



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:24 PM UTC

PDB ID : 2BSE / pdb_00002bse
Title : Structure of Lactococcal Bacteriophage p2 Receptor Binding Protein in complex with a llama VHH domain
Authors : Spinelli, S.; Desmyter, A.; Verrips, C.T.; de Haard, H.J.W.; Moineau, S.; Cambillau, C.
Deposited on : 2005-05-20
Resolution : 2.70 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

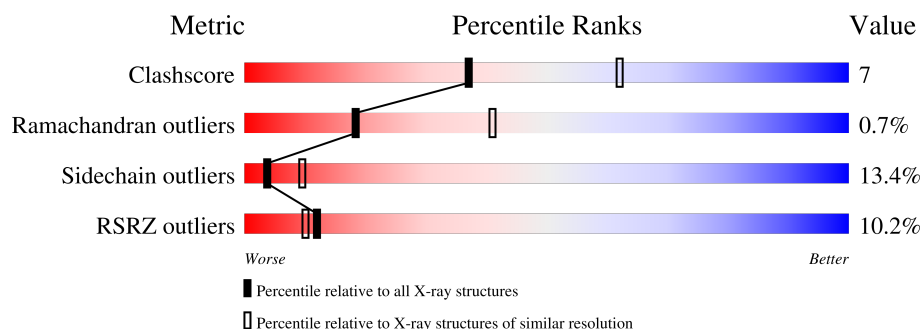
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	264	0% 34% 6% 59%
1	B	264	2% 33% 7% 59%
1	C	264	34% 6% 59%
2	D	123	20% 67% 28% 5%
2	E	123	12% 71% 24%
2	F	123	19% 64% 33%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5311 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 RECEPTOR BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			
1	B	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			
1	C	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			

- Molecule 2 is a protein called LLAMA IMMUNOGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			
2	E	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			
2	F	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			

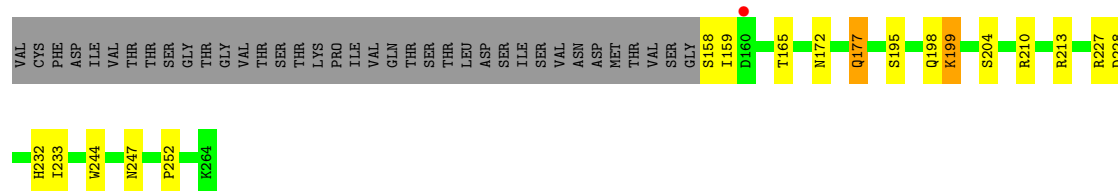
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	O	0	0
			1	1		

i

• Molecule 1: RECEPTOR BINDING PROTEIN





• Molecule 2: LLAMA IMMUNOGLOBULIN



• Molecule 2: LLAMA IMMUNOGLOBULIN



• Molecule 2: LLAMA IMMUNOGLOBULIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.76Å 83.94Å 137.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (15.00-2.70) 98.3 (15.00-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.251 , 0.294 0.243 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	52.5	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.1	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	0.89	EDS
Total number of atoms	5311	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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	0.42	0/853	0.78	0/1161
1	B	0.41	0/853	0.77	0/1161
1	C	0.40	0/853	0.77	0/1161
2	D	0.43	0/956	0.75	0/1289
2	E	0.40	0/956	0.74	0/1289
2	F	0.37	0/956	0.72	0/1289
All	All	0.40	0/5427	0.76	0/7350

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	832	0	819	9	0
1	B	832	0	819	11	0
1	C	832	0	819	15	0
2	D	938	0	891	14	0
2	E	938	0	891	13	0
2	F	938	0	891	20	0
3	D	1	0	0	0	0
All	All	5311	0	5130	74	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 7.

All (74) 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:F:108:GLU:CG	2:F:109:LEU:H	1.64	1.08
2:F:108:GLU:HG3	2:F:109:LEU:N	1.54	1.04
1:C:199:LYS:H	1:C:247:ASN:ND2	1.64	0.94
2:F:108:GLU:HG3	2:F:109:LEU:H	0.76	0.91
1:C:198:GLN:HA	1:C:247:ASN:HD22	1.42	0.83
2:F:91:THR:HG22	2:F:121:VAL:H	1.45	0.82
2:E:91:THR:HG22	2:E:121:VAL:H	1.47	0.80
1:B:198:GLN:HA	1:B:247:ASN:OD1	1.83	0.78
1:A:244:TRP:HE1	2:E:31:ASN:HD21	1.39	0.69
1:A:223:HIS:ND1	1:C:232:HIS:HD2	1.91	0.69
2:D:88:PRO:O	2:D:91:THR:HG22	1.95	0.66
1:C:198:GLN:CA	1:C:247:ASN:HD22	2.12	0.63
1:C:199:LYS:N	1:C:247:ASN:ND2	2.44	0.61
2:D:37:PHE:CE1	2:D:47:LEU:HD23	2.38	0.59
2:F:20:LEU:HD12	2:F:81:LEU:HD23	1.85	0.59
1:A:232:HIS:HD2	1:B:223:HIS:ND1	2.02	0.58
1:B:198:GLN:CA	1:B:247:ASN:OD1	2.51	0.56
1:C:199:LYS:H	1:C:247:ASN:HD21	1.52	0.56
2:E:36:TRP:HZ3	2:E:79:VAL:HG12	1.71	0.55
1:B:199:LYS:N	1:B:247:ASN:OD1	2.40	0.54
2:D:72:ARG:HH21	2:D:74:SER:HA	1.72	0.54
2:F:108:GLU:CG	2:F:109:LEU:N	2.38	0.54
2:D:20:LEU:HD12	2:D:81:LEU:HD23	1.90	0.53
1:B:244:TRP:HE1	2:D:31:ASN:HD21	1.58	0.52
2:E:99:ARG:HB3	2:E:110:TYR:CD2	2.45	0.52
2:E:55:TYR:HB3	2:E:57:MET:HE3	1.92	0.52
1:C:199:LYS:H	1:C:247:ASN:HD22	1.53	0.51
2:E:18:LEU:HB3	2:E:83:MET:HE3	1.92	0.51
2:F:99:ARG:HB3	2:F:110:TYR:HA	1.92	0.50
2:D:34:MET:HE3	2:D:79:VAL:HB	1.92	0.50
2:F:51:LEU:HD12	2:F:58:THR:HG22	1.93	0.50
1:A:223:HIS:ND1	1:C:232:HIS:CD2	2.76	0.50
2:F:49:VAL:HG11	2:F:81:LEU:HD13	1.94	0.50
1:C:244:TRP:HE1	2:F:31:ASN:HD21	1.58	0.50
1:C:172:ASN:HD21	1:C:204:SER:H	1.60	0.49
1:C:210:ARG:HA	1:C:213:ARG:HD2	1.95	0.49
2:F:107:ARG:N	2:F:107:ARG:HD3	2.29	0.48
2:F:55:TYR:HB3	2:F:57:MET:HE3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:23:THR:HG22	2:E:78:THR:HG23	1.95	0.47
2:F:34:MET:HG3	2:F:53:PHE:CE1	2.49	0.47
1:B:177:GLN:OE1	1:B:189:ARG:NH1	2.48	0.47
2:E:64:VAL:HA	2:E:67:ARG:HH11	1.79	0.46
2:E:91:THR:HG22	2:E:121:VAL:N	2.25	0.46
1:B:229:THR:HB	1:C:228:ASP:HB2	1.98	0.46
2:F:23:THR:HG22	2:F:78:THR:HG23	1.97	0.46
2:D:11:LEU:HG	2:D:120:THR:HB	1.97	0.45
1:A:173:GLY:HA3	1:A:193:SER:O	2.16	0.45
2:D:67:ARG:NH2	2:D:90:ASP:OD2	2.50	0.45
2:D:36:TRP:CZ3	2:D:79:VAL:HG12	2.52	0.44
1:A:198:GLN:HA	1:A:247:ASN:OD1	2.17	0.44
2:F:18:LEU:HD23	2:F:119:VAL:HG13	2.00	0.44
2:E:14:ALA:HB2	2:E:123:SER:HA	2.00	0.44
2:E:40:LEU:HB2	2:E:43:LYS:HB2	1.99	0.44
2:F:37:PHE:CE1	2:F:47:LEU:HD23	2.52	0.44
2:F:20:LEU:HB2	2:F:81:LEU:HB3	2.00	0.43
1:C:177:GLN:C	1:C:177:GLN:HE21	2.27	0.43
2:D:12:VAL:HB	2:D:18:LEU:HD13	2.00	0.43
1:B:186:VAL:O	1:B:260:SER:HA	2.19	0.42
1:C:199:LYS:N	1:C:247:ASN:HD22	2.13	0.42
1:A:232:HIS:CD2	1:B:223:HIS:ND1	2.85	0.42
2:E:36:TRP:CZ3	2:E:79:VAL:HG12	2.53	0.42
1:B:187:ILE:HG12	1:B:260:SER:HB3	2.00	0.42
1:C:195:SER:HB3	1:C:252:PRO:HA	2.01	0.41
1:A:209:ASP:HB3	1:A:211:PRO:HD2	2.03	0.41
2:D:45:PRO:HG2	2:D:107:ARG:HH22	1.85	0.41
2:F:39:GLN:HG3	2:F:45:PRO:HG3	2.02	0.41
2:D:53:PHE:CE2	2:D:72:ARG:HD2	2.56	0.41
2:F:106:ASN:HA	2:F:107:ARG:HH11	1.86	0.41
1:A:210:ARG:HA	1:A:213:ARG:HD2	2.02	0.41
2:D:38:ARG:HD2	2:D:94:TYR:OH	2.21	0.41
2:E:108:GLU:CG	2:E:109:LEU:N	2.83	0.41
2:D:97:ALA:HB1	2:D:110:TYR:CD2	2.57	0.40
2:F:36:TRP:CZ3	2:F:79:VAL:HG12	2.55	0.40
1:B:173:GLY:HA3	1:B:193:SER:O	2.21	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	105/264 (40%)	102 (97%)	3 (3%)	0	100	100
1	B	105/264 (40%)	102 (97%)	3 (3%)	0	100	100
1	C	105/264 (40%)	102 (97%)	3 (3%)	0	100	100
2	D	120/123 (98%)	114 (95%)	5 (4%)	1 (1%)	16	37
2	E	120/123 (98%)	114 (95%)	3 (2%)	3 (2%)	4	11
2	F	120/123 (98%)	113 (94%)	6 (5%)	1 (1%)	16	37
All	All	675/1161 (58%)	647 (96%)	23 (3%)	5 (1%)	18	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	74	SER
2	E	108	GLU
2	F	74	SER
2	E	41	ALA
2	E	74	SER

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	90/228 (40%)	82 (91%)	8 (9%)	9	23
1	B	90/228 (40%)	81 (90%)	9 (10%)	7	19
1	C	90/228 (40%)	83 (92%)	7 (8%)	11	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	99/100 (99%)	79 (80%)	20 (20%)	1	4
2	E	99/100 (99%)	83 (84%)	16 (16%)	2	6
2	F	99/100 (99%)	83 (84%)	16 (16%)	2	6
All	All	567/984 (58%)	491 (87%)	76 (13%)	4	9

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	ILE
1	A	165	THR
1	A	177	GLN
1	A	199	LYS
1	A	210	ARG
1	A	227	ARG
1	A	228	ASP
1	A	233	ILE
1	B	161	VAL
1	B	164	GLN
1	B	165	THR
1	B	177	GLN
1	B	197	ILE
1	B	199	LYS
1	B	227	ARG
1	B	228	ASP
1	B	233	ILE
1	C	158	SER
1	C	159	ILE
1	C	165	THR
1	C	177	GLN
1	C	199	LYS
1	C	227	ARG
1	C	233	ILE
2	D	2	VAL
2	D	5	GLN
2	D	11	LEU
2	D	23	THR
2	D	27	ARG
2	D	38	ARG
2	D	43	LYS
2	D	49	VAL
2	D	52	ASN

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Mol	Chain	Res	Type
2	D	65	LYS
2	D	73	ASP
2	D	77	ASN
2	D	79	VAL
2	D	86	LEU
2	D	91	THR
2	D	107	ARG
2	D	109	LEU
2	D	117	THR
2	D	122	SER
2	D	123	SER
2	E	23	THR
2	E	27	ARG
2	E	38	ARG
2	E	43	LYS
2	E	44	GLU
2	E	47	LEU
2	E	52	ASN
2	E	63	SER
2	E	65	LYS
2	E	70	VAL
2	E	74	SER
2	E	77	ASN
2	E	93	ILE
2	E	106	ASN
2	E	109	LEU
2	E	117	THR
2	F	11	LEU
2	F	26	ARG
2	F	27	ARG
2	F	43	LYS
2	F	52	ASN
2	F	65	LYS
2	F	73	ASP
2	F	77	ASN
2	F	89	GLU
2	F	93	ILE
2	F	105	SER
2	F	107	ARG
2	F	108	GLU
2	F	115	GLN
2	F	117	THR

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Mol	Chain	Res	Type
2	F	123	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	175	GLN
1	A	232	HIS
1	A	236	ASN
1	B	164	GLN
1	B	172	ASN
1	B	198	GLN
1	B	232	HIS
1	B	236	ASN
1	C	172	ASN
1	C	177	GLN
1	C	183	ASN
1	C	232	HIS
1	C	236	ASN
1	C	247	ASN
2	D	31	ASN
2	D	106	ASN
2	E	31	ASN
2	E	84	ASN
2	E	106	ASN
2	F	31	ASN
2	F	52	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 oligosaccharides in this entry.

5.6 Ligand geometry

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

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	107/264 (40%)	0.00	2 (1%) 66 63	11, 20, 31, 41	1 (0%)
1	B	107/264 (40%)	0.17	4 (3%) 45 41	11, 20, 31, 41	1 (0%)
1	C	107/264 (40%)	0.12	1 (0%) 81 80	11, 20, 31, 41	1 (0%)
2	D	122/123 (99%)	1.44	25 (20%) 2 2	18, 26, 34, 38	0
2	E	122/123 (99%)	0.85	15 (12%) 8 7	20, 26, 33, 37	0
2	F	122/123 (99%)	1.23	23 (18%) 3 3	19, 26, 34, 37	0
All	All	687/1161 (59%)	0.67	70 (10%) 12 10	11, 23, 34, 41	3 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	75	GLY	10.0
2	D	42	GLY	10.0
2	F	109	LEU	6.8
2	D	74	SER	5.2
2	E	41	ALA	5.1
2	D	123	SER	5.0
2	F	74	SER	4.5
2	D	41	ALA	4.3
2	F	123	SER	4.1
2	F	75	GLY	4.1
2	D	109	LEU	4.1
2	D	44	GLU	4.0
2	E	76	LYS	3.9
2	F	44	GLU	3.8
2	E	2	VAL	3.7
2	D	108	GLU	3.7
2	F	116	GLY	3.7
2	F	108	GLU	3.5
2	E	75	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
2	F	13	GLN	3.2
2	F	76	LYS	3.2
2	D	18	LEU	3.0
2	F	2	VAL	3.0
1	B	175	GLN	2.9
2	F	70	VAL	2.8
2	D	13	GLN	2.8
2	F	122	SER	2.8
2	D	9	GLY	2.8
2	F	115	GLN	2.7
1	B	160	ASP	2.7
2	D	39	GLN	2.7
1	B	158	SER	2.6
2	E	114	GLY	2.6
2	D	122	SER	2.6
2	E	39	GLN	2.6
1	C	160	ASP	2.6
2	F	106	ASN	2.6
2	F	121	VAL	2.6
2	D	46	GLU	2.6
2	E	21	SER	2.5
2	D	78	THR	2.5
2	D	111	ASP	2.5
2	F	90	ASP	2.5
2	E	45	PRO	2.5
2	F	39	GLN	2.5
2	D	26	ARG	2.4
2	D	79	VAL	2.3
2	D	4	LEU	2.3
2	F	51	LEU	2.3
2	F	50	ALA	2.2
2	F	96	CYS	2.2
2	D	45	PRO	2.2
2	E	9	GLY	2.2
2	E	11	LEU	2.2
2	E	70	VAL	2.2
2	E	108	GLU	2.2
2	D	56	ASP	2.2
2	F	73	ASP	2.2
2	D	2	VAL	2.2
2	D	72	ARG	2.1
2	E	42	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	121	VAL	2.1
2	E	111	ASP	2.1
2	D	10	GLY	2.1
2	F	49	VAL	2.1
2	E	96	CYS	2.1
1	A	209	ASP	2.1
1	A	158	SER	2.0
1	B	230	SER	2.0
2	F	64	VAL	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.