



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:21 AM UTC

PDB ID : 6EJG / pdb_00006ejg
Title : CRYSTAL STRUCTURE OF HUMAN CD81 LARGE EXTRACELLULAR LOOP IN COMPLEX WITH SINGLE CHAIN FV FRAGMENT 4
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Deposited on : 2017-09-21
Resolution : 2.82 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
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

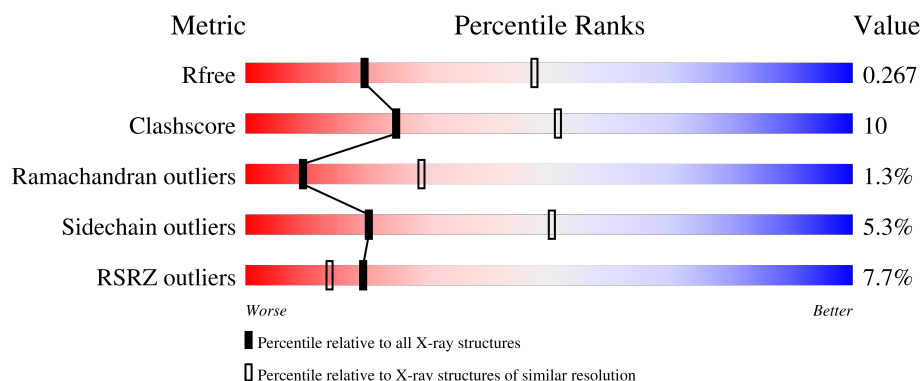
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	99	15% 67% 20% 10%
1	B	99	14% 69% 19% 10%
2	C	251	4% 76% 15% 8%
2	D	251	4% 74% 16% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4971 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 CD81 antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	89	Total	C	N	O	S	0	0	0
			683	424	115	140	4			
1	B	89	Total	C	N	O	S	0	0	0
			683	424	115	140	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	GLY	-	expression tag	UNP P60033
A	111	SER	-	expression tag	UNP P60033
A	203	HIS	-	expression tag	UNP P60033
A	204	HIS	-	expression tag	UNP P60033
A	205	HIS	-	expression tag	UNP P60033
A	206	HIS	-	expression tag	UNP P60033
A	207	HIS	-	expression tag	UNP P60033
A	208	HIS	-	expression tag	UNP P60033
B	110	GLY	-	expression tag	UNP P60033
B	111	SER	-	expression tag	UNP P60033
B	203	HIS	-	expression tag	UNP P60033
B	204	HIS	-	expression tag	UNP P60033
B	205	HIS	-	expression tag	UNP P60033
B	206	HIS	-	expression tag	UNP P60033
B	207	HIS	-	expression tag	UNP P60033
B	208	HIS	-	expression tag	UNP P60033

- Molecule 2 is a protein called SINGLE CHAIN FV FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	231	Total	C	N	O	S	0	1	0
			1774	1120	298	348	8			
2	D	231	Total	C	N	O	S	0	1	0
			1774	1120	298	348	8			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total 5	O 5	0	0
3	B	2	Total 2	O 2	0	0
3	C	23	Total 23	O 23	0	0
3	D	27	Total 27	O 27	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	78.64Å 170.91Å 185.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.83 – 2.82 46.83 – 2.82	Depositor EDS
% Data completeness (in resolution range)	88.2 (46.83-2.82) 88.1 (46.83-2.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.227 , 0.263 0.232 , 0.267	Depositor DCC
R_{free} test set	1355 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å ²)	47.8	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 17.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4971	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% 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](#)

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	0.41	0/691	0.69	0/933
1	B	0.43	0/691	0.70	0/933
2	C	0.41	0/1815	0.71	2/2453 (0.1%)
2	D	0.42	0/1815	0.73	3/2453 (0.1%)
All	All	0.42	0/5012	0.71	5/6772 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	195	GLY	N-CA-C	-6.13	104.88	111.93
2	C	73	SER	CA-C-N	5.66	131.88	121.70
2	C	73	SER	C-N-CA	5.66	131.88	121.70
2	D	73	SER	CA-C-N	5.15	130.97	121.70
2	D	73	SER	C-N-CA	5.15	130.97	121.70

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	683	0	665	25	0
1	B	683	0	665	16	0
2	C	1774	0	1731	29	0
2	D	1774	0	1731	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	5	0	0	1	0
3	B	2	0	0	1	0
3	C	23	0	0	0	0
3	D	27	0	0	2	0
All	All	4971	0	4792	93	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 10.

All (93) 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:C:217:ILE:HD13	2:C:250:MET:HE1	1.44	0.99
1:B:170:LEU:HD22	1:B:185:LEU:HD11	1.44	0.96
2:C:187:VAL:HG23	2:C:255:LEU:HD11	1.56	0.86
1:A:135:VAL:HG21	1:A:165:LEU:HD22	1.56	0.85
2:D:217:ILE:HD13	2:D:250:MET:CE	2.11	0.81
2:D:217:ILE:HD13	2:D:250:MET:HE1	1.63	0.80
2:C:256:THR:HG22	2:C:258:GLU:H	1.49	0.77
2:C:54:GLY:HA3	2:C:55:GLN:HB2	1.67	0.77
2:D:54:GLY:HA3	2:D:55:GLN:HB2	1.68	0.76
2:C:54:GLY:CA	2:C:55:GLN:HB2	2.18	0.73
2:C:250:MET:HE2	2:C:252:LEU:HD21	1.71	0.72
2:C:67:VAL:HG21	2:C:132:HIS:HB2	1.72	0.71
1:A:123:VAL:HG12	1:A:194:ILE:HD13	1.73	0.69
2:D:54:GLY:CA	2:D:55:GLN:HB2	2.22	0.69
1:A:133:GLN:HA	1:A:136:VAL:HG12	1.74	0.69
2:C:187:VAL:HG23	2:C:255:LEU:CD1	2.24	0.67
1:A:136:VAL:HG23	2:C:92:TYR:CZ	2.30	0.67
1:B:132:GLN:O	1:B:136:VAL:HG12	1.94	0.66
2:D:217:ILE:HG21	2:D:250:MET:HE3	1.78	0.66
1:B:136:VAL:HG23	2:D:92:TYR:CZ	2.31	0.66
2:C:217:ILE:HD13	2:C:250:MET:CE	2.23	0.65
1:B:170:LEU:HD11	1:B:180:ASN:HA	1.78	0.65
2:D:256:THR:HG22	2:D:258:GLU:H	1.61	0.65
2:D:51:VAL:HG21	2:D:120:VAL:HG21	1.79	0.63
2:D:73:SER:HA	2:D:74:TYR:HB2	1.81	0.63
1:A:180:ASN:O	1:A:181:ILE:CD1	2.47	0.62
2:C:67:VAL:HG11	2:C:75:MET:HE2	1.82	0.61
1:B:136:VAL:HG22	1:B:136:VAL:O	2.02	0.60
2:D:67:VAL:HG11	2:D:75:MET:HE2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:VAL:CG2	1:A:119:ILE:HD11	2.32	0.59
1:A:158:GLY:HA3	1:A:166:THR:HG23	1.84	0.59
2:C:73:SER:HA	2:C:74:TYR:HB2	1.84	0.58
2:D:67:VAL:HG21	2:D:132:HIS:HB2	1.85	0.58
1:A:170:LEU:HD11	1:A:180:ASN:HA	1.86	0.57
1:A:180:ASN:O	1:A:181:ILE:HD13	2.05	0.57
2:D:250:MET:HE2	2:D:252:LEU:HD21	1.86	0.56
2:C:217:ILE:HG21	2:C:250:MET:HE3	1.88	0.56
2:D:67:VAL:O	2:D:74:TYR:HB2	2.06	0.55
1:A:135:VAL:CG2	1:A:165:LEU:HD22	2.32	0.54
2:D:46:PRO:HG3	2:D:49:LEU:HD13	1.89	0.54
1:A:138:ASP:HA	2:C:271:THR:HG21	1.91	0.53
1:A:136:VAL:HG11	2:C:72:TYR:CE1	2.43	0.53
2:D:136:PHE:CE1	2:D:228:ILE:HD13	2.44	0.53
2:C:136:PHE:CE1	2:C:228:ILE:HD13	2.45	0.52
2:C:175:GLN:HE21	2:C:280:GLY:HA3	1.76	0.51
1:B:165:LEU:HD11	2:D:74:TYR:OH	2.11	0.50
2:D:54:GLY:HA3	2:D:55:GLN:CB	2.37	0.50
1:A:136:VAL:HG11	2:C:72:TYR:CZ	2.47	0.50
2:C:54:GLY:N	2:C:55:GLN:HB2	2.27	0.49
1:A:114:VAL:HG22	1:A:119:ILE:HD11	1.94	0.49
1:B:136:VAL:HG11	2:D:72:TYR:CE1	2.48	0.49
2:D:273:ASP:O	2:D:275:LEU:N	2.38	0.48
1:A:166:THR:HG22	1:A:185:LEU:HD13	1.97	0.47
2:D:146:LEU:HD23	2:D:147:GLU:N	2.29	0.47
2:D:67:VAL:HG23	2:D:134:ARG:HB2	1.97	0.46
2:C:181:VAL:HG21	2:C:255:LEU:HD13	1.96	0.46
1:A:114:VAL:HG21	1:A:119:ILE:HD11	1.98	0.46
1:B:127:TYR:OH	1:B:151:HIS:NE2	2.42	0.46
2:C:57:ALA:HB2	2:C:120:VAL:HG21	1.99	0.45
2:D:92:TYR:CE2	2:D:275:LEU:HD21	2.51	0.45
1:A:143:ALA:O	1:A:147:VAL:HG23	2.17	0.45
1:B:160:SER:O	1:B:163:THR:HG23	2.17	0.45
1:A:167:THR:HG21	2:C:228:ILE:HD11	1.98	0.45
2:C:67:VAL:O	2:C:74:TYR:HB2	2.17	0.45
2:D:139:THR:HG21	3:D:325:HOH:O	2.18	0.44
1:B:163:THR:HG22	3:B:302:HOH:O	2.17	0.44
1:B:175:CYS:HB3	1:B:176:PRO:HD2	2.00	0.44
2:C:273:ASP:OD1	2:C:275:LEU:HD22	2.18	0.43
1:B:179:SER:OG	1:B:180:ASN:N	2.51	0.43
2:D:217:ILE:HD13	2:D:250:MET:HE3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:80:GLN:O	2:C:126:ALA:HB1	2.18	0.43
2:D:171:VAL:HG13	3:D:327:HOH:O	2.19	0.43
1:B:156:CYS:HB3	1:B:193:LYS:HG3	2.01	0.43
1:A:113:PHE:N	3:A:301:HOH:O	2.52	0.43
2:C:73:SER:HA	2:C:74:TYR:CB	2.49	0.42
2:D:195:GLY:O	2:D:196:TYR:HB3	2.19	0.42
2:C:115:LEU:HD12	2:C:116:ASN:N	2.35	0.42
2:C:187:VAL:HG21	2:C:285:LEU:HD21	2.01	0.42
1:A:170:LEU:HD22	1:A:185:LEU:HD21	2.01	0.42
1:B:131:LEU:HD12	1:B:169:VAL:HG11	2.02	0.41
2:D:180:LEU:HD11	2:D:288:SER:HB3	2.02	0.41
1:A:168:SER:O	1:A:172:ASN:ND2	2.53	0.41
1:A:180:ASN:O	1:A:181:ILE:HD12	2.17	0.41
2:D:73:SER:HA	2:D:74:TYR:CB	2.49	0.41
2:D:256:THR:CG2	2:D:257:SER:N	2.82	0.41
2:D:73:SER:O	2:D:92:TYR:HA	2.20	0.41
1:A:172:ASN:HD22	1:A:172:ASN:N	2.18	0.41
1:A:158:GLY:HA3	1:A:166:THR:CG2	2.49	0.41
1:B:136:VAL:HG11	2:D:72:TYR:CZ	2.55	0.41
2:D:54:GLY:N	2:D:55:GLN:HB2	2.36	0.41
1:A:131:LEU:HD23	1:A:162:LEU:HD12	2.02	0.40
1:B:119:ILE:O	1:B:123:VAL:HG23	2.21	0.40
2:C:51:VAL:HG21	2:C:120:VAL:HG21	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	87/99 (88%)	83 (95%)	3 (3%)	1 (1%)	11	34
1	B	87/99 (88%)	77 (88%)	8 (9%)	2 (2%)	5	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	228/251 (91%)	215 (94%)	11 (5%)	2 (1%)	14	38
2	D	228/251 (91%)	213 (93%)	12 (5%)	3 (1%)	9	29
All	All	630/700 (90%)	588 (93%)	34 (5%)	8 (1%)	9	29

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	ILE
2	C	55	GLN
2	D	55	GLN
2	D	196	TYR
1	B	176	PRO
1	B	179	SER
2	C	54	GLY
2	D	274	LEU

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	79/87 (91%)	76 (96%)	3 (4%)	29	62
1	B	79/87 (91%)	77 (98%)	2 (2%)	42	74
2	C	194/197 (98%)	183 (94%)	11 (6%)	18	47
2	D	194/197 (98%)	180 (93%)	14 (7%)	13	37
All	All	546/568 (96%)	516 (94%)	30 (6%)	20	49

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168	SER
1	A	172	ASN
1	A	181	ILE
1	B	141	ASN

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Mol	Chain	Res	Type
1	B	173	ASN
2	C	73	SER
2	C	97	GLU
2	C	146	LEU
2	C	147	GLU
2	C	173	LEU
2	C	239	LEU
2	C	265[A]	CYS
2	C	265[B]	CYS
2	C	277	ARG
2	C	281	GLN
2	C	286	THR
2	D	52	SER
2	D	68	SER
2	D	73	SER
2	D	97	GLU
2	D	179	GLU
2	D	186	SER
2	D	194	SER
2	D	196	TYR
2	D	197	THR
2	D	239	LEU
2	D	251	GLN
2	D	277	ARG
2	D	281	GLN
2	D	286	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	GLN
1	A	141	ASN
1	A	142	ASN
1	A	172	ASN
1	B	129	GLN
1	B	132	GLN
1	B	172	ASN
1	B	180	ASN
1	B	184	ASN
2	C	55	GLN
2	C	79	GLN
2	C	80	GLN

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Mol	Chain	Res	Type
2	C	175	GLN
2	C	208	GLN
2	D	84	GLN
2	D	174	GLN
2	D	175	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 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	A	89/99 (89%)	0.80	15 (16%) 4 3	48, 56, 64, 65	0
1	B	89/99 (89%)	0.88	14 (15%) 5 4	47, 57, 65, 68	0
2	C	231/251 (92%)	0.40	11 (4%) 35 27	21, 45, 54, 57	1 (0%)
2	D	231/251 (92%)	0.33	9 (3%) 43 34	21, 43, 47, 58	1 (0%)
All	All	640/700 (91%)	0.50	49 (7%) 19 14	21, 46, 62, 68	2 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	ASP	6.1
1	B	178	GLY	5.0
1	B	140	ALA	5.0
2	D	170	GLN	4.7
2	D	171	VAL	4.4
1	B	113	PHE	4.2
2	C	122	GLU	3.8
2	C	170	GLN	3.3
1	B	138	ASP	3.2
1	A	177	SER	3.1
1	B	179	SER	3.1
1	A	178	GLY	3.0
1	B	141	ASN	3.0
1	B	177	SER	3.0
1	A	179	SER	2.9
1	B	139	ASP	2.7
2	C	60	SER	2.7
2	D	211	GLY	2.7
2	D	195	GLY	2.6
2	C	73	SER	2.6
2	C	289	SER	2.6

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Mol	Chain	Res	Type	RSRZ
2	C	49	LEU	2.6
2	C	147	GLU	2.6
2	D	174	GLN	2.6
1	A	141	ASN	2.5
1	A	139	ASP	2.5
2	D	281	GLN	2.5
2	C	53	LEU	2.5
1	B	137	ASP	2.5
1	A	125	GLN	2.5
1	A	152	GLU	2.4
2	D	172	GLN	2.4
1	A	113	PHE	2.4
1	B	152	GLU	2.4
1	A	137	ASP	2.3
2	D	270	LYS	2.3
1	A	201	LYS	2.2
1	B	114	VAL	2.2
1	B	201	LYS	2.2
1	A	133	GLN	2.2
2	C	149	LYS	2.2
1	A	180	ASN	2.1
2	C	210	PRO	2.1
1	B	186	PHE	2.1
1	A	148	LYS	2.0
2	C	245	SER	2.0
2	D	289	SER	2.0
1	B	180	ASN	2.0
1	A	142	ASN	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 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.