356	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 carbohydrates 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

### 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	343/375 (91%)	0.53	27 (7%) 15 24	22, 44, 72, 102	0
1	B	351/375 (93%)	0.76	42 (11%) 6 10	27, 49, 100, 112	0
All	All	694/750 (92%)	0.65	69 (9%) 9 16	22, 46, 89, 112	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	33	MET	8.0
1	B	181	GLY	7.8
1	A	310	LYS	7.5
1	B	309	ASP	7.4
1	B	310	LYS	7.4
1	B	185	GLY	6.6
1	B	187	ALA	6.6
1	A	311	ASP	6.5
1	A	286	LYS	6.3
1	A	306	ASN	6.3
1	A	309	ASP	6.3
1	B	311	ASP	6.2
1	A	287	GLY	6.1
1	A	308	GLU	5.8
1	B	308	GLU	5.6
1	B	312	ARG	5.6
1	B	286	LYS	5.5
1	B	287	GLY	5.4
1	A	312	ARG	5.4
1	B	182	GLU	5.3
1	A	307	SER	5.2
1	A	288	ALA	5.1
1	B	307	SER	4.4
1	B	199	LYS	4.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	192	SER	4.1
1	B	184	ARG	4.0
1	B	191	LYS	3.9
1	B	394	THR	3.9
1	B	48	GLU	3.7
1	B	195	GLU	3.7
1	B	395	ASP	3.6
1	A	113	LEU	3.6
1	B	397	TYR	3.5
1	B	396	ASP	3.2
1	B	35	ARG	3.1
1	B	188	LEU	3.1
1	B	186	ASN	3.1
1	B	183	MET	2.9
1	A	45	ASN	2.9
1	B	45	ASN	2.9
1	A	233	ASN	2.9
1	B	190	LYS	2.8
1	A	214	SER	2.8
1	A	109	GLU	2.7
1	B	313	LYS	2.7
1	A	60	ASP	2.6
1	A	114	ALA	2.6
1	B	162	GLN	2.6
1	A	216	LYS	2.5
1	B	200	ASP	2.5
1	A	289	ASN	2.5
1	A	285	ASP	2.5
1	B	91	GLN	2.5
1	B	139	GLU	2.4
1	B	189	GLU	2.4
1	A	305	SER	2.4
1	B	400	ILE	2.4
1	A	284	THR	2.4
1	B	196	VAL	2.3
1	A	46	SER	2.3
1	B	401	ILE	2.3
1	A	31	GLY	2.3
1	A	397	TYR	2.3
1	B	76	LYS	2.3
1	A	100	LEU	2.3
1	B	201	VAL	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	84	GLY	2.2
1	B	85	LEU	2.1
1	B	284	THR	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.