



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:58 PM UTC

PDB ID : 6F09 / pdb_00006f09
Title : Binary complex of 14-3-3 zeta with ubiquitin specific protease 8 (USP8)
pSer718 peptide
Authors : Centorrino, F.; Ballone, A.; Ottmann, C.; Guo, S.; Leysen, S.
Deposited on : 2017-11-17
Resolution : 1.59 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

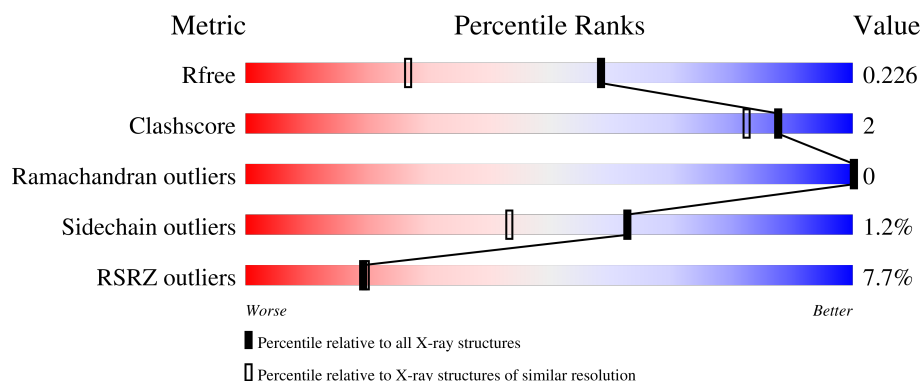
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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}	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	P	230	6% 94% 5%
1	Q	230	10% 95% ..
1	R	230	9% 91% 6% ..
1	S	230	2% 95% ..
2	A	13	15% 38% 15% 46%

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Mol	Chain	Length	Quality of chain
2	B	13	38%38%31%31%
2	C	13	8%38%8%54%
2	D	13	31%69%8%23%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15047 atoms, of which 7050 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 14-3-3 protein zeta/delta.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	P	229	Total	C	H	N	O	S	0	0	0
			3553	1127	1755	304	358	9			
1	Q	226	Total	C	H	N	O	S	0	0	1
			3479	1112	1709	293	356	9			
1	R	226	Total	C	H	N	O	S	0	0	0
			3363	1087	1635	291	341	9			
1	S	228	Total	C	H	N	O	S	0	0	0
			3522	1120	1735	300	358	9			

- Molecule 2 is a protein called Ubiquitin carboxyl-terminal hydrolase 8.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	7	Total	C	H	N	O	P	0	0	0
			101	33	44	7	16	1			
2	B	9	Total	C	H	N	O	P	0	0	0
			138	43	63	12	19	1			
2	C	6	Total	C	H	N	O	P	0	0	0
			93	29	41	9	13	1			
2	D	10	Total	C	H	N	O	P	0	0	0
			153	48	68	14	22	1			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	175	Total	O	0	0
			175	175		
3	A	2	Total	O	0	0
			2	2		
3	Q	147	Total	O	0	0
			147	147		
3	B	10	Total	O	0	0
			10	10		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	R	120	Total 120	O 120	0	0
3	C	4	Total 4	O 4	0	0
3	S	178	Total 178	O 178	0	0
3	D	9	Total 9	O 9	0	0

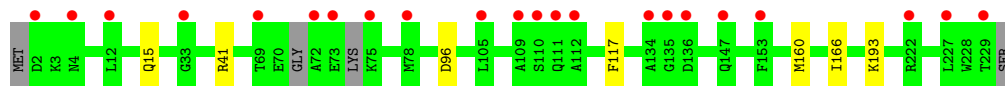
3 Residue-property plots [i](#)

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.

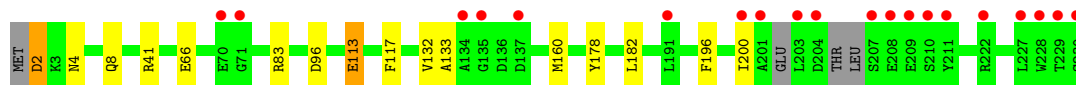
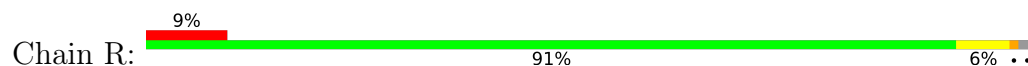
- Molecule 1: 14-3-3 protein zeta/delta



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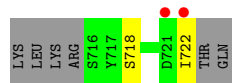
- Molecule 1: 14-3-3 protein zeta/delta



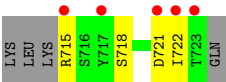
- Molecule 1: 14-3-3 protein zeta/delta



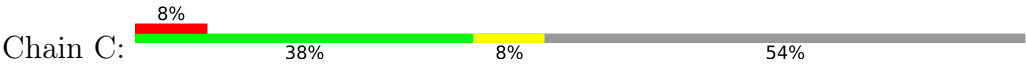
- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 8



- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 8



• Molecule 2: Ubiquitin carboxyl-terminal hydrolase 8



• Molecule 2: Ubiquitin carboxyl-terminal hydrolase 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.38Å 64.89Å 71.52Å 99.71° 114.22° 108.79°	Depositor
Resolution (Å)	61.14 – 1.59 61.14 – 1.59	Depositor EDS
% Data completeness (in resolution range)	91.5 (61.14-1.59) 91.5 (61.14-1.59)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 1.59Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.180 , 0.225 0.183 , 0.226	Depositor DCC
R_{free} test set	5243 reflections (4.47%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15047	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.15% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	P	0.48	0/1821	0.60	0/2452
1	Q	0.42	0/1793	0.56	0/2418
1	R	0.43	0/1749	0.58	0/2360
1	S	0.51	0/1811	0.64	0/2443
2	A	0.44	0/47	0.59	0/62
2	B	0.40	0/65	0.53	0/86
2	C	0.57	0/42	0.63	0/54
2	D	0.55	0/75	0.84	0/98
All	All	0.46	0/7403	0.60	0/9973

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	P	1798	1755	1755	8	0
1	Q	1770	1709	1708	4	0
1	R	1728	1635	1631	9	0
1	S	1787	1735	1734	8	0
2	A	57	44	43	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	75	63	63	0	0
2	C	52	41	41	0	0
2	D	85	68	71	1	0
3	A	2	0	0	0	0
3	B	10	0	0	0	0
3	C	4	0	0	0	0
3	D	9	0	0	0	0
3	P	175	0	0	4	4
3	Q	147	0	0	2	1
3	R	120	0	0	1	4
3	S	178	0	0	2	1
All	All	7997	7050	7046	29	5

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 2.

All (29) 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:Q:193:LYS:NZ	3:Q:301:HOH:O	2.20	0.74
1:S:137:ASP:OD2	3:S:301:HOH:O	2.14	0.66
1:S:64:SER:OG	1:S:68:LYS:NZ	2.30	0.64
1:R:96:ASP:OD2	3:R:301:HOH:O	2.15	0.64
1:R:132:VAL:CA	1:R:133:ALA:N	2.63	0.62
1:P:66:GLU:O	1:P:76:GLN:NE2	2.31	0.60
1:R:2:ASP:N	1:R:2:ASP:OD1	2.34	0.59
1:P:113:GLU:HA	1:P:160:MET:CE	2.32	0.59
1:Q:160:MET:HE1	1:Q:166:ILE:HB	1.89	0.53
1:R:66:GLU:OE1	1:R:83:ARG:NE	2.32	0.52
1:R:196:PHE:CE2	1:R:200:ILE:HD11	2.45	0.51
1:S:156:SER:OG	1:S:157:LYS:NZ	2.45	0.49
1:R:113:GLU:HA	1:R:160:MET:CE	2.42	0.49
1:P:2:ASP:N	3:P:306:HOH:O	2.46	0.48
1:S:49:LYS:NZ	2:D:720:PRO:O	2.45	0.48
1:P:191:LEU:HD12	3:P:326:HOH:O	2.16	0.45
1:S:96:ASP:CB	3:S:322:HOH:O	2.65	0.44
1:P:41:ARG:HG2	1:P:117:PHE:CE1	2.53	0.44
1:S:153:PHE:CZ	1:S:157:LYS:HE2	2.54	0.43
1:P:49:LYS:HD2	3:P:384:HOH:O	2.20	0.42
1:S:153:PHE:O	1:S:157:LYS:HG2	2.19	0.42
1:R:41:ARG:HG2	1:R:117:PHE:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:178:TYR:CD1	1:R:182:LEU:HD12	2.55	0.42
1:S:182:LEU:O	1:S:183:ASN:C	2.62	0.41
1:P:91:ARG:NH1	3:P:307:HOH:O	2.48	0.41
1:P:90:LEU:C	1:P:90:LEU:HD23	2.46	0.41
1:R:4:ASN:O	1:R:8:GLN:HG2	2.21	0.40
1:Q:15:GLN:NE2	3:Q:304:HOH:O	2.34	0.40
1:Q:41:ARG:HG2	1:Q:117:PHE:CE1	2.57	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:306:HOH:O	3:R:391:HOH:O[1_554]	1.98	0.22
3:P:440:HOH:O	3:R:416:HOH:O[1_554]	1.98	0.22
3:Q:405:HOH:O	3:S:450:HOH:O[1_445]	2.06	0.14
3:P:407:HOH:O	3:R:396:HOH:O[1_554]	2.07	0.13
3:P:466:HOH:O	3:R:372:HOH:O[1_554]	2.07	0.13

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	P	225/230 (98%)	219 (97%)	6 (3%)	0	100	100
1	Q	220/230 (96%)	217 (99%)	3 (1%)	0	100	100
1	R	217/230 (94%)	215 (99%)	2 (1%)	0	100	100
1	S	224/230 (97%)	220 (98%)	4 (2%)	0	100	100
2	A	4/13 (31%)	3 (75%)	1 (25%)	0	100	100
2	B	6/13 (46%)	6 (100%)	0	0	100	100
2	C	3/13 (23%)	3 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	7/13 (54%)	7 (100%)	0	0	100	100
All	All	906/972 (93%)	890 (98%)	16 (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	P	190/200 (95%)	189 (100%)	1 (0%)	81	70
1	Q	185/200 (92%)	184 (100%)	1 (0%)	81	70
1	R	172/200 (86%)	170 (99%)	2 (1%)	63	43
1	S	188/200 (94%)	187 (100%)	1 (0%)	81	70
2	A	6/12 (50%)	5 (83%)	1 (17%)	2	0
2	B	8/12 (67%)	5 (62%)	3 (38%)	0	0
2	C	5/12 (42%)	5 (100%)	0	100	100
2	D	9/12 (75%)	9 (100%)	0	100	100
All	All	763/848 (90%)	754 (99%)	9 (1%)	63	43

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	96	ASP
2	A	722	ILE
1	Q	96	ASP
2	B	715	ARG
2	B	721	ASP
2	B	722	ILE
1	R	2	ASP
1	R	113	GLU
1	S	49	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	P	38	ASN
1	P	108	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SEP	A	718	2	8,9,10	1.39	1 (12%)	7,12,14	1.37	0
2	SEP	B	718	2	8,9,10	1.27	1 (12%)	7,12,14	1.89	3 (42%)
2	SEP	C	718	2	8,9,10	1.54	1 (12%)	7,12,14	1.47	1 (14%)
2	SEP	D	718	2	8,9,10	0.93	0	7,12,14	1.14	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	A	718	2	-	0/6/8/10	-
2	SEP	B	718	2	-	0/6/8/10	-
2	SEP	C	718	2	-	0/6/8/10	-
2	SEP	D	718	2	-	0/6/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	718	SEP	P-O1P	3.52	1.61	1.50
2	A	718	SEP	P-O1P	3.01	1.59	1.50
2	B	718	SEP	P-O1P	2.68	1.58	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	718	SEP	OG-CB-CA	3.14	111.20	108.14
2	C	718	SEP	OG-P-O1P	-3.01	98.30	106.44
2	B	718	SEP	O3P-P-OG	-2.76	99.48	106.67
2	B	718	SEP	O2P-P-OG	2.20	112.40	106.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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, 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	P	229/230 (99%)	0.39	14 (6%) 27 27	12, 27, 58, 84	0
1	Q	226/230 (98%)	0.63	22 (9%) 13 13	17, 31, 66, 95	0
1	R	226/230 (98%)	0.59	20 (8%) 15 15	15, 32, 66, 97	0
1	S	228/230 (99%)	0.14	4 (1%) 67 71	13, 25, 50, 78	0
2	A	6/13 (46%)	1.80	2 (33%) 1 1	25, 37, 64, 80	0
2	B	8/13 (61%)	2.15	5 (62%) 0 0	35, 42, 81, 88	0
2	C	5/13 (38%)	1.32	1 (20%) 3 2	27, 33, 46, 61	0
2	D	9/13 (69%)	1.47	4 (44%) 0 0	25, 42, 53, 58	0
All	All	937/972 (96%)	0.47	72 (7%) 19 20	12, 29, 64, 97	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	75	LYS	11.0
1	R	204	ASP	7.0
1	R	201	ALA	6.8
1	R	203	LEU	6.0
1	S	135	GLY	5.0
1	P	34	ALA	4.6
1	Q	72	ALA	4.6
1	R	71	GLY	4.5
1	R	134	ALA	4.5
2	A	722	ILE	4.3
2	B	722	ILE	4.3
1	Q	112	ALA	3.7
1	S	134	ALA	3.6
1	Q	2	ASP	3.5
1	Q	73	GLU	3.5
2	B	723	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	Q	111	GLN	3.4
2	A	721	ASP	3.4
1	R	229	THR	3.3
1	R	135	GLY	3.3
1	Q	109	ALA	3.3
1	R	200	ILE	3.2
1	Q	78	MET	3.2
1	P	29	VAL	3.0
1	Q	12	LEU	3.0
1	Q	227	LEU	3.0
2	D	715	ARG	3.0
1	R	207	SER	2.9
1	R	230	SER	2.9
1	P	4	ASN	2.8
1	R	137	ASP	2.8
1	R	228	TRP	2.8
1	Q	134	ALA	2.7
2	B	721	ASP	2.7
1	Q	135	GLY	2.7
1	P	135	GLY	2.6
1	R	191	LEU	2.6
1	P	201	ALA	2.6
1	Q	153	PHE	2.6
1	P	32	GLN	2.6
1	R	210	SER	2.5
1	Q	229	THR	2.5
1	P	6	LEU	2.5
1	P	229	THR	2.5
1	Q	4	ASN	2.5
1	P	76	GLN	2.5
1	R	227	LEU	2.4
2	D	721	ASP	2.4
1	P	158	LYS	2.3
2	D	722	ILE	2.3
1	Q	33	GLY	2.3
1	Q	147	GLN	2.3
1	R	209	GLU	2.2
1	P	33	GLY	2.2
1	S	230	SER	2.2
1	Q	69	THR	2.2
2	B	715	ARG	2.2
1	P	134	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	Q	222	ARG	2.1
1	R	222	ARG	2.1
2	C	715	ARG	2.1
1	Q	110	SER	2.1
1	S	206	LEU	2.1
2	B	717	TYR	2.1
1	Q	136	ASP	2.1
1	R	208	GLU	2.1
1	P	2	ASP	2.1
1	P	227	LEU	2.0
1	R	70	GLU	2.0
2	D	719	SER	2.0
1	Q	105	LEU	2.0
1	R	211	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	B-factors(Å ²)	Q<0.9
2	SEP	D	718	10/11	0.97	0.09	20,20,20,20	0
2	SEP	C	718	10/11	0.98	0.06	17,17,23,27	0
2	SEP	B	718	10/11	0.98	0.07	18,22,28,29	0
2	SEP	A	718	10/11	0.99	0.04	13,16,20,24	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.