

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 15, 2023 – 07:38 AM EDT

PDB ID : 7T87

Title : CRYSTAL STRUCTURE OF LEUKOCIDIN AB/CENTYRIN S17/FAB

214F COMPLEX

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Deposited on : 2021-12-15

Resolution : 3.00 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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467 Xtriage (Phenix) : 1.13

Phenix) : 1.13 EDS : 2.36

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)

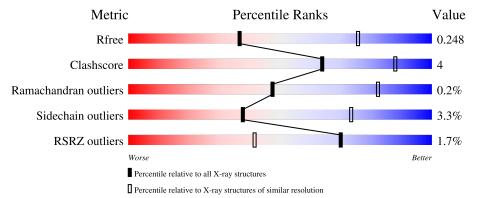
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 3.00 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 <=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	309	78%	16% • 6%
2	В	332	68% 17%	15%
3	L	213	92%	7%
4	Н	233	84%	10% 6%
5	С	98	7% 81%	15% •



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8641 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 Leukocidin B.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	290	Total 2346	C 1470	N 411	O 460	S 5	0	0	0

• Molecule 2 is a protein called Leukocidin A.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
2	В	283	Total 2291	C 1447	N 398	O 446	0	0	0

• Molecule 3 is a protein called Antibody Fab B214 Light Chain.

M	ol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	3	L	213	Total 1624	C 1018	N 272	O 327	S 7	0	0	0

• Molecule 4 is a protein called Antibody Fab B214 Heavy Chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
4	Н	220	Total 1654	C 1049	N 268	O 330	S 7	0	0	0

• Molecule 5 is a protein called Centyrin S17.

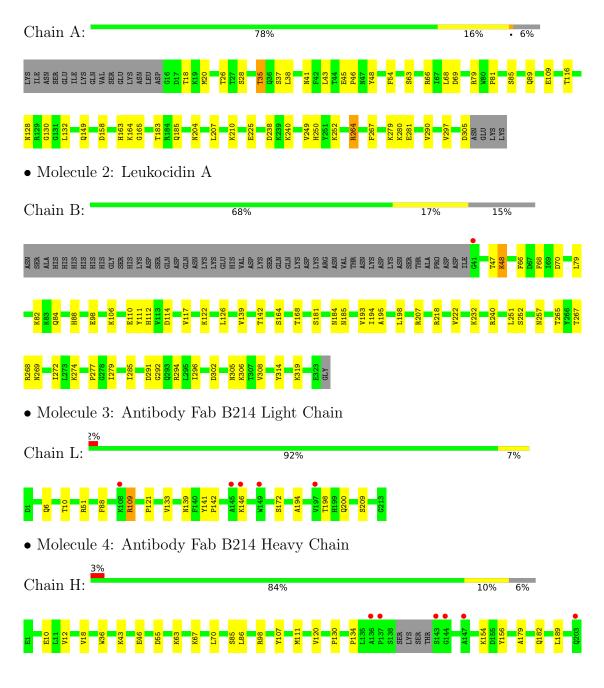
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
5	С	94	Total 726	C 471	N 119	O 135	S 1	0	0	0



# 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.

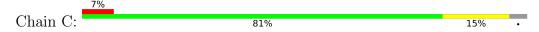
• Molecule 1: Leukocidin B







• Molecule 5: Centyrin S17







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	92.98Å 173.74Å 174.31Å	Donasiton
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.16 - 3.00	Depositor
Resolution (A)	49.16 - 3.00	EDS
% Data completeness	95.0 (49.16-3.00)	Depositor
(in resolution range)	95.0 (49.16-3.00)	EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.72 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
D D.	0.196 , 0.247	Depositor
$R, R_{free}$	0.196 , 0.248	DCC
$R_{free}$ test set	1361 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.8	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.34, 58.5	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8641	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.18% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.26	0/2404	0.45	0/3253	
2	В	0.26	0/2343	0.45	0/3172	
3	L	0.26	0/1660	0.46	0/2254	
4	Н	0.26	0/1697	0.46	0/2308	
5	С	0.28	0/749	0.48	0/1023	
All	All	0.26	0/8853	0.46	0/12010	

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	2346	0	2219	21	0
2	В	2291	0	2184	28	0
3	L	1624	0	1583	6	0
4	Н	1654	0	1590	13	0
5	С	726	0	701	9	0
All	All	8641	0	8277	71	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 4.

All (71) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



A 4 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}\ (\mathring{\rm A})$	overlap (Å)
2:B:302:ASP:OD2	2:B:305:ASN:ND2	2.19	0.76
5:C:4:ALA:HB2	5:C:82:TRP:HB2	1.68	0.74
2:B:181:SER:O	2:B:184:ASN:ND2	2.20	0.74
1:A:38:LEU:HD21	1:A:249:VAL:HG21	1.73	0.70
1:A:85:SER:HB2	1:A:252:LYS:HG3	1.75	0.68
4:H:12:VAL:HG11	4:H:18:VAL:HB	1.75	0.68
1:A:264:ARG:NH2	5:C:37:GLU:OE2	2.26	0.66
2:B:70:ASP:OD2	2:B:306:LYS:NZ	2.20	0.66
1:A:26:THR:HG22	1:A:37:SER:HA	1.77	0.65
2:B:122:LYS:HD3	2:B:257:ASN:HB2	1.79	0.65
1:A:264:ARG:HG2	5:C:35:THR:HG21	1.77	0.64
1:A:89:GLN:HG3	1:A:165:GLY:HA3	1.80	0.64
2:B:112:HIS:HB2	2:B:267:THR:HB	1.81	0.63
5:C:72:ILE:HG23	5:C:84:LEU:HB3	1.80	0.62
1:A:45:GLU:OE1	2:B:48:LYS:NZ	2.33	0.61
1:A:183:THR:HG23	1:A:185:GLN:H	1.64	0.61
3:L:146:LYS:HB3	3:L:198:THR:HB	1.84	0.58
1:A:41:ASN:HB2	1:A:54:PHE:HB2	1.86	0.58
2:B:110:GLU:HB2	2:B:269:ASN:HB2	1.85	0.57
5:C:29:PHE:HA	5:C:76:LYS:HB2	1.85	0.57
1:A:290:VAL:HG22	1:A:297:VAL:HG22	1.87	0.56
2:B:232:LYS:HD2	2:B:240:ARG:NH1	2.20	0.56
1:A:18:THR:HG22	1:A:46:PRO:HD3	1.88	0.56
2:B:294:ARG:HH21	2:B:319:LYS:HG3	1.72	0.55
3:L:121:PRO:HD3	3:L:133:VAL:HG22	1.89	0.55
4:H:179:ALA:HB2	4:H:189:LEU:HD23	1.89	0.54
4:H:134:PRO:HD3	4:H:220:LYS:HE2	1.90	0.54
5:C:34:ILE:HG12	5:C:72:ILE:HD13	1.90	0.54
2:B:82:LYS:HD2	2:B:84:GLN:HE21	1.72	0.54
3:L:6:GLN:HE22	3:L:88:PHE:HA	1.74	0.53
2:B:274:LYS:HB2	2:B:285:ILE:HB	1.89	0.53
2:B:106:LYS:HG2	2:B:272:ILE:HG12	1.91	0.52
2:B:222:VAL:HG22	2:B:277:PRO:HG2	1.92	0.52
1:A:132:LEU:HD12	2:B:164:SER:HA	1.92	0.52
1:A:163:HIS:CD2	1:A:164:LYS:HG3	2.45	0.51
2:B:291:ASP:OD1	2:B:292:GLY:N	2.41	0.50
3:L:194:ALA:HB2	3:L:209:SER:HB3	1.94	0.49
2:B:114:ASP:HB3	2:B:265:THR:HB	1.94	0.48
1:A:20:MET:HE2	1:A:43:LEU:HD13	1.96	0.48
1:A:281:GLU:HB2	4:H:107:TYR:CE1	2.49	0.48
1:A:63:SER:HB2	1:A:81:PRO:HG3	1.96	0.47
5:C:25:PRO:HB2	5:C:28:ALA:HB2	1.95	0.47

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A.		Interatomic	Clash
Atom-1	Atom-2	${ m distance} \; ({ m \AA})$	overlap (Å)
2:B:126:LEU:HD22	2:B:252:SER:HB3	1.97	0.47
2:B:218:ARG:HG2	2:B:279:ILE:HA	1.96	0.47
2:B:79:LEU:HD23	2:B:251:LEU:HD12	1.95	0.47
2:B:88:HIS:O	2:B:268:ARG:NH1	2.46	0.47
4:H:67:LYS:NZ	4:H:85:SER:O	2.47	0.47
1:A:280:LYS:NZ	4:H:55:ASP:OD2	2.45	0.46
4:H:46:GLU:OE2	4:H:63:LYS:NZ	2.46	0.46
2:B:111:TYR:HB2	2:B:193:VAL:HB	1.97	0.46
4:H:154:LYS:NZ	4:H:182:GLN:OE1	2.49	0.46
2:B:47:THR:HB	2:B:68:PHE:HB2	1.98	0.45
1:A:68:LEU:HD21	1:A:79:ARG:HB2	1.99	0.45
1:A:28:SER:HA	1:A:35:THR:HA	1.98	0.44
1:A:128:ASN:OD1	1:A:130:GLY:N	2.31	0.44
2:B:195:ALA:HB1	2:B:198:LEU:HD21	1.99	0.44
4:H:130:PRO:HB3	4:H:156:TYR:HB3	1.98	0.44
2:B:294:ARG:NH1	2:B:296:ILE:HD11	2.33	0.44
4:H:12:VAL:HG21	4:H:86:LEU:HD13	2.00	0.43
2:B:110:GLU:HG2	2:B:194:ILE:HG23	2.01	0.43
4:H:179:ALA:HA	4:H:189:LEU:HB3	1.99	0.43
2:B:142:THR:HG22	2:B:168:THR:HG22	2.00	0.43
5:C:32:PHE:HB2	5:C:50:VAL:HG22	1.99	0.43
5:C:32:PHE:HB3	5:C:72:ILE:HD11	2.00	0.43
4:H:36:TRP:CD1	4:H:70:LEU:HD22	2.53	0.42
2:B:296:ILE:HB	2:B:314:TYR:HB3	2.01	0.42
2:B:66:PHE:CE1	2:B:308:VAL:HG11	2.54	0.42
3:L:109:ARG:HG2	3:L:172:SER:HB2	2.01	0.42
4:H:10:GLU:HB2	4:H:120:VAL:HG22	2.02	0.42
3:L:141:TYR:CD1	3:L:142:PRO:HA	2.54	0.42
1:A:238:ASP:CG	1:A:240:LYS:HG2	2.41	0.41

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	Perce	ntiles
1	A	288/309 (93%)	270 (94%)	18 (6%)	0	100	100
2	В	281/332 (85%)	262 (93%)	19 (7%)	0	100	100
3	L	211/213 (99%)	196 (93%)	14 (7%)	1 (0%)	29	68
4	Н	216/233 (93%)	210 (97%)	6 (3%)	0	100	100
5	С	92/98 (94%)	86 (94%)	5 (5%)	1 (1%)	14	50
All	All	1088/1185 (92%)	1024 (94%)	62 (6%)	2 (0%)	47	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	С	3	PRO
3	L	139	ASN

#### 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	Percent	iles
1	A	258/281 (92%)	241 (93%)	17 (7%)	16	19
2	В	248/308 (80%)	242 (98%)	6 (2%)	49 7	79
3	L	185/185 (100%)	181 (98%)	4 (2%)	52 8	31
4	Н	181/195 (93%)	178 (98%)	3 (2%)	60 8	35
5	$\mathbf{C}$	75/81~(93%)	74 (99%)	1 (1%)	69 8	39
All	All	947/1050 (90%)	916 (97%)	31 (3%)	38 7	73

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\operatorname{Res}$	Type
1	A	35	THR
1	A	48	TYR
1	A	66	ARG
1	A	69	ASP
1	A	109	GLU
1	A	116	THR

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Mol	Chain	Res	$egin{array}{c}  ext{Type} \end{array}$
1	A	149	GLN
1	A	158	ASP
1	A	204	ASN
1	A	207	LEU
1	A	210	LYS
1	A	225	GLU
1	A	250	HIS
1	A	264	ARG
1	A	267	PHE
1	A	279	LYS
1	A	305	ASP
2	В	48	LYS
2	В	98	GLU
2	В	117	VAL
2	В	139	VAL
2	В	185	ASN
2	В	207	ARG
3	L	10	THR
3	L	51	ARG
3	L	109	ARG
3	L	200	GLN
4	Н	43	LYS
4	Н	98	ARG
4	Н	111	MET
5	С	12	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	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 monosaccharides 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 (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,  $95^{th}$  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>	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	A	290/309 (93%)	-0.24	0 100 100	24, 47, 81, 101	0
2	В	283/332 (85%)	-0.20	1 (0%) 92 79	32, 59, 91, 106	0
3	L	213/213 (100%)	0.38	5 (2%) 60 31	46, 81, 122, 129	0
4	Н	220/233 (94%)	0.08	6 (2%) 54 26	33, 64, 98, 135	0
5	С	94/98~(95%)	0.35	7 (7%) 14 4	39, 75, 94, 111	0
All	All	1100/1185~(92%)	0.01	19 (1%) 70 41	24, 62, 106, 135	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	41	GLY	3.8
5	С	77	GLY	3.7
4	Н	144	GLY	3.6
4	Н	203	GLN	3.2
3	L	145	ALA	3.1
5	С	49	THR	3.1
5	С	78	GLY	3.0
5	С	31	SER	3.0
5	С	30	ASP	2.9
3	L	149	TRP	2.8
4	Н	143	SER	2.6
3	L	197	VAL	2.5
3	L	108	LYS	2.4
4	Н	137	PRO	2.2
4	Н	136	ALA	2.2
3	L	146	LYS	2.2
4	Н	147	ALA	2.0
5	С	25	PRO	2.0
5	С	27	ALA	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 monosaccharides 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.

