



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:50 PM UTC

PDB ID : 3L6W / pdb_00003l6w
Title : Structure of the collar functional unit (KLH1-H) of keyhole limpet hemocyanin
Authors : Jaenicke, E.; Buechler, K.; Markl, J.; Decker, H.; Barends, T.R.M.
Deposited on : 2009-12-27
Resolution : 4.00 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 ⓘ 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

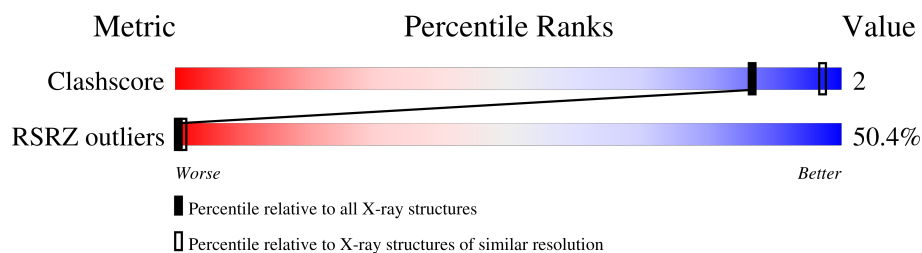
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1129 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)

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	491	48% 97% .
1	B	491	49% 96% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 954 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 Hemocyanin 1.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
1	A	479	Total	C	0	0	479
			479	479			
1	B	475	Total	C	0	0	475
			475	475			

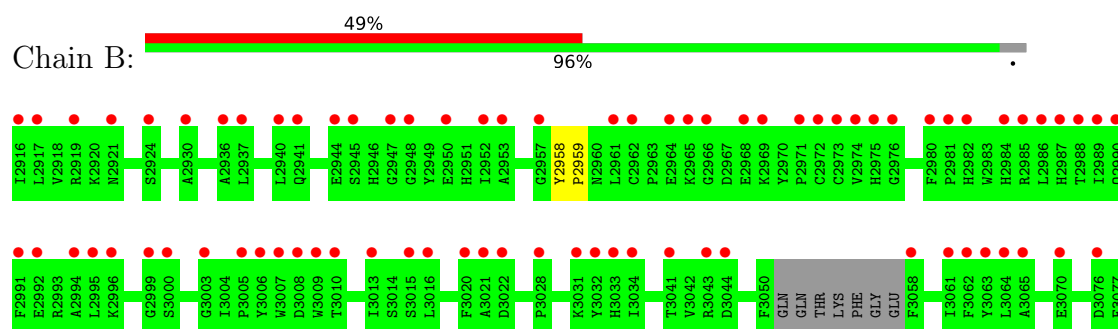
3 Residue-property plots [i](#)

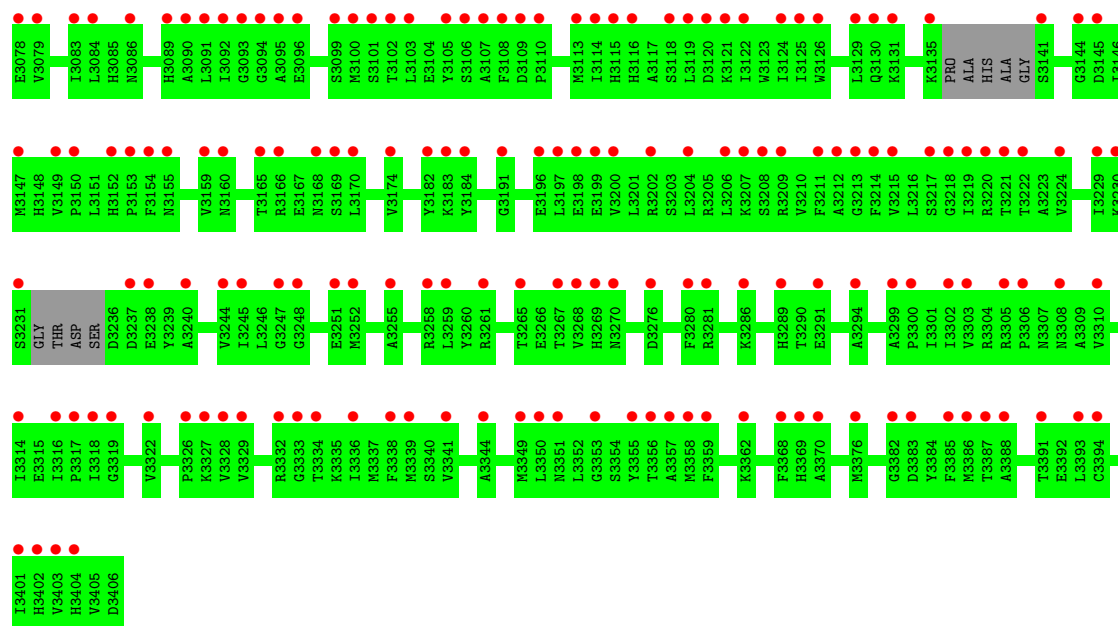
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Hemocyanin 1



• Molecule 1: Hemocyanin 1





4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, α , β , γ	251.02Å 251.02Å 251.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 4.00 177.50 – 4.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-4.00) 99.7 (177.50-4.00)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 3.98Å)	Xtriage
Refinement program		Depositor
R, R_{free}	(Not available) , (Not available) 0.418 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	122.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.28 , 93.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.055 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.63	EDS
Total number of atoms	954	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.70% 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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	479	0	0	1	0
1	B	475	0	0	1	0
All	All	954	0	0	2	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 2.

All (2) 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:B:2958:TYR:CA	1:B:2959:PRO:CA	2.94	0.46
1:A:2958:TYR:CA	1:A:2959:PRO:CA	2.94	0.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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	479/491 (97%)	2.85	238 (49%) 0 1	0, 0, 0, 0	0
1	B	475/491 (96%)	2.91	243 (51%) 0 1	0, 0, 0, 0	0
All	All	954/982 (97%)	2.88	481 (50%) 0 1	0, 0, 0, 0	0

All (481) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3101	SER	31.3
1	A	3006	TYR	27.1
1	B	3353	GLY	26.8
1	B	3103	LEU	22.9
1	A	3007	TRP	22.1
1	B	3382	GLY	22.0
1	B	3327	LYS	21.8
1	B	3096	GLU	19.5
1	A	3235	SER	18.2
1	A	2953	ALA	18.2
1	A	2957	GLY	18.0
1	A	2975	HIS	17.1
1	B	2965	LYS	16.9
1	B	3101	SER	16.0
1	B	3006	TYR	15.7
1	B	3155	ASN	15.5
1	B	3386	MET	15.3
1	A	3093	GLY	14.6
1	A	3032	TYR	14.5
1	B	3095	ALA	14.3
1	B	3093	GLY	14.1
1	B	3102	THR	13.9
1	A	3400	ARG	13.0
1	A	3089	HIS	12.2

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Mol	Chain	Res	Type	RSRZ
1	A	3387	THR	12.1
1	B	2947	GLY	12.0
1	B	3370	ALA	12.0
1	A	3332	ARG	11.8
1	B	3230	LYS	11.8
1	B	3032	TYR	11.8
1	A	3353	GLY	11.6
1	A	3383	ASP	11.4
1	B	3099	SER	11.1
1	A	3341	VAL	10.9
1	A	3354	SER	10.9
1	A	3327	LYS	10.6
1	A	3002	LEU	10.6
1	A	3386	MET	10.4
1	A	3102	THR	10.1
1	B	3076	ASP	10.1
1	B	3308	ASN	10.1
1	B	2972	CYS	9.9
1	B	2984	HIS	9.6
1	A	2917	LEU	9.6
1	B	3387	THR	9.3
1	A	3073	ASN	9.2
1	A	3005	PRO	9.0
1	A	3068	ALA	8.9
1	A	3008	ASP	8.8
1	A	2992	GLU	8.7
1	A	3309	ALA	8.7
1	B	3333	GLY	8.7
1	B	3261	ARG	8.6
1	B	3222	THR	8.5
1	B	3022	ASP	8.4
1	B	3357	ALA	8.4
1	A	2999	GLY	8.4
1	A	3095	ALA	8.2
1	A	3106	SER	8.2
1	A	2940	LEU	8.0
1	A	2976	GLY	8.0
1	A	3394	CYS	7.9
1	B	3105	TYR	7.9
1	A	3319	GLY	7.9
1	B	2975	HIS	7.8
1	A	3114	ILE	7.7

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Mol	Chain	Res	Type	RSRZ
1	B	3394	CYS	7.6
1	A	3388	ALA	7.6
1	B	3326	PRO	7.4
1	B	3184	TYR	7.4
1	B	3106	SER	7.3
1	B	3078	GLU	7.3
1	A	3144	GLY	7.1
1	B	3221	THR	7.1
1	B	3109	ASP	7.1
1	A	3223	ALA	7.0
1	B	2971	PRO	7.0
1	B	3125	ILE	7.0
1	A	3011	GLN	7.0
1	B	3043	ARG	6.9
1	B	3212	ALA	6.9
1	A	3169	SER	6.9
1	B	3403	VAL	6.8
1	B	2964	GLU	6.8
1	A	3357	ALA	6.8
1	A	3113	MET	6.8
1	B	3383	ASP	6.8
1	A	3293	ASP	6.7
1	B	3135	LYS	6.7
1	B	3169	SER	6.7
1	B	2980	PHE	6.7
1	B	3268	VAL	6.6
1	A	3232	GLY	6.6
1	B	3245	ILE	6.6
1	A	2920	LYS	6.6
1	B	2919	ARG	6.5
1	B	3144	GLY	6.5
1	A	3109	ASP	6.4
1	B	2976	GLY	6.3
1	B	3116	HIS	6.3
1	B	3183	LYS	6.3
1	A	2964	GLU	6.3
1	A	2947	GLY	6.1
1	A	3371	PHE	6.1
1	A	2981	PRO	6.1
1	B	3332	ARG	6.1
1	A	3346	THR	6.1
1	B	3094	GLY	6.0

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Mol	Chain	Res	Type	RSRZ
1	B	2936	ALA	6.0
1	B	2992	GLU	6.0
1	B	2990	GLN	6.0
1	A	3307	ASN	5.9
1	A	2967	ASP	5.9
1	A	3385	PHE	5.9
1	B	3092	ILE	5.9
1	A	2985	ARG	5.9
1	A	3090	ALA	5.9
1	B	3209	ARG	5.8
1	B	3281	ARG	5.8
1	B	2987	HIS	5.8
1	B	2957	GLY	5.8
1	B	3090	ALA	5.8
1	A	3043	ARG	5.7
1	B	2994	ALA	5.7
1	A	3203	SER	5.7
1	B	3291	GLU	5.7
1	A	3334	THR	5.7
1	B	3255	ALA	5.7
1	B	2969	LYS	5.6
1	B	3000	SER	5.6
1	B	3021	ALA	5.6
1	B	3391	THR	5.6
1	A	3104	GLU	5.6
1	B	3368	PHE	5.6
1	A	3308	ASN	5.6
1	B	2995	LEU	5.6
1	B	3159	VAL	5.5
1	A	3103	LEU	5.4
1	A	3100	MET	5.4
1	A	3222	THR	5.4
1	A	2960	ASN	5.4
1	A	3359	PHE	5.4
1	A	3074	TYR	5.3
1	A	3316	ILE	5.3
1	A	3247	GLY	5.3
1	B	2948	GLY	5.3
1	A	2989	ILE	5.3
1	A	3288	ASP	5.2
1	B	3154	PHE	5.2
1	B	3086	ASN	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	3021	ALA	5.2
1	B	3388	ALA	5.2
1	B	3113	MET	5.2
1	A	2959	PRO	5.2
1	B	3401	ILE	5.2
1	B	2924	SER	5.1
1	A	3117	ALA	5.1
1	B	3229	ILE	5.1
1	B	3160	ASN	5.1
1	A	2988	THR	5.1
1	B	3247	GLY	5.0
1	A	3384	TYR	5.0
1	B	2966	GLY	5.0
1	A	2984	HIS	5.0
1	A	3128	GLU	5.0
1	A	3086	ASN	5.0
1	B	3269	HIS	4.9
1	A	3338	PHE	4.9
1	A	2986	LEU	4.9
1	B	2988	THR	4.9
1	B	3170	LEU	4.9
1	A	3312	ASP	4.8
1	B	3084	LEU	4.8
1	A	3094	GLY	4.8
1	B	2917	LEU	4.8
1	A	3029	PHE	4.7
1	B	3310	VAL	4.7
1	A	3076	ASP	4.7
1	A	3178	HIS	4.7
1	A	3397	ASN	4.7
1	B	3213	GLY	4.7
1	A	2978	SER	4.7
1	A	3211	PHE	4.6
1	B	2991	PHE	4.6
1	B	3369	HIS	4.6
1	A	3221	THR	4.6
1	A	2956	HIS	4.6
1	B	2961	LEU	4.5
1	B	3165	THR	4.5
1	B	3191	GLY	4.5
1	B	3358	MET	4.5
1	A	2949	TYR	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	3092	ILE	4.4
1	A	2971	PRO	4.4
1	B	3206	LEU	4.4
1	A	2941	GLN	4.4
1	A	3127	GLN	4.4
1	B	2982	HIS	4.4
1	A	2934	ARG	4.4
1	A	3350	LEU	4.4
1	B	3145	ASP	4.3
1	A	3351	ASN	4.3
1	A	2994	ALA	4.3
1	A	2919	ARG	4.3
1	B	3265	THR	4.3
1	B	2953	ALA	4.3
1	A	2991	PHE	4.3
1	B	3306	PRO	4.2
1	A	3129	LEU	4.2
1	A	3268	VAL	4.2
1	B	3349	MET	4.2
1	B	3214	PHE	4.1
1	B	3385	PHE	4.1
1	A	3082	GLU	4.1
1	A	3340	SER	4.1
1	B	3122	ILE	4.1
1	B	3339	MET	4.1
1	B	2945	SER	4.1
1	A	3125	ILE	4.1
1	A	3126	TRP	4.1
1	A	3078	GLU	4.0
1	A	3016	LEU	4.0
1	A	3403	VAL	4.0
1	B	3166	ARG	4.0
1	A	3191	GLY	4.0
1	B	3338	PHE	4.0
1	A	3099	SER	4.0
1	B	2989	ILE	4.0
1	B	3079	VAL	4.0
1	B	3267	THR	4.0
1	B	3062	PHE	4.0
1	A	3024	GLY	4.0
1	A	3020	PHE	3.9
1	B	3007	TRP	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	3358	MET	3.9
1	B	3376	MET	3.9
1	B	3115	HIS	3.9
1	B	3238	GLU	3.9
1	B	3091	LEU	3.9
1	A	3226	LYS	3.9
1	B	3322	VAL	3.9
1	A	2966	GLY	3.9
1	A	3105	TYR	3.9
1	B	3174	VAL	3.9
1	A	3065	ALA	3.8
1	A	3166	ARG	3.8
1	B	3207	LYS	3.8
1	A	3367	SER	3.8
1	A	2972	CYS	3.8
1	A	3231	SER	3.8
1	A	2961	LEU	3.8
1	B	3248	GLY	3.7
1	B	3118	SER	3.7
1	A	2937	LEU	3.7
1	B	3061	ILE	3.7
1	A	3237	ASP	3.7
1	A	3269	HIS	3.7
1	A	2977	MET	3.7
1	A	3259	LEU	3.7
1	A	3075	CYS	3.7
1	A	3382	GLY	3.7
1	A	3044	ASP	3.7
1	A	3050	PHE	3.7
1	B	3119	LEU	3.7
1	A	2987	HIS	3.6
1	B	3200	VAL	3.6
1	B	3393	LEU	3.6
1	A	3310	VAL	3.6
1	B	3351	ASN	3.6
1	A	3163	ASP	3.6
1	A	3022	ASP	3.6
1	B	2999	GLY	3.6
1	A	3225	VAL	3.6
1	A	3289	HIS	3.6
1	B	3107	ALA	3.6
1	A	3405	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	3058	PHE	3.5
1	A	2921	ASN	3.5
1	A	2990	GLN	3.5
1	A	3081	TYR	3.5
1	B	3141	SER	3.5
1	A	3318	ILE	3.5
1	A	3165	THR	3.5
1	B	3259	LEU	3.5
1	A	2945	SER	3.5
1	A	3087	GLU	3.5
1	B	2940	LEU	3.5
1	B	3208	SER	3.5
1	A	3347	THR	3.5
1	A	3214	PHE	3.4
1	B	3258	ARG	3.4
1	B	3280	PHE	3.4
1	A	2968	GLU	3.4
1	B	3034	ILE	3.4
1	B	3005	PRO	3.4
1	A	3015	SER	3.4
1	A	3119	LEU	3.4
1	B	3120	ASP	3.3
1	B	2944	GLU	3.3
1	B	2962	CYS	3.3
1	A	3399	LEU	3.3
1	B	3198	GLU	3.3
1	A	3066	LEU	3.3
1	A	3063	TYR	3.3
1	A	2924	SER	3.2
1	B	3336	ILE	3.2
1	B	3153	PRO	3.2
1	A	3213	GLY	3.2
1	B	3231	SER	3.2
1	A	2995	LEU	3.2
1	B	3341	VAL	3.2
1	B	3020	PHE	3.2
1	B	3197	LEU	3.2
1	B	3126	TRP	3.1
1	B	3089	HIS	3.1
1	A	3253	PRO	3.1
1	B	3318	ILE	3.1
1	B	3152	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	3015	SER	3.1
1	B	3003	GLY	3.1
1	A	2980	PHE	3.1
1	B	3063	TYR	3.1
1	B	3302	ILE	3.1
1	B	3244	VAL	3.0
1	A	3201	LEU	3.0
1	A	3331	LYS	3.0
1	A	3317	PRO	3.0
1	A	2938	TYR	3.0
1	A	3393	LEU	3.0
1	A	3306	PRO	3.0
1	A	2950	GLU	3.0
1	A	3212	ALA	3.0
1	B	3008	ASP	3.0
1	A	3348	PRO	3.0
1	B	3402	HIS	3.0
1	A	3112	PHE	3.0
1	B	3344	ALA	3.0
1	A	3025	ASN	3.0
1	A	3154	PHE	3.0
1	A	3157	GLU	3.0
1	B	3305	ARG	3.0
1	B	2968	GLU	2.9
1	A	2982	HIS	2.9
1	A	3083	ILE	2.9
1	B	3252	MET	2.9
1	B	2985	ARG	2.9
1	A	2998	HIS	2.9
1	B	3356	THR	2.9
1	A	3402	HIS	2.9
1	B	3121	LYS	2.9
1	B	3294	ALA	2.9
1	A	2939	LYS	2.9
1	B	3131	LYS	2.8
1	B	3204	LEU	2.8
1	A	3123	TRP	2.8
1	A	3164	PHE	2.8
1	B	3033	HIS	2.8
1	A	3298	PRO	2.8
1	B	3100	MET	2.8
1	B	3286	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	3174	VAL	2.8
1	B	3289	HIS	2.7
1	B	3182	TYR	2.7
1	B	3355	TYR	2.7
1	A	3120	ASP	2.7
1	A	3034	ILE	2.7
1	A	3370	ALA	2.7
1	B	3359	PHE	2.7
1	B	2937	LEU	2.7
1	B	3350	LEU	2.7
1	A	3062	PHE	2.7
1	B	3220	ARG	2.7
1	A	3300	PRO	2.7
1	A	2970	TYR	2.7
1	B	3114	ILE	2.7
1	B	3334	THR	2.7
1	B	2952	ILE	2.6
1	A	2954	GLY	2.6
1	A	3279	LYS	2.6
1	A	3396	ASP	2.6
1	A	3010	THR	2.6
1	A	3320	LYS	2.6
1	A	3042	VAL	2.6
1	A	3227	VAL	2.6
1	A	2979	ILE	2.6
1	B	2916	ILE	2.6
1	B	3013	ILE	2.6
1	B	2973	CYS	2.6
1	B	3110	PRO	2.6
1	B	2941	GLN	2.6
1	A	3363	VAL	2.6
1	B	3065	ALA	2.6
1	B	3070	GLU	2.6
1	B	3314	ILE	2.6
1	B	3219	ILE	2.6
1	B	3064	LEU	2.5
1	A	3252	MET	2.5
1	A	3339	MET	2.5
1	B	3299	ALA	2.5
1	A	3098	TYR	2.5
1	B	3218	GLY	2.5
1	B	3317	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	3362	LYS	2.5
1	A	3079	VAL	2.5
1	B	3199	GLU	2.5
1	B	3217	SER	2.5
1	A	3315	GLU	2.5
1	A	3228	TYR	2.5
1	B	2930	ALA	2.5
1	A	2932	GLU	2.5
1	A	3236	ASP	2.5
1	A	3263	ASP	2.5
1	B	3147	MET	2.5
1	B	2986	LEU	2.4
1	B	3196	GLU	2.4
1	B	3028	PRO	2.4
1	B	2950	GLU	2.4
1	A	3329	VAL	2.4
1	A	3286	LYS	2.4
1	A	3084	LEU	2.4
1	A	3110	PRO	2.4
1	B	2996	LYS	2.4
1	A	3170	LEU	2.4
1	A	2973	CYS	2.4
1	B	2974	VAL	2.4
1	B	3276	ASP	2.4
1	B	2921	ASN	2.4
1	B	3211	PHE	2.3
1	B	3202	ARG	2.3
1	A	3291	GLU	2.3
1	B	3009	TRP	2.3
1	B	3328	VAL	2.3
1	B	3237	ASP	2.3
1	B	3124	ILE	2.3
1	B	3300	PRO	2.3
1	B	3031	LYS	2.3
1	B	3016	LEU	2.3
1	B	3215	VAL	2.3
1	A	2935	ASP	2.3
1	A	3040	ASP	2.3
1	A	3172	ASN	2.2
1	B	3108	PHE	2.2
1	A	3264	ILE	2.2
1	B	3316	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	3059	SER	2.2
1	A	3360	LYS	2.2
1	B	3319	GLY	2.2
1	A	3107	ALA	2.2
1	A	3153	PRO	2.2
1	B	3130	GLN	2.2
1	A	3398	ASN	2.2
1	B	3329	VAL	2.2
1	B	3240	ALA	2.2
1	A	3142	CYS	2.2
1	B	3168	ASN	2.2
1	A	3058	PHE	2.2
1	A	3185	ASP	2.2
1	B	3149	VAL	2.2
1	B	3303	VAL	2.2
1	B	3010	THR	2.1
1	B	3041	THR	2.1
1	A	3267	THR	2.1
1	A	3116	HIS	2.1
1	B	2981	PRO	2.1
1	B	3224	VAL	2.1
1	B	3270	ASN	2.1
1	A	3335	LYS	2.1
1	A	3122	ILE	2.1
1	B	3083	ILE	2.1
1	B	3044	ASP	2.1
1	A	3155	ASN	2.1
1	B	3129	LEU	2.1
1	B	3251	GLU	2.1
1	A	2944	GLU	2.1
1	A	3215	VAL	2.1
1	A	3328	VAL	2.1
1	B	3150	PRO	2.0
1	A	3108	PHE	2.0
1	A	3033	HIS	2.0
1	A	3158	SER	2.0
1	B	3404	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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.