



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 12:23 AM UTC

PDB ID : 6E7D / pdb_00006e7d
Title : Structure of the inhibitory NKR-P1B receptor bound to the host-encoded ligand, Clr-b
Authors : Balaji, G.R.; Rossjohn, J.; Berry, R.
Deposited on : 2018-07-26
Resolution : 2.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

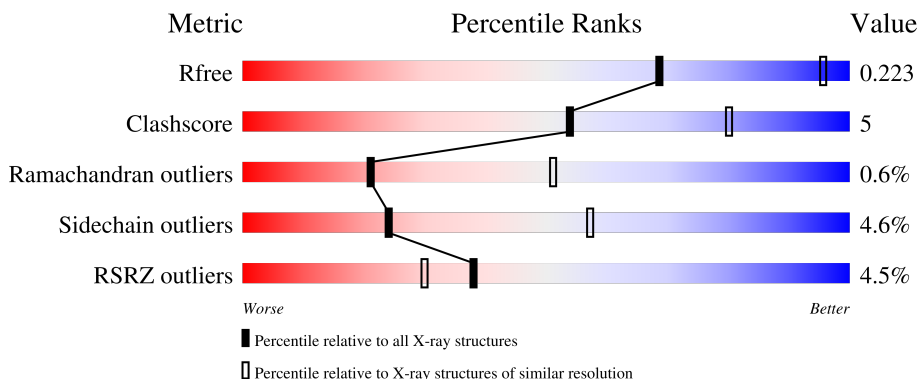
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	124	73% 24% ..
1	B	124	4% 84% 14% .
1	C	124	2% 81% 15% ..
1	D	124	% 77% 19% ..
1	E	124	3% 78% 19% ..

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Mol	Chain	Length	Quality of chain
1	F	124	 2% 77% 21% ..
1	G	124	 % 75% 18% . .
1	H	124	 2% 81% 14% ..
1	I	124	 % 72% 23% ..
1	J	124	 5% 81% 17% ..
1	K	124	 % 73% 19% .. 5%
1	L	124	 6% 85% 12% ..
1	M	124	 82% 14% .
1	N	124	 6% 80% 18% ..
1	O	124	 % 81% 14% . 5%
1	P	124	 4% 81% 18% .
2	Q	137	 5% 76% 9% . 15%
2	R	137	 12% 75% 5% . 18%
2	S	137	 % 80% 7% . 11%
2	T	137	 9% 82% 7% . 11%
2	U	137	 7% 72% 9% .. 15%
2	V	137	 5% 75% 11% .. 12%
2	W	137	 3% 79% 6% . 14%
2	X	137	 17% 81% .. 13%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 22989 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 C-type lectin domain family 2 member D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	121	997	635	171	184	7	0	0	0
1	B	121	974	624	169	173	8	0	0	0
1	C	120	979	625	166	181	7	0	0	0
1	D	121	1006	641	173	185	7	0	0	0
1	E	122	994	637	175	175	7	0	0	0
1	F	122	982	629	170	176	7	0	0	0
1	G	119	986	630	170	179	7	0	0	0
1	H	122	984	632	168	177	7	0	0	0
1	I	119	993	634	171	181	7	0	0	0
1	J	122	987	634	170	175	8	0	0	0
1	K	118	984	625	171	181	7	0	0	0
1	L	122	993	639	172	174	8	0	0	0
1	M	119	983	628	170	178	7	0	0	0
1	N	122	979	628	170	174	7	0	0	0
1	O	118	960	615	167	171	7	0	0	0
1	P	122	1002	639	175	181	7	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	MET	-	initiating methionine	UNP Q91V08
A	195	ALA	-	expression tag	UNP Q91V08
A	196	SER	-	expression tag	UNP Q91V08
B	73	MET	-	initiating methionine	UNP Q91V08
B	195	ALA	-	expression tag	UNP Q91V08
B	196	SER	-	expression tag	UNP Q91V08
C	73	MET	-	initiating methionine	UNP Q91V08
C	195	ALA	-	expression tag	UNP Q91V08
C	196	SER	-	expression tag	UNP Q91V08
D	73	MET	-	initiating methionine	UNP Q91V08
D	195	ALA	-	expression tag	UNP Q91V08
D	196	SER	-	expression tag	UNP Q91V08
E	73	MET	-	initiating methionine	UNP Q91V08
E	195	ALA	-	expression tag	UNP Q91V08
E	196	SER	-	expression tag	UNP Q91V08
F	73	MET	-	initiating methionine	UNP Q91V08
F	195	ALA	-	expression tag	UNP Q91V08
F	196	SER	-	expression tag	UNP Q91V08
G	73	MET	-	initiating methionine	UNP Q91V08
G	195	ALA	-	expression tag	UNP Q91V08
G	196	SER	-	expression tag	UNP Q91V08
H	73	MET	-	initiating methionine	UNP Q91V08
H	195	ALA	-	expression tag	UNP Q91V08
H	196	SER	-	expression tag	UNP Q91V08
I	73	MET	-	initiating methionine	UNP Q91V08
I	195	ALA	-	expression tag	UNP Q91V08
I	196	SER	-	expression tag	UNP Q91V08
J	73	MET	-	initiating methionine	UNP Q91V08
J	195	ALA	-	expression tag	UNP Q91V08
J	196	SER	-	expression tag	UNP Q91V08
K	73	MET	-	initiating methionine	UNP Q91V08
K	195	ALA	-	expression tag	UNP Q91V08
K	196	SER	-	expression tag	UNP Q91V08
L	73	MET	-	initiating methionine	UNP Q91V08
L	195	ALA	-	expression tag	UNP Q91V08
L	196	SER	-	expression tag	UNP Q91V08
M	73	MET	-	initiating methionine	UNP Q91V08
M	195	ALA	-	expression tag	UNP Q91V08
M	196	SER	-	expression tag	UNP Q91V08
N	73	MET	-	initiating methionine	UNP Q91V08
N	195	ALA	-	expression tag	UNP Q91V08
N	196	SER	-	expression tag	UNP Q91V08

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Chain	Residue	Modelled	Actual	Comment	Reference
O	73	MET	-	initiating methionine	UNP Q91V08
O	195	ALA	-	expression tag	UNP Q91V08
O	196	SER	-	expression tag	UNP Q91V08
P	73	MET	-	initiating methionine	UNP Q91V08
P	195	ALA	-	expression tag	UNP Q91V08
P	196	SER	-	expression tag	UNP Q91V08

- Molecule 2 is a protein called Killer cell lectin-like receptor subfamily B member 1B allele B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	Q	117	892	561	152	173	6	0	0	0
2	R	112	812	514	136	157	5	0	0	0
2	S	122	918	573	154	184	7	0	0	0
2	T	122	924	579	155	183	7	0	0	0
2	U	116	861	541	149	164	7	0	0	0
2	V	121	897	564	151	175	7	0	0	0
2	W	118	876	546	149	174	7	0	0	0
2	X	119	861	538	144	172	7	0	0	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	87	THR	-	expression tag	UNP Q99JB4
Q	88	GLY	-	expression tag	UNP Q99JB4
Q	118	GLY	CYS	engineered mutation	UNP Q99JB4
Q	216	GLY	-	expression tag	UNP Q99JB4
Q	217	THR	-	expression tag	UNP Q99JB4
Q	218	HIS	-	expression tag	UNP Q99JB4
Q	219	HIS	-	expression tag	UNP Q99JB4
Q	220	HIS	-	expression tag	UNP Q99JB4
Q	221	HIS	-	expression tag	UNP Q99JB4
Q	222	HIS	-	expression tag	UNP Q99JB4
Q	223	HIS	-	expression tag	UNP Q99JB4
R	87	THR	-	expression tag	UNP Q99JB4

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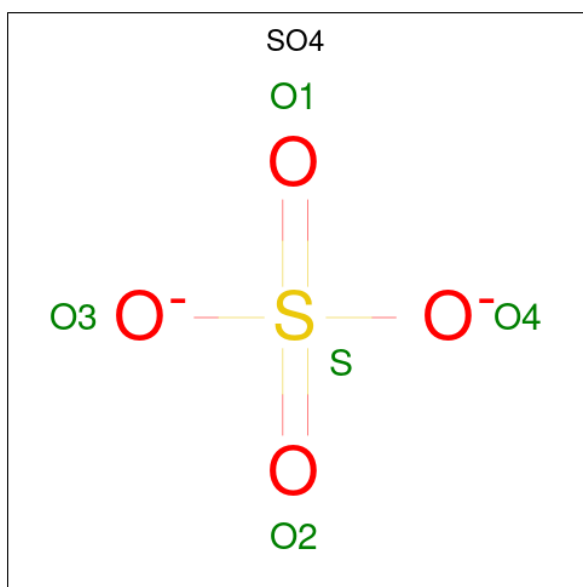
Chain	Residue	Modelled	Actual	Comment	Reference
R	88	GLY	-	expression tag	UNP Q99JB4
R	118	GLY	CYS	engineered mutation	UNP Q99JB4
R	216	GLY	-	expression tag	UNP Q99JB4
R	217	THR	-	expression tag	UNP Q99JB4
R	218	HIS	-	expression tag	UNP Q99JB4
R	219	HIS	-	expression tag	UNP Q99JB4
R	220	HIS	-	expression tag	UNP Q99JB4
R	221	HIS	-	expression tag	UNP Q99JB4
R	222	HIS	-	expression tag	UNP Q99JB4
R	223	HIS	-	expression tag	UNP Q99JB4
S	87	THR	-	expression tag	UNP Q99JB4
S	88	GLY	-	expression tag	UNP Q99JB4
S	118	GLY	CYS	engineered mutation	UNP Q99JB4
S	216	GLY	-	expression tag	UNP Q99JB4
S	217	THR	-	expression tag	UNP Q99JB4
S	218	HIS	-	expression tag	UNP Q99JB4
S	219	HIS	-	expression tag	UNP Q99JB4
S	220	HIS	-	expression tag	UNP Q99JB4
S	221	HIS	-	expression tag	UNP Q99JB4
S	222	HIS	-	expression tag	UNP Q99JB4
S	223	HIS	-	expression tag	UNP Q99JB4
T	87	THR	-	expression tag	UNP Q99JB4
T	88	GLY	-	expression tag	UNP Q99JB4
T	118	GLY	CYS	engineered mutation	UNP Q99JB4
T	216	GLY	-	expression tag	UNP Q99JB4
T	217	THR	-	expression tag	UNP Q99JB4
T	218	HIS	-	expression tag	UNP Q99JB4
T	219	HIS	-	expression tag	UNP Q99JB4
T	220	HIS	-	expression tag	UNP Q99JB4
T	221	HIS	-	expression tag	UNP Q99JB4
T	222	HIS	-	expression tag	UNP Q99JB4
T	223	HIS	-	expression tag	UNP Q99JB4
U	87	THR	-	expression tag	UNP Q99JB4
U	88	GLY	-	expression tag	UNP Q99JB4
U	118	GLY	CYS	engineered mutation	UNP Q99JB4
U	216	GLY	-	expression tag	UNP Q99JB4
U	217	THR	-	expression tag	UNP Q99JB4
U	218	HIS	-	expression tag	UNP Q99JB4
U	219	HIS	-	expression tag	UNP Q99JB4
U	220	HIS	-	expression tag	UNP Q99JB4
U	221	HIS	-	expression tag	UNP Q99JB4
U	222	HIS	-	expression tag	UNP Q99JB4

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Chain	Residue	Modelled	Actual	Comment	Reference
U	223	HIS	-	expression tag	UNP Q99JB4
V	87	THR	-	expression tag	UNP Q99JB4
V	88	GLY	-	expression tag	UNP Q99JB4
V	118	GLY	CYS	engineered mutation	UNP Q99JB4
V	216	GLY	-	expression tag	UNP Q99JB4
V	217	THR	-	expression tag	UNP Q99JB4
V	218	HIS	-	expression tag	UNP Q99JB4
V	219	HIS	-	expression tag	UNP Q99JB4
V	220	HIS	-	expression tag	UNP Q99JB4
V	221	HIS	-	expression tag	UNP Q99JB4
V	222	HIS	-	expression tag	UNP Q99JB4
V	223	HIS	-	expression tag	UNP Q99JB4
W	87	THR	-	expression tag	UNP Q99JB4
W	88	GLY	-	expression tag	UNP Q99JB4
W	118	GLY	CYS	engineered mutation	UNP Q99JB4
W	216	GLY	-	expression tag	UNP Q99JB4
W	217	THR	-	expression tag	UNP Q99JB4
W	218	HIS	-	expression tag	UNP Q99JB4
W	219	HIS	-	expression tag	UNP Q99JB4
W	220	HIS	-	expression tag	UNP Q99JB4
W	221	HIS	-	expression tag	UNP Q99JB4
W	222	HIS	-	expression tag	UNP Q99JB4
W	223	HIS	-	expression tag	UNP Q99JB4
X	87	THR	-	expression tag	UNP Q99JB4
X	88	GLY	-	expression tag	UNP Q99JB4
X	118	GLY	CYS	engineered mutation	UNP Q99JB4
X	216	GLY	-	expression tag	UNP Q99JB4
X	217	THR	-	expression tag	UNP Q99JB4
X	218	HIS	-	expression tag	UNP Q99JB4
X	219	HIS	-	expression tag	UNP Q99JB4
X	220	HIS	-	expression tag	UNP Q99JB4
X	221	HIS	-	expression tag	UNP Q99JB4
X	222	HIS	-	expression tag	UNP Q99JB4
X	223	HIS	-	expression tag	UNP Q99JB4

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		
3	Q	1	Total	O	S	0	0
			5	4	1		
3	R	1	Total	O	S	0	0
			5	4	1		
3	S	1	Total	O	S	0	0
			5	4	1		
3	T	1	Total	O	S	0	0
			5	4	1		
3	U	1	Total	O	S	0	0
			5	4	1		
3	V	1	Total	O	S	0	0
			5	4	1		
3	W	1	Total	O	S	0	0
			5	4	1		
3	X	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	Q	1	Total 14	C 8	N 1	O 5	0	0
4	R	1	Total 14	C 8	N 1	O 5	0	0
4	S	1	Total 14	C 8	N 1	O 5	0	0
4	T	1	Total 14	C 8	N 1	O 5	0	0
4	U	1	Total 14	C 8	N 1	O 5	0	0
4	V	1	Total 14	C 8	N 1	O 5	0	0
4	W	1	Total 14	C 8	N 1	O 5	0	0
4	X	1	Total 14	C 8	N 1	O 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
5	C	2	Total 2	O 2	0	0
5	F	1	Total 1	O 1	0	0
5	H	1	Total 1	O 1	0	0
5	K	2	Total 2	O 2	0	0

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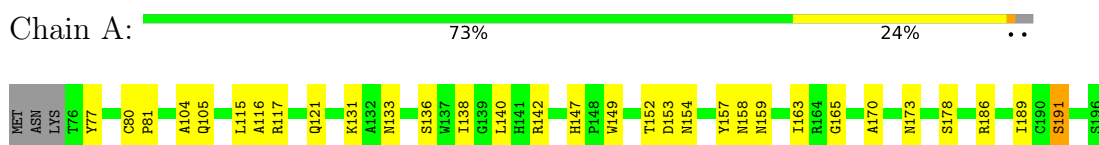
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	M	1	Total O 1 1	0	0
5	O	1	Total O 1 1	0	0

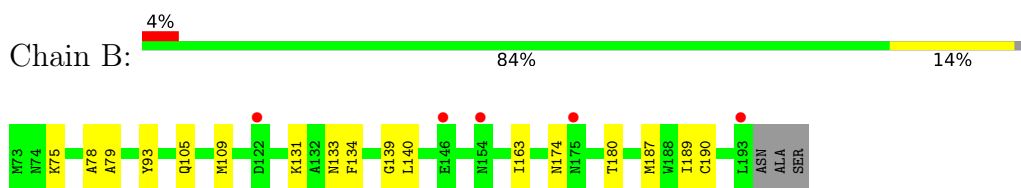
3 Residue-property plots [i](#)

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.

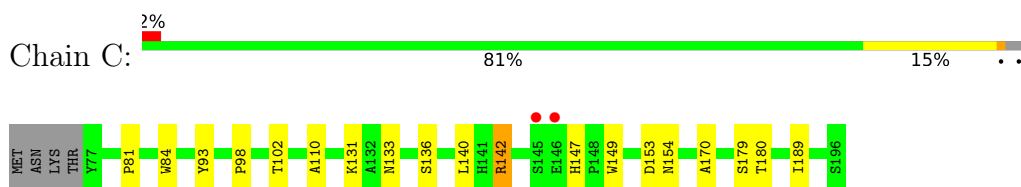
- Molecule 1: C-type lectin domain family 2 member D



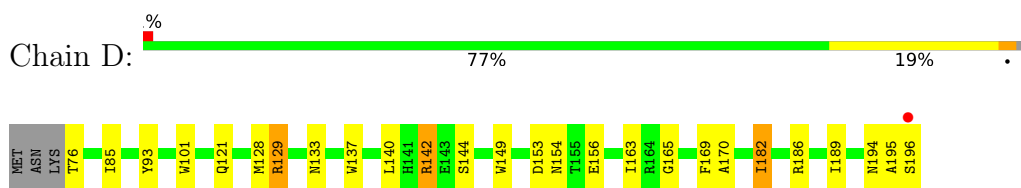
- Molecule 1: C-type lectin domain family 2 member D



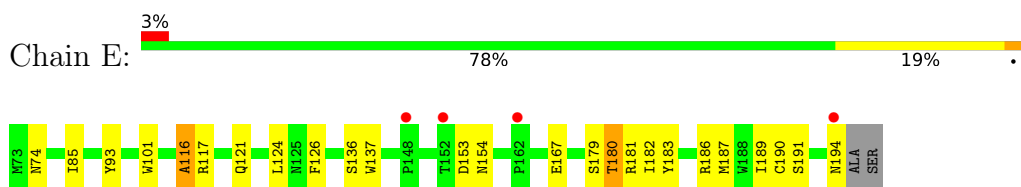
- Molecule 1: C-type lectin domain family 2 member D



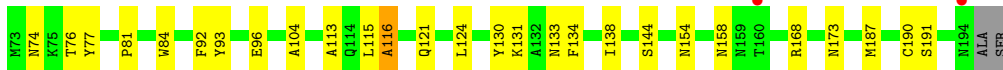
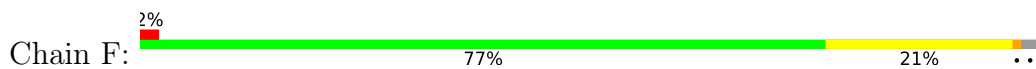
- Molecule 1: C-type lectin domain family 2 member D



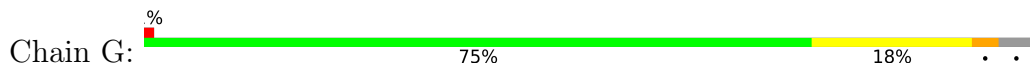
- Molecule 1: C-type lectin domain family 2 member D



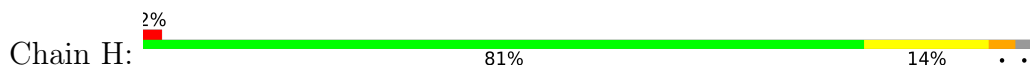
- Molecule 1: C-type lectin domain family 2 member D



- Molecule 1: C-type lectin domain family 2 member D



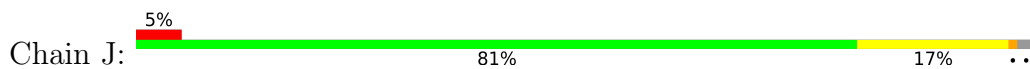
- Molecule 1: C-type lectin domain family 2 member D



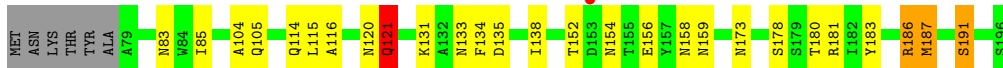
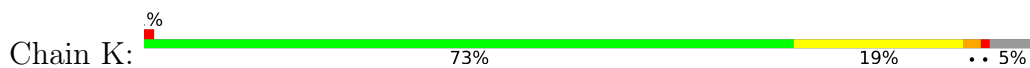
- Molecule 1: C-type lectin domain family 2 member D



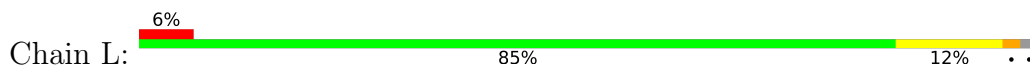
- Molecule 1: C-type lectin domain family 2 member D




- Molecule 1: C-type lectin domain family 2 member D

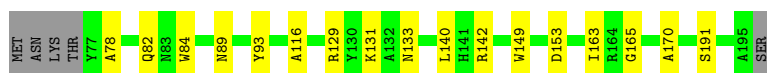


- Molecule 1: C-type lectin domain family 2 member D




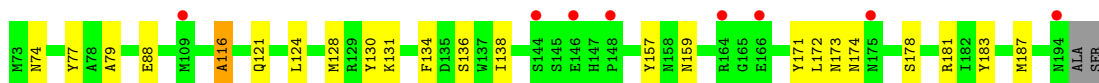
- Molecule 1: C-type lectin domain family 2 member D

Chain M:  82% 14%




- Molecule 1: C-type lectin domain family 2 member D

Chain N:  6% 80% 18%




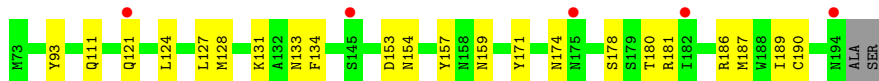
- Molecule 1: C-type lectin domain family 2 member D

Chain O:  1% 81% 14% 5%




- Molecule 1: C-type lectin domain family 2 member D

Chain P:  4% 81% 18%




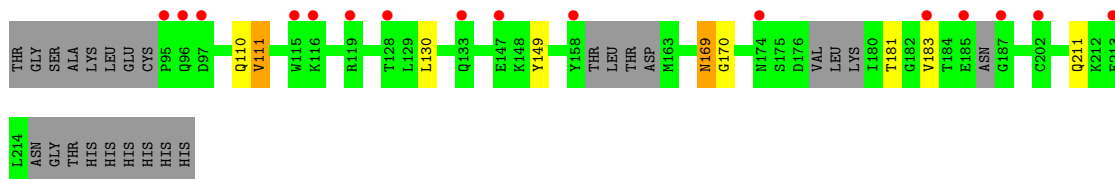
- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B

Chain Q:  5% 76% 9% 15%




- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B

Chain R:  12% 75% 5% 18%



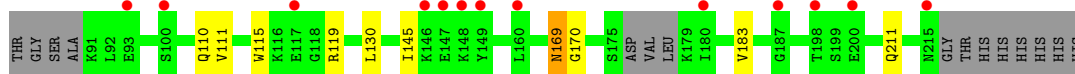
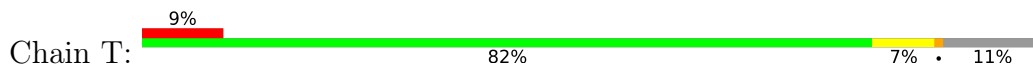
- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B

Chain S:  1% 80% 7% 11%

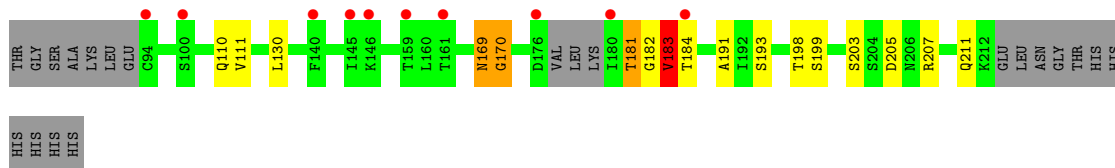




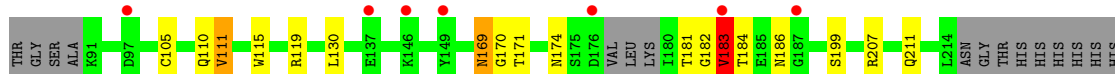
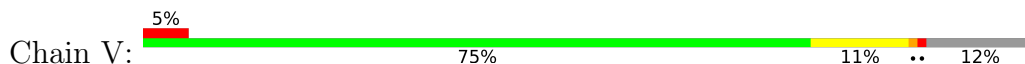
- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B



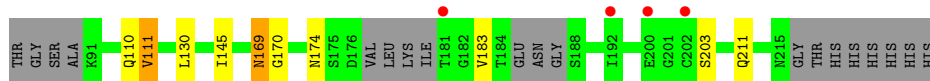
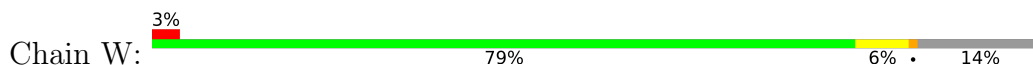
- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B



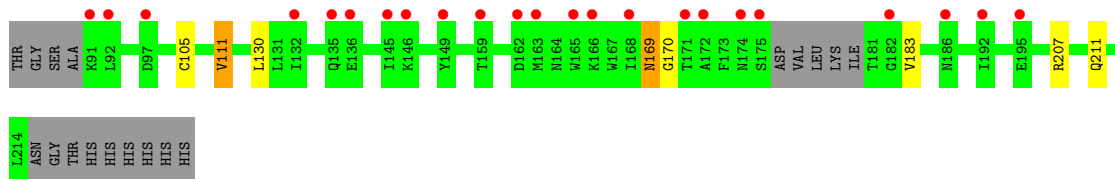
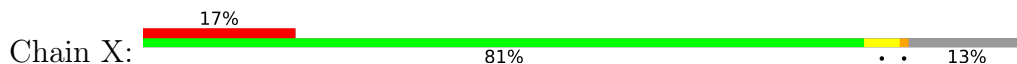
- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B



- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B



- Molecule 2: Killer cell lectin-like receptor subfamily B member 1B allele B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.93Å 122.07Å 131.56Å 73.12° 82.08° 84.46°	Depositor
Resolution (Å)	42.46 – 2.90 42.46 – 2.90	Depositor EDS
% Data completeness (in resolution range)	92.6 (42.46-2.90) 92.5 (42.46-2.90)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.91Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.186 , 0.225 0.205 , 0.223	Depositor DCC
R_{free} test set	4057 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	40.2	Xtrriage
Anisotropy	0.529	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	22989	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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: NAG, SO4

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	0.95	0/1029	1.27	3/1399 (0.2%)
1	B	0.88	0/1006	1.25	0/1370
1	C	0.88	1/1011 (0.1%)	1.24	3/1377 (0.2%)
1	D	1.00	2/1038 (0.2%)	1.31	2/1410 (0.1%)
1	E	0.89	0/1026	1.28	4/1396 (0.3%)
1	F	0.93	0/1014	1.23	3/1381 (0.2%)
1	G	0.94	0/1018	1.27	3/1384 (0.2%)
1	H	0.96	0/1016	1.25	6/1385 (0.4%)
1	I	0.94	1/1025 (0.1%)	1.31	9/1392 (0.6%)
1	J	0.91	1/1019 (0.1%)	1.22	3/1387 (0.2%)
1	K	0.94	1/1015 (0.1%)	1.34	8/1377 (0.6%)
1	L	0.89	0/1025	1.24	3/1393 (0.2%)
1	M	0.84	0/1015	1.23	1/1379 (0.1%)
1	N	0.84	0/1011	1.22	2/1378 (0.1%)
1	O	0.90	0/990	1.28	0/1345
1	P	0.91	1/1034 (0.1%)	1.22	1/1406 (0.1%)
2	Q	0.85	0/910	1.31	7/1235 (0.6%)
2	R	0.81	0/829	1.26	6/1128 (0.5%)
2	S	0.87	0/937	1.29	6/1276 (0.5%)
2	T	0.86	1/943 (0.1%)	1.28	5/1282 (0.4%)
2	U	0.90	2/880 (0.2%)	1.34	7/1197 (0.6%)
2	V	0.99	2/916 (0.2%)	1.35	9/1248 (0.7%)
2	W	0.82	0/894	1.27	7/1216 (0.6%)
2	X	0.84	0/880	1.30	4/1202 (0.3%)
All	All	0.90	12/23481 (0.1%)	1.27	102/31943 (0.3%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	V	174	ASN	CA-C	6.38	1.58	1.52
1	D	85	ILE	CG1-CD1	-6.26	1.27	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	V	169	ASN	CA-C	5.74	1.60	1.52
1	D	128	MET	SD-CE	5.62	1.93	1.79
2	U	169	ASN	CA-C	5.55	1.60	1.52

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	180	THR	CA-C-N	7.84	132.59	120.75
1	E	180	THR	C-N-CA	7.84	132.59	120.75
1	H	153	ASP	CA-CB-CG	6.73	119.33	112.60
1	D	153	ASP	CA-CB-CG	6.52	119.12	112.60
2	X	169	ASN	CA-CB-CG	6.47	119.07	112.60

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	997	0	899	22	0
1	B	974	0	861	7	0
1	C	979	0	867	9	0
1	D	1006	0	917	10	0
1	E	994	0	898	12	0
1	F	982	0	873	17	0
1	G	986	0	892	12	0
1	H	984	0	873	12	0
1	I	993	0	905	15	0
1	J	987	0	877	8	0
1	K	984	0	895	14	0
1	L	993	0	897	4	0
1	M	983	0	888	13	0
1	N	979	0	855	14	0
1	O	960	0	875	10	0
1	P	1002	0	899	9	0
2	Q	892	0	795	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	812	0	685	3	0
2	S	918	0	800	5	0
2	T	924	0	818	3	0
2	U	861	0	756	26	0
2	V	897	0	786	17	0
2	W	876	0	735	3	0
2	X	861	0	709	4	0
3	D	5	0	0	0	0
3	Q	5	0	0	0	0
3	R	5	0	0	0	0
3	S	5	0	0	0	0
3	T	5	0	0	0	0
3	U	5	0	0	0	0
3	V	5	0	0	0	0
3	W	5	0	0	0	0
3	X	5	0	0	0	0
4	Q	14	0	13	0	0
4	R	14	0	13	0	0
4	S	14	0	13	0	0
4	T	14	0	13	0	0
4	U	14	0	13	0	0
4	V	14	0	13	0	0
4	W	14	0	13	0	0
4	X	14	0	13	0	0
5	C	2	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
5	K	2	0	0	0	0
5	M	1	0	0	0	0
5	O	1	0	0	0	0
All	All	22989	0	20359	213	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 5.

The worst 5 of 213 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:U:183:VAL:HG21	2:U:199:SER:N	1.65	1.11
2:V:183:VAL:HG21	2:V:199:SER:N	1.66	1.11
2:U:183:VAL:HG21	2:U:199:SER:H	0.98	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:183:VAL:HG21	2:V:199:SER:H	1.01	1.08
2:U:183:VAL:CG2	2:U:199:SER:H	1.79	0.95

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	119/124 (96%)	111 (93%)	8 (7%)	0	100	100
1	B	119/124 (96%)	110 (92%)	8 (7%)	1 (1%)	16	44
1	C	118/124 (95%)	109 (92%)	9 (8%)	0	100	100
1	D	119/124 (96%)	113 (95%)	6 (5%)	0	100	100
1	E	120/124 (97%)	111 (92%)	8 (7%)	1 (1%)	16	44
1	F	120/124 (97%)	113 (94%)	6 (5%)	1 (1%)	16	44
1	G	117/124 (94%)	110 (94%)	6 (5%)	1 (1%)	14	41
1	H	120/124 (97%)	111 (92%)	8 (7%)	1 (1%)	16	44
1	I	117/124 (94%)	113 (97%)	3 (3%)	1 (1%)	14	41
1	J	120/124 (97%)	110 (92%)	10 (8%)	0	100	100
1	K	116/124 (94%)	111 (96%)	5 (4%)	0	100	100
1	L	120/124 (97%)	111 (92%)	8 (7%)	1 (1%)	16	44
1	M	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
1	N	120/124 (97%)	112 (93%)	7 (6%)	1 (1%)	16	44
1	O	116/124 (94%)	110 (95%)	6 (5%)	0	100	100
1	P	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
2	Q	111/137 (81%)	102 (92%)	8 (7%)	1 (1%)	14	41
2	R	104/137 (76%)	97 (93%)	6 (6%)	1 (1%)	12	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S	118/137 (86%)	108 (92%)	9 (8%)	1 (1%)	16	44
2	T	118/137 (86%)	108 (92%)	9 (8%)	1 (1%)	16	44
2	U	112/137 (82%)	103 (92%)	8 (7%)	1 (1%)	14	41
2	V	117/137 (85%)	105 (90%)	11 (9%)	1 (1%)	14	41
2	W	112/137 (82%)	104 (93%)	7 (6%)	1 (1%)	14	41
2	X	115/137 (84%)	106 (92%)	8 (7%)	1 (1%)	14	41
All	All	2805/3080 (91%)	2613 (93%)	176 (6%)	16 (1%)	21	51

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	116	ALA
2	Q	183	VAL
2	R	183	VAL
2	S	183	VAL
2	T	183	VAL

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	Percentiles	
1	A	103/110 (94%)	98 (95%)	5 (5%)	22	54
1	B	95/110 (86%)	91 (96%)	4 (4%)	26	60
1	C	99/110 (90%)	94 (95%)	5 (5%)	21	53
1	D	105/110 (96%)	96 (91%)	9 (9%)	10	30
1	E	99/110 (90%)	95 (96%)	4 (4%)	28	62
1	F	97/110 (88%)	94 (97%)	3 (3%)	35	69
1	G	101/110 (92%)	92 (91%)	9 (9%)	9	28
1	H	97/110 (88%)	92 (95%)	5 (5%)	21	52
1	I	103/110 (94%)	95 (92%)	8 (8%)	11	35
1	J	96/110 (87%)	91 (95%)	5 (5%)	21	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	103/110 (94%)	96 (93%)	7 (7%)	14	42
1	L	98/110 (89%)	91 (93%)	7 (7%)	13	40
1	M	100/110 (91%)	98 (98%)	2 (2%)	48	78
1	N	93/110 (84%)	91 (98%)	2 (2%)	45	77
1	O	97/110 (88%)	90 (93%)	7 (7%)	13	39
1	P	101/110 (92%)	94 (93%)	7 (7%)	14	41
2	Q	91/122 (75%)	89 (98%)	2 (2%)	45	77
2	R	76/122 (62%)	74 (97%)	2 (3%)	40	73
2	S	94/122 (77%)	92 (98%)	2 (2%)	47	77
2	T	95/122 (78%)	93 (98%)	2 (2%)	47	77
2	U	85/122 (70%)	82 (96%)	3 (4%)	32	66
2	V	90/122 (74%)	87 (97%)	3 (3%)	33	67
2	W	85/122 (70%)	83 (98%)	2 (2%)	43	75
2	X	81/122 (66%)	80 (99%)	1 (1%)	63	86
All	All	2284/2736 (84%)	2178 (95%)	106 (5%)	24	57

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	121	GLN
1	M	131	LYS
2	U	183	VAL
1	K	154	ASN
1	L	131	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	133	ASN
2	W	215	ASN
1	P	173	ASN
2	T	211	GLN
1	G	194	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 [i](#)

17 ligands 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
3	SO4	W	301	-	4,4,4	0.31	0	6,6,6	0.17	0
4	NAG	S	300	2	14,14,15	0.29	0	17,19,21	0.84	2 (11%)
4	NAG	V	300	2	14,14,15	0.29	0	17,19,21	0.92	1 (5%)
4	NAG	Q	300	2	14,14,15	0.33	0	17,19,21	0.86	2 (11%)
4	NAG	T	300	2	14,14,15	0.34	0	17,19,21	0.74	1 (5%)
3	SO4	U	301	-	4,4,4	0.30	0	6,6,6	0.22	0
3	SO4	X	302	-	4,4,4	0.29	0	6,6,6	0.29	0
3	SO4	V	301	-	4,4,4	0.23	0	6,6,6	0.30	0
3	SO4	S	301	-	4,4,4	0.36	0	6,6,6	0.28	0
4	NAG	U	300	2	14,14,15	0.31	0	17,19,21	0.98	2 (11%)
4	NAG	X	301	2	14,14,15	0.33	0	17,19,21	0.78	2 (11%)
3	SO4	R	301	-	4,4,4	0.27	0	6,6,6	0.16	0
4	NAG	W	300	2	14,14,15	0.31	0	17,19,21	0.76	1 (5%)
4	NAG	R	300	2	14,14,15	0.33	0	17,19,21	0.92	2 (11%)
3	SO4	T	301	-	4,4,4	0.39	0	6,6,6	0.19	0
3	SO4	Q	301	-	4,4,4	0.48	0	6,6,6	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	D	201	-	4,4,4	0.17	0	6,6,6	0.22	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
4	NAG	V	300	2	-	0/6/23/26	0/1/1/1
4	NAG	Q	300	2	-	0/6/23/26	0/1/1/1
4	NAG	T	300	2	-	0/6/23/26	0/1/1/1
4	NAG	U	300	2	-	0/6/23/26	0/1/1/1
4	NAG	X	301	2	-	0/6/23/26	0/1/1/1
4	NAG	W	300	2	-	0/6/23/26	0/1/1/1
4	NAG	R	300	2	-	0/6/23/26	0/1/1/1
4	NAG	S	300	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	300	NAG	C1-O5-C5	2.81	115.95	112.19
4	U	300	NAG	C1-O5-C5	2.65	115.74	112.19
4	V	300	NAG	C1-O5-C5	2.64	115.73	112.19
4	U	300	NAG	O5-C1-C2	-2.56	107.33	111.29
4	Q	300	NAG	C1-O5-C5	2.42	115.43	112.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	121/124 (97%)	-0.01	0 100 100	20, 40, 71, 81	1 (0%)
1	B	121/124 (97%)	0.55	5 (4%) 41 33	24, 55, 101, 117	1 (0%)
1	C	120/124 (96%)	0.24	2 (1%) 69 61	27, 52, 83, 107	1 (0%)
1	D	121/124 (97%)	-0.14	1 (0%) 82 77	16, 34, 60, 82	1 (0%)
1	E	122/124 (98%)	0.29	4 (3%) 49 40	19, 48, 90, 102	0
1	F	122/124 (98%)	0.08	2 (1%) 70 62	15, 40, 88, 106	1 (0%)
1	G	119/124 (95%)	-0.13	1 (0%) 82 77	19, 35, 66, 86	1 (0%)
1	H	122/124 (98%)	0.19	2 (1%) 70 62	14, 42, 89, 111	1 (0%)
1	I	119/124 (95%)	-0.14	1 (0%) 82 77	10, 33, 60, 87	1 (0%)
1	J	122/124 (98%)	0.27	6 (4%) 35 27	11, 47, 94, 106	1 (0%)
1	K	118/124 (95%)	-0.13	1 (0%) 82 77	12, 32, 65, 87	1 (0%)
1	L	122/124 (98%)	0.19	8 (6%) 24 19	12, 43, 95, 114	1 (0%)
1	M	119/124 (95%)	0.00	0 100 100	22, 47, 74, 97	1 (0%)
1	N	122/124 (98%)	0.45	8 (6%) 24 19	23, 51, 96, 114	1 (0%)
1	O	118/124 (95%)	0.10	1 (0%) 82 77	28, 48, 77, 94	1 (0%)
1	P	122/124 (98%)	0.26	5 (4%) 41 33	18, 45, 81, 96	1 (0%)
2	Q	117/137 (85%)	0.65	7 (5%) 27 21	29, 62, 85, 100	1 (0%)
2	R	112/137 (81%)	0.99	16 (14%) 6 5	43, 81, 103, 110	0
2	S	122/137 (89%)	0.62	2 (1%) 70 62	26, 59, 94, 120	2 (1%)
2	T	122/137 (89%)	0.65	13 (10%) 11 9	20, 56, 88, 124	1 (0%)
2	U	116/137 (84%)	0.62	10 (8%) 16 13	24, 62, 99, 125	0
2	V	121/137 (88%)	0.48	7 (5%) 29 22	17, 51, 83, 101	1 (0%)
2	W	118/137 (86%)	0.78	4 (3%) 48 39	38, 67, 103, 125	2 (1%)
2	X	119/137 (86%)	1.16	23 (19%) 3 2	42, 77, 119, 144	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	2877/3080 (93%)	0.33	129 (4%) 38 30	10, 51, 95, 144	22 (0%)

The worst 5 of 129 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	194	ASN	5.6
1	J	194	ASN	5.3
1	H	194	ASN	4.0
2	X	146	LYS	4.0
1	B	122	ASP	3.8

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](#)

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
4	NAG	R	300	14/15	0.74	0.14	93,97,108,111	0
4	NAG	X	301	14/15	0.74	0.16	114,125,136,136	0
4	NAG	S	300	14/15	0.81	0.13	72,86,97,97	0
4	NAG	W	300	14/15	0.86	0.11	79,93,100,101	0
4	NAG	U	300	14/15	0.86	0.13	80,98,114,119	0
3	SO4	D	201	5/5	0.88	0.12	109,109,110,110	0
3	SO4	R	301	5/5	0.90	0.13	86,88,89,93	0
3	SO4	U	301	5/5	0.91	0.14	77,78,84,85	0
4	NAG	V	300	14/15	0.92	0.12	43,58,75,76	0
4	NAG	T	300	14/15	0.92	0.10	46,62,76,78	0
4	NAG	Q	300	14/15	0.92	0.09	58,68,71,73	0
3	SO4	Q	301	5/5	0.93	0.10	52,57,58,62	0
3	SO4	X	302	5/5	0.93	0.08	65,67,67,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	W	301	5/5	0.95	0.08	62,64,65,67	0
3	SO4	S	301	5/5	0.97	0.07	62,63,64,66	0
3	SO4	T	301	5/5	0.98	0.06	50,52,54,56	0
3	SO4	V	301	5/5	0.98	0.10	50,51,53,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.